(54) Title: SECRETORY MOLECULES

(57) Abstract: The invention provides purified secretory polynucleotides (sptm). Also encompassed are the polypeptides (SPTM) encoded by sptm. The invention also provides for the use of sptm, or complements, oligonucleotides, or fragments thereof in diagnostic assays. The invention further provides for vectors and host cells containing sptm for the expression of SPTM. The invention additionally provides for the use of isolated and purified SPTM to induce antibodies and to screen libraries of compounds and the use of anti-SPTM antibodies in diagnostic assays. Also provided are microarrays containing sptm and methods of use.

SECRETORY MOLECULES

TECHNICAL FIELD

5   The present invention relates to secretory molecules and to the use of these sequences in the

diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of

exogenous compounds on, the expression of secretory molecules.

BACKGROUND OF THE INVENTION

10   Both protein transport and secretion are involved in cellular function. Protein transport is

mediated by a signal peptide located at the amino terminus of the protein to be transported or secreted.

The signal peptide is comprised of about ten to twenty hydrophobic amino acids which target the

nascent protein from the ribosome to a particular membrane bound compartment such as the

endoplasmic reticulum (ER). Proteins targeted to the ER may either proceed through the secretory

15   pathway or remain in any of the secretory organelles such as the ER, Golgi apparatus, or lysosomes.

Proteins that transit through the secretory pathway are either secreted into the extracellular space or

retained in the plasma membrane. Proteins that are retained in the plasma membrane contain one or

more transmembrane domains, each comprised of about 20 hydrophobic amino acid residues. Proteins

that are secreted from the cell are generally synthesized as inactive precursors that are activated by

20   post-translational processing events during transit through the secretory pathway. Such events include

glycosylation, proteolysis, and removal of the signal peptide by a signal peptidase. Other events that

may occur during protein transport include chaperone-dependent unfolding and folding of the nascent

protein and interaction of the protein with a receptor or pore complex. Examples of secretory proteins

with amino terminal signal peptides are discussed below and include proteins with important roles in

25   cell-to-cell signaling. Such proteins include transmembrane receptors and cell surface markers,

extracellular matrix molecules, cytokines, hormones, growth and differentiation factors, neuropeptides,

vasomediators, ion channels, transporters/pumps, and proteases. (Reviewed in Alberts, B. et al.

(1994) Molecular Biology of The Cell, Garland Publishing, New York NY, pp. 557-560, 582-592.)

         G-protein coupled receptors (GPCRs) comprise a superfamily of integral membrane proteins

30   which transduce extracellular signals. Not all GPCRs contain N-terminal signal peptides. GPCRs

include receptors for biogenic amines such as dopamine, epinephrine, histamine, glutamate

(metabotropic-type), acetylcholine (muscarinic-type), and serotonin; for lipid mediators of inflammation

such as prostaglandins, platelet activating factor, and leukotrienes; for peptide hormones such as

calcitonin, C5a anaphylatoxin, follicle stimulating hormone, gonadotropin releasing hormone, neurokinin,

35   oxytocin, and thrombin; and for sensory signal mediators such as retinal photopigments and olfactory

stimulatory molecules. The structure of these highly conserved receptors consists of seven

hydrophobic transmembrane regions, cysteine disulfide bridges between the second and third

extracellular loops, an extracellular N-terminus, and a cytoplasmic C-terminus. The N-terminus

interacts with ligands, the disulfide bridges interact with agonists and antagonists, and the large third

5   intracellular loop interacts with G proteins to activate second messengers such as cyclic AMP,

phospholipase C, inositol triphosphate, or ion channels. (Reviewed in Watson, S. and Arkinstall, S.

(1994) The G-protein Linked Receptor Facts Book, Academic Press, San Diego CA, pp. 2-6; and

Bolander, F.F. (1994) Molecular Endocrinology, Academic Press, San Diego CA, pp. 162-176.)

        Other types of receptors include cell surface antigens identified on leukocytic cells of the

10   immune system. These antigens have been identified using systematic, monoclonal antibody (mAb)-

based "shot gun" techniques. These techniques have resulted in the production of hundreds of mAbs

directed against unknown cell surface leukocytic antigens. These antigens have been grouped into

"clusters of differentiation" based on common immunocytochemical localization patterns in various

differentiated and undifferentiated leukocytic cell types. Antigens in a given cluster are presumed to

15   identify a single cell surface protein and are assigned a "cluster of differentiation" or "CD"

designation. Some of the genes encoding proteins identified by CD antigens have been cloned and

verified by standard molecular biology techniques. CD antigens have been characterized as both

transmembrane proteins and cell surface proteins anchored to the plasma membrane via covalent

attachment to fatty acid-containing glycolipids such as glycosylphosphatidylinositol (GPI). (Reviewed

20   in Barclay, A.N. et al. (1995) The Leucocyte Antigen Facts Book, Academic Press, San Diego CA,

pp. 17-20.)

        Matrix proteins (MPs) are transmembrane and extracellular proteins which function in

formation, growth, remodeling, and maintenance of tissues and as important mediators and regulators

of the inflammatory response. The expression and balance of MPs may be perturbed by biochemical

25   changes that result from congenital, epigenetic, or infectious diseases. In addition, MPs affect

leukocyte migration, proliferation, differentiation, and activation in the immune response. MPs are

frequently characterized by the presence of one or more domains which may include collagen-like

domains, EGF-like domains, immunoglobulin-like domains, and fibronectin-like domains. In addition,

MPs may be heavily glycosylated and may contain an Arginine-Glycine-Aspartate (RGD) tripeptide

30   motif which may play a role in adhesive interactions. MPs include extracellular proteins such as

fibronectin, collagen, galectin, vitronectin and its proteolytic derivative somatomedin B; and cell

adhesion receptors such as cell adhesion molecules (CAMs), cadherins, and integrins. (Reviewed in

Ayad, S. et al. (1994) The Extracellular Matrix Facts Book, Academic Press, San Diego CA, pp. 2-

16; Ruoslahti, E. (1997) Kidney Int. 51:1413-1417; Sjaastad, M.D. and Nelson, W.J. (1997) BioEssays

19:47-55.)

Cytokines are secreted by hematopoietic cells in response to injury or infection. Interleukins, neurotrophins, growth factors, interferons, and chemokines all define cytokine families that work in conjunction with cellular receptors to regulate cell proliferation and differentiation. In addition,
5   cytokines effect activities such as leukocyte migration and function, hematopoietic cell proliferation, temperature regulation, acute response to infection, tissue remodeling, and apoptosis.

Chemokines, in particular, are small chemoattractant cytokines involved in inflammation, leukocyte proliferation and migration, angiogenesis and angiostasis, regulation of hematopoiesis, HIV infectivity, and stimulation of cytokine secretion. Chemokines generally contain 70-100 amino acids
10   and are subdivided into four subfamilies based on the presence of conserved cysteine-based motifs. (Callard, R. and Gearing, A. (1994) The Cytokine Facts Book, Academic Press, New York NY, pp. 181-190, 210-213, 223-227.)

Growth and differentiation factors are secreted proteins which function in intercellular communication. Some factors require oligomerization or association with MPs for activity. Complex
15   interactions among these factors and their receptors trigger intracellular signal transduction pathways that stimulate or inhibit cell division, cell differentiation, cell signaling, and cell motility. Most growth and differentiation factors act on cells in their local environment (paracrine signaling). There are three broad classes of growth and differentiation factors. The first class includes the large polypeptide growth factors such as epidermal growth factor, fibroblast growth factor, transforming growth factor,
20   insulin-like growth factor, and platelet-derived growth factor. The second class includes the hematopoietic growth factors such as the colony stimulating factors (CSFs). Hematopoietic growth factors stimulate the proliferation and differentiation of blood cells such as B-lymphocytes, T-lymphocytes, erythrocytes, platelets, eosinophils, basophils, neutrophils, macrophages, and their stem cell precursors. The third class includes small peptide factors such as bombesin, vasopressin,
25   oxytocin, endothelin, transferrin, angiotensin II, vasoactive intestinal peptide, and bradykinin which function as hormones to regulate cellular functions other than proliferation.

Growth and differentiation factors play critical roles in neoplastic transformation of cells in vitro and in tumor progression in vivo. Inappropriate expression of growth factors by tumor cells may contribute to vascularization and metastasis of tumors. During hematopoiesis, growth factor
30   misregulation can result in anemias, leukemias, and lymphomas. Certain growth factors such as interferon are cytotoxic to tumor cells both in vivo and in vitro. Moreover, some growth factors and growth factor receptors are related both structurally and functionally to oncoproteins. In addition, growth factors affect transcriptional regulation of both proto-oncogenes and oncosuppressor genes. (Reviewed in Pimentel, E. (1994) Handbook of Growth Factors, CRC Press, Ann Arbor MI, pp. 1-9.)

Proteolytic enzymes or proteases either activate or deactivate proteins by hydrolyzing peptide bonds. Proteases are found in the cytosol, in membrane-bound compartments, and in the extracellular space. The major families are the zinc, serine, cysteine, thiol, and carboxyl proteases.

Ion channels, ion pumps, and transport proteins mediate the transport of molecules across

5   cellular membranes. Transport can occur by a passive, concentration-dependent mechanism or can be linked to an energy source such as ATP hydrolysis. Symporters and antiporters transport ions and small molecules such as amino acids, glucose, and drugs. Symporters transport molecules and ions unidirectionally, and antiporters transport molecules and ions bidirectionally. Transporter superfamilies include facilitative transporters and active ATP-binding cassette transporters which are involved in

10   multiple-drug resistance and the targeting of antigenic peptides to MHC Class I molecules. These transporters bind to a specific ion or other molecule and undergo a conformational change in order to transfer the ion or molecule across the membrane. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York NY, pp. 523-546.)

Ion channels are formed by transmembrane proteins which create a lined passageway across

15   the membrane through which water and ions, such as Na^+, K^+, Ca^{2+}, and Cl^-, enter and exit the cell. For example, chloride channels are involved in the regulation of the membrane electric potential as well as absorption and secretion of ions across the membrane. Chloride channels also regulate the internal pH of membrane-bound organelles.

Ion pumps are ATPases which actively maintain membrane gradients. Ion pumps are

20   classified as P, V, or F according to their structure and function. All have one or more binding sites for ATP in their cytosolic domains. The P-class ion pumps include Ca^{2+} ATPase and Na^+/K^+ ATPase and function in transporting H^+, Na^+, K^+, and Ca^{2+} ions. P-class pumps consist of two α and two β transmembrane subunits. The V- and F-class ion pumps have similar structures but transport only H^+. F class H^+ pumps mediate transport across the membranes of mitochondria and chloroplasts, while V-

25   class H^+ pumps regulate acidity inside lysosomes, endosomes, and plant vacuoles.

A family of structurally related intrinsic membrane proteins known as facilitative glucose transporters catalyze the movement of glucose and other selected sugars across the plasma membrane. The proteins in this family contain a highly conserved, large transmembrane domain comprised of 12 α-helices, and several weakly conserved, cytoplasmic and exoplasmic domains.

30   (Pessin, J.E. and Bell, G.I. (1992) Annu. Rev. Physiol. 54:911-930.)

Amino acid transport is mediated by Na^+ dependent amino acid transporters. These transporters are involved in gastrointestinal and renal uptake of dietary and cellular amino acids and in neuronal reuptake of neurotransmitters. Transport of cationic amino acids is mediated by the system y+ family and the cationic amino acid transporter (CAT) family. Members of the CAT family share a

high degree of sequence homology, and each contains 12-14 putative transmembrane domains. (Ito, K. and Groudine, M. (1997) J. Biol. Chem. 272:26780-26786.)

Hormones are secreted molecules that travel through the circulation and bind to specific receptors on the surface of, or within, target cells. Although they have diverse biochemical

5   compositions and mechanisms of action, hormones can be grouped into two categories. One category includes small lipophilic hormones that diffuse through the plasma membrane of target cells, bind to cytosolic or nuclear receptors, and form a complex that alters gene expression. Examples of these molecules include retinoic acid, thyroxine, and the cholesterol-derived steroid hormones such as progesterone, estrogen, testosterone, cortisol, and aldosterone. The second category includes

10   hydrophilic hormones that function by binding to cell surface receptors that transduce signals across the plasma membrane. Examples of such hormones include amino acid derivatives such as catecholamines and peptide hormones such as glucagon, insulin, gastrin, secretin, cholecystokinin, adrenocorticotropic hormone, follicle stimulating hormone, luteinizing hormone, thyroid stimulating hormone, and vasopressin. (See, for example, Lodish et al. (1995) Molecular Cell Biology, Scientific

15   American Books Inc., New York NY, pp. 856-864.)

Neuropeptides and vasomediators (NP/VM) comprise a large family of endogenous signaling molecules. Included in this family are neuropeptides and neuropeptide hormones such as bombesin, neuropeptide Y, neurotensin, neuromedin N, melanocortins, opioids, galanin, somatostatin, tachykinins, urotensin II and related peptides involved in smooth muscle stimulation, vasopressin, vasoactive

20   intestinal peptide, and circulatory system-borne signaling molecules such as angiotensin, complement, . calcitonin, endothelins, formyl-methionyl peptides, glucagon, cholecystokinin and gastrin. NP/VMs can transduce signals directly, modulate the activity or release of other neurotransmitters and hormones, and act as catalytic enzymes in cascades. The effects of NP/VMs range from extremely brief to long-lasting. (Reviewed in Martin, C.R. et al. (1985) Endocrine Physiology, Oxford University Press,

25   New York, NY, pp. 57-62.)

The discovery of new secretory molecules provide new compositions which are useful in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, cell signaling and the expression of secretory molecules.

30   **SUMMARY OF THE INVENTION**

Embodiments of the invention relate to nucleic acid sequences comprising human polynucleotides encoding secretory polypeptides that can contain signal peptides and/or transmembrane domains. These human polynucleotides (sptm) as presented in the Sequence Listing uniquely identify partial or full length genes encoding structural, functional, and regulatory polypeptides

involved in cell signaling.

An embodiment of the invention provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; b) a polynucleotide comprising a naturally occurring polynucleotide

5   sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In one alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567. In another alternative, the polynucleotide comprises at least 30 contiguous

10 nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; b) a polynucleotide comprising a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the

15 polynucleotide of b); and e) an RNA equivalent of a) through d). In another alternative, the polynucleotide comprises at least 60 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; b) a polynucleotide comprising a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected

20 from the group consisting of SEQ ID NO:1-567; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). Another embodiment provides a composition for the detection of expression of secretory polynucleotides comprising at least one isolated polynucleotide comprising a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; b) a polynucleotide comprising a

25 naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d); and a detectable label.

30 An embodiment of the invention also provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a polynucleotide sequence of a polyneucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of SEQ ID NO:1-567; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide

sequence selected from the group consisting of SEQ ID NO:1-567; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the

5   presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

Another embodiment also provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a polynucleotide sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group

10   consisting of SEQ ID NO:1-567; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides

15   comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof. In an alternative·   · · embodiment, the invention provides a composition comprising a target polynucleotide of the method,

20   wherein said probe comprises at least 30 contiguous nucleotides. In an alternative embodiment, the   . invention provides a composition comprising a target polynucleotide of the method, wherein said probe comprises at least 60 contiguous nucleotides.

Another embodiment provides a recombinant polynucleotide comprising a promoter sequence operably linked to an isolated polynucleotide selected from the group consisting of a) a polynucleotide

25   comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In an alternative embodiment, the invention provides a

30   cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

Yet another embodiment provides a method for producing a secretory polypeptide, the method comprising a) culturing a cell under conditions suitable for expression of the secretory polypeptide, wherein said cell is transformed with a recombinant polynucleotide, said recombinant polynucleotide

comprising an isolated polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; iii) a polynucleotide

5   complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv), and b) recovering the secretory polypeptide so expressed. The invention additionally provides a method wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146.

Still another embodiment provides an isolated secretory polypeptide (SPTM) encoded by at

10   least one polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567. The invention further provides a method of screening for a test compound that specifically binds to the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146. The method comprises a) combining the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146 with at least one test compound

15   under suitable conditions, and b) detecting binding of the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146 to the test compound, thereby identifying a compound that specifically binds to the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146.

. : Still yet another embodiment provides a microarray wherein at least one element of the . ·

20   microarray is an isolated polynucleotide comprising at least 30 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; c) a polynucleotide complementary to the

25   polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The invention also provides a method for generating a transcript image of a sample which contains polynucleotides. The method comprises a) labeling the polynucleotides of the sample, b) contacting the elements of the microarray with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and c) quantifying the

30   expression of the polynucleotides in the sample.

Still yet another embodiment provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; b) a polynucleotide comprising a

naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) exposing a sample comprising the target
5   polynucleotide to a compound, b) detecting altered expression of the target polynucleotide, and c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

    Another embodiment provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b)
10 hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; iii) a polynucleotide
15 complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence
20 selected from the group consisting of SEQ ID NO:1-567; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-567; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv), and alternatively, the target polynucleotide comprises a polynucleotide sequence of a
25 fragment of a polynucleotide selected from the group consisting of i-v above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.
30   Another embodiment provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group

consisting of SEQ ID NO:568-1146, and d) an immunogenic fragment of a polypeptide having an

amino acid sequence selected from the group consisting of SEQ ID NO:568-1146. In an alternative

embodiment, the invention provides an isolated polypeptide comprising an amino acid sequence

selected from the group consisting of SEQ ID NO:568-1146.

5   Still another embodiment provides an isolated polynucleotide encoding a polypeptide selected

from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the

group consisting of SEQ ID NO:568-1146, b) a polypeptide comprising a naturally occurring amino

acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of

SEQ ID NO:568-1146, c) a biologically active fragment of a polypeptide having an amino acid

10   sequence selected from the group consisting of SEQ ID NO:568-1146, and d) an immunogenic

fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ

ID NO:568-1146. In one alternative, the polynucleotide encodes a polypeptide comprising an amino

acid sequence selected from the group consisting of SEQ ID NO:568-1146. In another alternative, the

polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID

15   NO:1-567.

          Another embodiment provides an isolated antibody which specifically binds to a polypeptide

selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected

from the group consisting of SEQ ID NO:568-1146, b) a polypeptide comprising a naturally occurring.

amino acid sequence at least 90% identical to an amino acid sequence selected from the group

20   consisting of SEQ ID NO:568-1146, c) a biologically active fragment of a polypeptide having an amino

acid sequence selected from the group consisting of SEQ ID NO:568-1146, and d) an immunogenic

fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ

ID NO:568-1146.

          Another embodiment provides a composition comprising a polypeptide selected from the group

25   consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of

SEQ ID NO:568-1146, b) a polypeptide comprising a naturally occurring amino acid sequence at least

90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146,

c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the

group consisting of SEQ ID NO:568-1146, and d) an immunogenic fragment of a polypeptide having

30   an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, and a

pharmaceutically acceptable excipient. In an embodiment, the composition comprises a polypeptide

having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146. Another

embodiment provides a method of treating a disease or condition associated with decreased expression

of functional SPTM, comprising administering to a patient in need of such treatment the composition.

Another embodiment provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence

5   selected from the group consisting of SEQ ID NO:568-1146, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In an

10   alternative embodiment, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative embodiment, the invention provides a method of treating a disease or condition associated with decreased expression of functional SPTM, comprising administering to a patient in need of such ·   treatment the composition.

15   Another embodiment provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, c) a biologically active fragment of a

20   polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In an alternative, the invention provides a composition comprising an antagonist compound identified by the

25   method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional SPTM, comprising administering to a patient in need of such treatment the composition.

Another embodiment provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino

30   acid sequence selected from the group consisting of SEQ ID NO:568-1146, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from

35   the group consisting of SEQ ID NO:568-1146. The method comprises a) combining the polypeptide

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with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence

5   of the test compound is indicative of a compound that modulates the activity of the polypeptide.

DESCRIPTION OF THE TABLES

Table 1 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with the

10   sequence identification numbers (SEQ ID NO:s) and open reading frame identification numbers (ORF IDs) corresponding to polypeptides encoded by the template ID.

Table 2 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with polynucleotide segments of each template sequence as defined by the indicated "start" and "stop"

15   nucleotide positions. The reading frames of the polynucleotide segments are shown, and the polypeptides encoded by the polynucleotide segments constitute either signal peptide (SP) or transmembrane (TM) domains, as indicated. For TM domains, the membrane topology of the encoded polypeptide sequence is indicated as being transmembrane or on the cytosolic or non-cytosolic side of the cell membrane or organelle.

20   Table 3 shows the sequence identification numbers and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with component sequence identification spans corresponding to each template. The component sequences, which were used to assemble the template sequences, are defined by the spans indicating the nucleotide positions along each template.

25   Table 4 shows the tissue distribution profiles for the templates of the invention.

Table 5 shows the sequence identification numbers (SEQ ID NO:s) corresponding to the polypeptides of the present invention, along with the reading frames used to obtain the polypeptide segments, the lengths of the polypeptide segments, the "start" and "stop" nucleotide positions of the polynucleotide sequences used to define the encoded polypeptide segments, the GenBank hits (GI

30   Numbers), probability scores, and functional annotations corresponding to the GenBank hits.

Table 6 summarizes the bioinformatics tools which are useful for analysis of the polynucleotides of the present invention. The first column of Table 6 lists analytical tools, programs, and algorithms, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the

35   fourth column presents, where applicable, the scores, probability values, and other parameters used to

evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences).

DETAILED DESCRIPTION OF THE INVENTION

Before the nucleic acid sequences and methods are presented, it is to be understood that this invention is not limited to the particular machines, methods, and materials described. Although particular embodiments are described, machines, methods, and materials similar or equivalent to these embodiments may be used to practice the invention. The preferred machines, methods, and materials set forth are not intended to limit the scope of the invention which is limited only by the appended claims.

The singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. All technical and scientific terms have the meanings commonly understood by one of ordinary skill in the art. All publications are incorporated by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are presented and which might be used in connection with the invention. Nothing in the specification is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

Definitions

As used herein, the lower case "sptm" refers to a nucleic acid sequence, while the upper case "SPTM" refers to an amino acid sequence encoded by sptm. A "full-length" sptm refers to a nucleic acid sequence containing the entire coding region of a gene endogenously expressed in human tissue.

"Adjuvants" are materials such as Freund's adjuvant, mineral gels (aluminum hydroxide), and surface active substances (lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol) which may be administered to increase a host's immunological response.

"Allele" refers to an alternative form of a nucleic acid sequence. Alleles result from a "mutation," a change or an alternative reading of the genetic code. Any given gene may have none, one, or many allelic forms. Mutations which give rise to alleles include deletions, additions, or substitutions of nucleotides. Each of these changes may occur alone, or in combination with the others, one or more times in a given nucleic acid sequence. The present invention encompasses allelic sptm.

An "allelic variant" is an alternative form of the gene encoding SPTM. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to

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allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding SPTM include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as SPTM or a polypeptide with at least one functional characteristic of SPTM. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding SPTM, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding SPTM. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent SPTM. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of SPTM is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

"Amino acid sequence" refers to a peptide, a polypeptide, or a protein of either natural or synthetic origin. The amino acid sequence is not limited to the complete, endogenous amino acid sequence and may be a fragment, epitope, variant, or derivative of a protein expressed by a nucleic acid sequence.

"Amplification" refers to the production of additional copies of a sequence and is carried out using polymerase chain reaction (PCR) technologies well known in the art.

"Antibody" refers to intact molecules as well as to fragments thereof, such as Fab, F(ab')$_2$, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind SPTM polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or peptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "aptamer" refers to a nucleic acid or oligonucleotide molecule that binds to a specific molecular target. Aptamers are derived from an in vitro evolutionary process (e.g., SELEX

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(Systematic Evolution of Ligands by EXponential Enrichment), described in U.S. Patent No. 5,270,163), which selects for target-specific aptamer sequences from large combinatorial libraries. Aptamer compositions may be double-stranded or single-stranded, and may include deoxyribonucleotides, ribonucleotides, nucleotide derivatives, or other nucleotide-like molecules. The

5   nucleotide components of an aptamer may have modified sugar groups (e.g., the 2'-OH group of a ribonucleotide may be replaced by 2'-F or 2'-NH$_2$), which may improve a desired property, e.g., resistance to nucleases or longer lifetime in blood. Aptamers may be conjugated to other molecules, e.g., a high molecular weight carrier to slow clearance of the aptamer from the circulatory system. Aptamers may be specifically cross-linked to their cognate ligands, e.g., by photo-activation of a

10 cross-linker. (See, e.g., Brody, E.N. and L. Gold (2000) J. Biotechnol. 74:5-13.)

The term "intramer" refers to an aptamer which is expressed in vivo. For example, a vaccinia virus-based RNA expression system has been used to express specific RNA aptamers at high levels in the cytoplasm of leukocytes (Blind, M. et al. (1999) Proc. Natl Acad. Sci. USA 96:3606-3610).

The term "spiegelmer" refers to an aptamer which includes L-DNA, L-RNA, or other left-

15 handed nucleotide derivatives or nucleotide-like molecules. Aptamers containing left-handed nucleotides are resistant to degradation by naturally occurring enzymes, which normally act on substrates containing right-handed nucleotides.

"Antisense sequence" refers to a sequence capable of specifically hybridizing to a target sequence. The antisense sequence may include DNA, RNA, or any nucleic acid mimic or analog

20 such as peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified base.

"Antisense technology" refers to any technology which relies on the specific hybridization of

25 an antisense sequence to a target sequence.

A "bin" is a portion of computer memory space used by a computer program for storage of data, and bounded in such a manner that data stored in a bin may be retrieved by the program.

"Biologically active" refers to an amino acid sequence having a structural, regulatory, or biochemical function of a naturally occurring amino acid sequence.

30 "Clone joining" is a process for combining gene bins based upon the bins' containing sequence information from the same clone. The sequences may assemble into a primary gene transcript as well as one or more splice variants.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing (5'-A-G-T-3' pairs with its complement 3'-T-C-A-5').

35 A "component sequence" is a nucleic acid sequence selected by a computer program such as

PHRED and used to assemble a consensus or template sequence from one or more component sequences.

A "consensus sequence" or "template sequence" is a nucleic acid sequence which has been assembled from overlapping sequences, using a computer program for fragment assembly such as the

5   GELVIEW fragment assembly system (Genetics Computer Group (GCG), Madison WI) or using a relational database management system (RDMS).

"Conservative amino acid substitutions" are those substitutions that, when made, least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino

10   acids which may be substituted for an original amino acid in a protein and which are regarded as conservative substitutions.

Original Residue	Conservative Substitution
Ala	Gly, Ser
Arg	His, Lys
Asn	Asp, Gln, His
Asp	Asn, Glu
Cys	Ala, Ser
Gln	Asn, Glu, His
Glu	Asp, Gln, His
Gly	Ala
His	Asn, Arg, Gln, Glu
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	His, Met, Leu, Trp, Tyr
Ser	Cys, Thr
Thr	Ser, Val
Trp	Phe, Tyr
Tyr	His, Phe, Trp
Val	Ile, Leu, Thr

35   Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

"Deletion" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or amino acid residue, respectively, is absent.

40   "Derivative" refers to the chemical modification of a nucleic acid sequence, such as by replacement of hydrogen by an alkyl, acyl, amino, hydroxyl, or other group.

"Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of SPTM. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of SPTM.

"E-value" refers to the statistical probability that a match between two sequences occurred by chance.

"Exon shuffling" refers to the recombination of different coding regions (exons). Since an exon may represent a structural or functional domain of the encoded protein, new proteins may be assembled through the novel reassortment of stable substructures, thus allowing acceleration of the evolution of new protein functions.

A "fragment" is a unique portion of sptm or SPTM which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 10 to 1000 contiguous amino acid residues or nucleotides. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous amino acid residues or nucleotides in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing and the figures, may be encompassed by the present embodiments.

A fragment of sptm comprises a region of unique polynucleotide sequence that specifically identifies sptm, for example, as distinct from any other sequence in the same genome. A fragment of sptm is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish sptm from related polynucleotide sequences. The precise length of a fragment of sptm and the region of sptm to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SPTM is encoded by a fragment of sptm. A fragment of SPTM comprises a region of unique amino acid sequence that specifically identifies SPTM. For example, a fragment of SPTM is useful as an immunogenic peptide for the development of antibodies that specifically

recognize SPTM. The precise length of a fragment of SPTM and the region of SPTM to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

5   A "full length" nucleotide sequence is one containing at least a start site for translation to a protein sequence, followed by an open reading frame and a stop site, and encoding a "full length" polypeptide.

"Hit" refers to a sequence whose annotation will be used to describe a given template. Criteria for selecting the top hit are as follows: if the template has one or more exact nucleic acid matches, the top hit is the exact match with highest percent identity. If the template has no exact

10   matches but has significant protein hits, the top hit is the protein hit with the lowest E-value. If the template has no significant protein hits, but does have significant non-exact nucleotide hits, the top hit is the nucleotide hit with the lowest E-value.

"Homology" refers to sequence similarity either between a reference nucleic acid sequence and at least a fragment of an sptm or between a reference amino acid sequence and a fragment of an

15   SPTM.

"Hybridization" refers to the process by which a strand of nucleotides anneals with a complementary strand through base pairing. Specific hybridization is an indication that two nucleic acid sequences share a high degree of identity. Specific hybridization complexes form under defined annealing conditions, and remain hybridized after the "washing" step. The defined hybridization

20   conditions include the annealing conditions and the washing step(s), the latter of which is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid probes that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable and may be consistent among hybridization experiments, whereas wash conditions may

25   be varied among experiments to achieve the desired stringency.

Generally, stringency of hybridization is expressed with reference to the temperature under which the wash step is carried out. Generally, such wash temperatures are selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target

30   sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization is well known and can be found in Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention

35   include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour.

Alternatively, temperatures of about 65°C, 60°C, or 55°C may be used. SSC concentration may be varied from about 0.2 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, denatured salmon sperm DNA at about 100-200 μg/ml. Useful variations on these conditions will be readily
5 apparent to those skilled in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their resultant proteins.

Other parameters, such as temperature, salt concentration, and detergent concentration may be varied to achieve the desired stringency. Denaturants, such as formamide at a concentration of
10 about 35-50% v/v, may also be used under particular circumstances, such as RNA:DNA hybridizations. Appropriate hybridization conditions are routinely determinable by one of ordinary skill in the art.

"Immunologically active" or "immunogenic" describes the potential for a natural, recombinant, or synthetic peptide, epitope, polypeptide, or protein to induce antibody production in appropriate
15 animals, cells, or cell lines.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

20 An "immunogenic fragment" is a polypeptide or oligopeptide fragment of SPTM which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of SPTM which is useful in any of the antibody production methods disclosed herein or known in the art.

25 "Insertion" or "addition" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or residue, respectively, is added to the sequence.

"Labeling" refers to the covalent or noncovalent joining of a polynucleotide, polypeptide, or antibody with a reporter molecule capable of producing a detectable or measurable signal.

"Microarray" is any arrangement of nucleic acids, amino acids, antibodies, etc., on a
30 substrate. The substrate may be a solid support such as beads, glass, paper, nitrocellulose, nylon, or an appropriate membrane.

"Linkers" are short stretches of nucleotide sequence which may be added to a vector or an sptm to create restriction endonuclease sites to facilitate cloning. "Polylinkers" are engineered to incorporate multiple restriction enzyme sites and to provide for the use of enzymes which leave 5' or 3'

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overhangs (e.g., BamHI, EcoRI, and HindIII) and those which provide blunt ends (e.g., EcoRV, SnaBI, and StuI).

"Naturally occurring" refers to an endogenous polynucleotide or polypeptide that may be isolated from viruses or prokaryotic or eukaryotic cells.

5   "Nucleic acid sequence" refers to the specific order of nucleotides joined by phosphodiester bonds in a linear, polymeric arrangement. Depending on the number of nucleotides, the nucleic acid sequence can be considered an oligomer, oligonucleotide, or polynucleotide. The nucleic acid can be DNA, RNA, or any nucleic acid analog, such as PNA, may be of genomic or synthetic origin, may be either double-stranded or single-stranded, and can represent either the sense or antisense

10   (complementary) strand.

"Oligomer" refers to a nucleic acid sequence of at least about 6 nucleotides and as many as about 60 nucleotides, preferably about 15 to 40 nucleotides, and most preferably between about 20 and 30 nucleotides, that may be used in hybridization or amplification technologies. Oligomers may be used as, e.g., primers for PCR, and are usually chemically synthesized.

15   "Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

20   · "Peptide nucleic acid" (PNA) refers to a DNA mimic in which nucleotide bases are attached to a pseudopeptide backbone to increase stability. PNAs, also designated antigene agents, can prevent gene expression by targeting complementary messenger RNA.

The phrases "percent identity" and "% identity", as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a

25   standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e

30   sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and Sharp, P.M. (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue

weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequence pairs.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at http://www.ncbi.nlm.nih.gov/BLAST/. The BLAST software suite includes various sequence analysis programs including "BLASTN," that is used to determine alignment between a known polynucleotide sequence and other sequences on a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at http://www.ncbi.nlm.nih.gov/gorf/bl2/. The "BLAST 2 Sequences" tool can be used for both BLASTN and BLASTP (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use BLASTN with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example:

> *Matrix: BLOSUM62*
>
> *Reward for match: 1*
>
> *Penalty for mismatch: -2*
>
> *Open Gap: 5 and Extension Gap: 2 penalties*
>
> *Gap x drop-off: 50*
>
> *Expect: 10*
>
> *Word Size: 11*
>
> *Filter: on*

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity", as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions,

5 explained in more detail above, generally preserve the hydrophobicity and acidity of the substituted residue, thus preserving the structure (and therefore function) of the folded polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of

10 polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise

15 comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) with BLASTP set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalty

20 *Gap x drop-off: 50*

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence,

25 for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to

30 describe a length over which percentage identity may be measured.

"Post-translational modification" of an SPTM may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu and the SPTM.

"Probe" refers to sptm or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA

5   oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous

10   nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the figures and Sequence Listing, may be used.

15   Methods for preparing and using probes and primers are described in the references, for example Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel et al.,1987, Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis et al., 1990, PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be

20   derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000

25   nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer

30   selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The

35   PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource

Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing
selection of primers that hybridize to either the most conserved or least conserved regions of aligned
nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved
oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments

5   identified by any of the above selection methods are useful in hybridization technologies, for example,
as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially
complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are
not limited to those described above.

"Purified" refers to molecules, either polynucleotides or polypeptides that are isolated or

10   separated from their natural environment and are at least about 60% free, preferably at least about
75% free, and most preferably at least about 90% free from other compounds with which they are
naturally associated.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence
that is made by an artificial combination of two or more otherwise separated segments of sequence.

15   This artificial combination is often accomplished by chemical synthesis or, more commonly, by the
artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques
such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have
been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a
recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence.

20   Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a
vaccinia virus, that could be use to vaccinate a mammal wherein the recombinant nucleic acid is
expressed, inducing a protective immunological response in the mammal.

"Regulatory element" refers to a nucleic acid sequence from nontranslated regions of a gene,

25   and includes enhancers, promoters, introns, and 3' untranslated regions, which interact with host
proteins to carry out or regulate transcription or translation.

"Reporter" molecules are chemical or biochemical moieties used for labeling a nucleic acid, an
amino acid, or an antibody. They include radionuclides; enzymes; fluorescent, chemiluminescent, or
chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in

30   the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear
sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of
the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose
instead of deoxyribose.

"Sample" is used in its broadest sense. Samples may contain nucleic or amino acids, antibodies, or other materials, and may be derived from any source (e.g., bodily fluids including, but not limited to, saliva, blood, and urine; chromosome(s), organelles, or membranes isolated from a cell; genomic DNA, RNA, or cDNA in solution or bound to a substrate; and cleared cells or tissues or blots or imprints from such cells or tissues).

"Specific binding" or "specifically binding" refers to the interaction between a protein or peptide and its agonist, antibody, antagonist, or other binding partner. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

"Substitution" refers to the replacement of at least one nucleotide or amino acid by a different nucleotide or amino acid.

"Substrate" refers to any suitable rigid or semi-rigid support including, e.g., membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles or capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" refers to the collective pattern of gene expression by a particular tissue or cell type under given conditions at a given time.

"Transformation" refers to a process by which exogenous DNA enters a recipient cell. Transformation may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed.

"Transformants" include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as cells which transiently express inserted DNA or RNA.

A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or _in vitro_ fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic

organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, and plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms

5   are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 25% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using BLASTN with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 30%,

10   at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. The variant may result in "conservative" amino acid changes which do not affect structural and/or chemical properties. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic"

15   variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid

20   identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

25   In an alternative, variants of the polynucleotides of the present invention may be generated through recombinant methods. One possible method is a DNA shuffling technique such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve

30   the biological properties of SPTM, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and

35   selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular

evolution. For example, fragments of a single gene containing random point mutations may be

recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively,

fragments of a given gene may be recombined with fragments of homologous genes in the same gene

family, either from the same or different species, thereby maximizing the genetic diversity of multiple

5   naturally occurring genes in a directed and controllable manner.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having

at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of

the polypeptide sequences using BLASTP with the "BLAST 2 Sequences" tool Version 2.0.9 (May-

07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%,

10   at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at

least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence

identity over a certain defined length of one of the polypeptides.

THE INVENTION

15   In a particular embodiment, cDNA sequences derived from human tissues and cell lines were

aligned based on nucleotide sequence identity and assembled into "consensus" or "template"

sequences which are designated by the template identification numbers (template IDs) in column 2 of

Table 2. The sequence identification numbers (SEQ ID NO:s) corresponding to the template IDs are

shown in column 1. Segments of the template sequences are defined by the "start" and "stop"

20   nucleotide positions listed in columns 3 and 4. These segments, when translated in the reading frames

indicated in column 5, have similarity to signal peptide (SP) or transmembrane (TM) domain consensus

sequences, as indicated in column 6.

The invention incorporates the nucleic acid sequences of these templates as disclosed in the

Sequence Listing and the use of these sequences in the diagnosis and treatment of disease states

25   characterized by defects in cell signaling. The invention further utilizes these sequences in

hybridization and amplification technologies, and in particular, in technologies which assess gene

expression patterns correlated with specific cells or tissues and their responses in vivo or in vitro to

pharmaceutical agents, toxins, and other treatments. In this manner, the sequences of the present

invention are used to develop a transcript image for a particular cell or tissue.

30

Derivation of Nucleic Acid Sequences

cDNA was isolated from libraries constructed using RNA derived from normal and diseased

human tissues and cell lines. The human tissues and cell lines used for cDNA library construction

were selected from a broad range of sources to provide a diverse population of cDNAs representative

35   of gene transcription throughout the human body. Descriptions of the human tissues and cell lines

used for cDNA library construction are provided in the LIFESEQ database (Incyte Genomics, Inc. (Incyte), Palo Alto CA). Human tissues were broadly selected from, for example, cardiovascular, dermatologic, endocrine, gastrointestinal, hematopoietic/immune system, musculoskeletal, neural, reproductive, and urologic sources.

5   Cell lines used for cDNA library construction were derived from, for example, leukemic cells, teratocarcinomas, neuroepitheliomas, cervical carcinoma, lung fibroblasts, and endothelial cells. Such cell lines include, for example, THP-1, Jurkat, HUVEC, hNT2, WI38, HeLa, and other cell lines commonly used and available from public depositories (American Type Culture Collection, Manassas VA). Prior to mRNA isolation, cell lines were untreated, treated with a pharmaceutical agent such as
10   5'-aza-2'-deoxycytidine, treated with an activating agent such as lipopolysaccharide in the case of leukocytic cell lines, or, in the case of endothelial cell lines, subjected to shear stress.

Sequencing of the cDNAs

    Methods for DNA sequencing are well known in the art. Conventional enzymatic methods
15   employ the Klenow fragment of DNA polymerase I, SEQUENASE DNA polymerase (U.S. Biochemical Corporation, Cleveland OH), Taq polymerase (Applied Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Inc. (Amersham Pharmacia Biotech), Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies Inc. (Life Technologies), Gaithersburg
20   MD), to extend the nucleic acid sequence from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both single-stranded and double-stranded templates. Chain termination reaction products may be electrophoresed on urea-polyacrylamide gels and detected either by autoradiography (for radioisotope-labeled nucleotides) or by fluorescence (for fluorophore-labeled nucleotides). Automated methods for mechanized reaction
25   preparation, sequencing, and analysis using fluorescence detection methods have been developed. Machines used to prepare cDNAs for sequencing can include the MICROLAB 2200 liquid transfer system (Hamilton Company (Hamilton), Reno NV), Peltier thermal cycler (PTC200; MJ Research, Inc. (MJ Research), Watertown MA), and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing can be carried out using, for example, the ABI 373 or 377 (Applied
30   Biosystems) or MEGABACE 1000 (Molecular Dynamics, Inc. (Molecular Dynamics), Sunnyvale CA) DNA sequencing systems, or other automated and manual sequencing systems well known in the art.

    The nucleotide sequences of the Sequence Listing have been prepared by current, state-of-the-art, automated methods and, as such, may contain occasional sequencing errors or unidentified
35   nucleotides. Such unidentified nucleotides are designated by an N. These infrequent unidentified

bases do not represent a hindrance to practicing the invention for those skilled in the art. Several methods employing standard recombinant techniques may be used to correct errors and complete the missing sequence information. (See, e.g., those described in Ausubel, F.M. et al. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY; and Sambrook, J. et al. (1989)
5   Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY.)

Assembly of cDNA Sequences

Human polynucleotide sequences may be assembled using programs or algorithms well known in the art. Sequences to be assembled are related, wholly or in part, and may be derived from a single
10   or many different transcripts. Assembly of the sequences can be performed using such programs as PHRAP (Phils Revised Assembly Program) and the GELVIEW fragment assembly system (GCG), or other methods known in the art.

Alternatively, cDNA sequences are used as "component" sequences that are assembled into "template" or "consensus" sequences as follows. Sequence chromatograms are processed, verified,
15   and quality scores are obtained using PHRED. Raw sequences are edited using an editing pathway known as Block 1 (See, e.g., the LIFESEQ Assembled User Guide, Incyte Genomics, Palo Alto, CA). A series of BLAST comparisons is performed and low-information segments and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) are replaced by "n's", or masked, to prevent spurious matches. Mitochondrial and ribosomal RNA sequences are also removed. The processed sequences
20   are then loaded into a relational database management system (RDMS) which assigns edited sequences to existing templates, if available. When additional sequences are added into the RDMS, a process is initiated which modifies existing templates or creates new templates from works in progress (i.e., nonfinal assembled sequences) containing queued sequences or the sequences themselves. After the new sequences have been assigned to templates, the templates can be merged into bins. If
25   multiple templates exist in one bin, the bin can be split and the templates reannotated.

Once gene bins have been generated based upon sequence alignments, bins are "clone joined" based upon clone information. Clone joining occurs when the 5' sequence of one clone is present in one bin and the 3' sequence from the same clone is present in a different bin, indicating that the two bins should be merged into a single bin. Only bins which share at least two different clones are
30   merged.

A resultant template sequence may contain either a partial or a full length open reading frame, or all or part of a genetic regulatory element. This variation is due in part to the fact that the full length cDNAs of many genes are several hundred, and sometimes several thousand, bases in length. With current technology, cDNAs comprising the coding regions of large genes cannot be cloned
35   because of vector limitations, incomplete reverse transcription of the mRNA, or incomplete "second

strand" synthesis. Template sequences may be extended to include additional contiguous sequences derived from the parent RNA transcript using a variety of methods known to those of skill in the art. Extension may thus be used to achieve the full length coding sequence of a gene.

5   Analysis of the cDNA Sequences

The cDNA sequences are analyzed using a variety of programs and algorithms which are well known in the art. (See, e.g., Ausubel, 1997, supra, Chapter 7.7; Meyers, R.A. (Ed.) (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853; and Table 6.) These analyses comprise both reading frame determinations, e.g., based on triplet codon periodicity for

10   particular organisms (Fickett, J.W. (1982) Nucleic Acids Res. 10:5303-5318); analyses of potential start and stop codons; and homology searches.

Computer programs known to those of skill in the art for performing computer-assisted searches for amino acid and nucleic acid sequence similarity, include, for example, Basic Local Alignment Search Tool (BLAST; Altschul, S.F. (1993) J. Mol. Evol. 36:290-300; Altschul, S.F. et al.

15   (1990) J. Mol. Biol. 215:403-410). BLAST is especially useful in determining exact matches and comparing two sequence fragments of arbitrary but equal lengths, whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user (Karlin, S. et al. (1988) Proc. Natl. Acad. Sci. USA 85:841-845). Using an appropriate search tool (e.g., BLAST or HMM), GenBank, SwissProt, BLOCKS, PFAM and other databases may be

20   searched for sequences containing regions of homology to a query sptm or SPTM of the present invention.

Other approaches to the identification, assembly, storage, and display of nucleotide and polypeptide sequences are provided in "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence

25   Database," U.S. Patent Number 5,953,727; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein in their entirety.

Protein hierarchies can be assigned to the putative encoded polypeptide based on, e.g., motif, BLAST, or biological analysis. Methods for assigning these hierarchies are described, for example, in

30   "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S. Patent Number 6,023,659, incorporated herein by reference.

Human Secretory Sequences

The sptm of the present invention may be used for a variety of diagnostic and therapeutic

35   purposes. For example, an sptm may be used to diagnose a particular condition, disease, or disorder

associated with cell signaling. Such conditions, diseases, and disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including

5   adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an immune system disorder such as such as inflammation, actinic keratosis, acquired immunodeficiency syndrome

10   (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease,

15   Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus

20   erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma; and a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other

25   extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker

30   syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorder of the central nervous system, cerebral palsy, a neuroskeletal disorder, an autonomic nervous system disorder, a cranial nerve disorder, a spinal cord disease, muscular dystrophy and other neuromuscular disorder, a peripheral nervous

35   system disorder, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic

31

myopathy, myasthenia gravis, periodic paralysis, a mental disorder including mood, anxiety, and

schizophrenic disorder, seasonal affective disorder (SAD), akathesia, amnesia, catatonia, diabetic

neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's

disorder. The sptm can be used to detect the presence of, or to quantify the amount of, an sptm-

5   related polynucleotide in a sample. This information is then compared to information obtained from

appropriate reference samples, and a diagnosis is established. Alternatively, a polynucleotide

complementary to a given sptm can inhibit or inactivate a therapeutically relevant gene related to the

sptm.

10 Analysis of sptm Expression Patterns

The expression of sptm may be routinely assessed by hybridization-based methods to

determine, for example, the tissue-specificity, disease-specificity, or developmental stage-specificity of

sptm expression. For example, the level of expression of sptm may be compared among different cell

types or tissues, among diseased and normal cell types or tissues, among cell types or tissues at

15 different developmental stages, or among cell types or tissues undergoing various treatments. This

type of analysis is useful, for example, to assess the relative levels of sptm expression in fully or

partially differentiated cells or tissues, to determine if changes in sptm expression levels are correlated

with the development or progression of specific disease states, and to assess the response of a cell or

tissue to a specific therapy, for example, in pharmacological or toxicological studies. Methods for the

20 analysis of sptm expression are based on hybridization and amplification technologies and include

membrane-based procedures such as northern blot analysis, high-throughput procedures that utilize, for

example, microarrays, and PCR-based procedures.

Hybridization and Genetic Analysis

25   The sptm, their fragments, or complementary sequences, may be used to identify the presence

of and/or to determine the degree of similarity between two (or more) nucleic acid sequences. The

sptm may be hybridized to naturally occurring or recombinant nucleic acid sequences under

appropriately selected temperatures and salt concentrations. Hybridization with a probe based on the

nucleic acid sequence of at least one of the sptm allows for the detection of nucleic acid sequences,

30 including genomic sequences, which are identical or related to the sptm of the Sequence Listing.

Probes may be selected from non-conserved or unique regions of at least one of the polynucleotides of

SEQ ID NO:1-567 and tested for their ability to identify or amplify the target nucleic acid sequence

using standard protocols.

Polynucleotide sequences that are capable of hybridizing, in particular, to those shown in SEQ

35 ID NO:1-567 and fragments thereof, can be identified using various conditions of stringency. (See,

e.g., Wahl, G.M. and S.L. Berger (1987) Methods Enzymol. 152:399-407; Kimmel, A.R. (1987) Methods Enzymol. 152:507-511.) Hybridization conditions are discussed in "Definitions."

A probe for use in Southern or northern hybridization may be derived from a fragment of an sptm sequence, or its complement, that is up to several hundred nucleotides in length and is either single-stranded or double-stranded. Such probes may be hybridized in solution to biological materials such as plasmids, bacterial, yeast, or human artificial chromosomes, cleared or sectioned tissues, or to artificial substrates containing sptm. Microarrays are particularly suitable for identifying the presence of and detecting the level of expression for multiple genes of interest by examining gene expression correlated with, e.g., various stages of development, treatment with a drug or compound, or disease progression. An array analogous to a dot or slot blot may be used to arrange and link polynucleotides to the surface of a substrate using one or more of the following: mechanical (vacuum), chemical, thermal, or UV bonding procedures. Such an array may contain any number of sptm and may be produced by hand or by using available devices, materials, and machines.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

Probes may be labeled by either PCR or enzymatic techniques using a variety of commercially available reporter molecules. For example, commercial kits are available for radioactive and chemiluminescent labeling (Amersham Pharmacia Biotech) and for alkaline phosphatase labeling (Life Technologies). Alternatively, sptm may be cloned into commercially available vectors for the production of RNA probes. Such probes may be transcribed in the presence of at least one labeled nucleotide (e.g., ^{32}P-ATP, Amersham Pharmacia Biotech).

Additionally the polynucleotides of SEQ ID NO:1-567 or suitable fragments thereof can be used to isolate full length cDNA sequences utilizing hybridization and/or amplification procedures well known in the art, e.g., cDNA library screening, PCR amplification, etc. The molecular cloning of such full length cDNA sequences may employ the method of cDNA library screening with probes using the hybridization, stringency, washing, and probing strategies described above and in Ausubel, supra, Chapters 3, 5, and 6. These procedures may also be employed with genomic libraries to isolate genomic sequences of sptm in order to analyze, e.g., regulatory elements.

Genetic Mapping

Gene identification and mapping are important in the investigation and treatment of almost all conditions, diseases, and disorders. Cancer, cardiovascular disease, Alzheimer's disease, arthritis,

diabetes, and mental illnesses are of particular interest. Each of these conditions is more complex than the single gene defects of sickle cell anemia or cystic fibrosis, with select groups of genes being predictive of predisposition for a particular condition, disease, or disorder. For example, cardiovascular disease may result from malfunctioning receptor molecules that fail to clear cholesterol

5 from the bloodstream, and diabetes may result when a particular individual's immune system is activated by an infection and attacks the insulin-producing cells of the pancreas. In some studies, Alzheimer's disease has been linked to a gene on chromosome 21; other studies predict a different gene and location. Mapping of disease genes is a complex and reiterative process and generally proceeds from genetic linkage analysis to physical mapping.

10   As a condition is noted among members of a family, a genetic linkage map traces parts of chromosomes that are inherited in the same pattern as the condition. Statistics link the inheritance of particular conditions to particular regions of chromosomes, as defined by RFLP or other markers. (See, for example, Lander, E. S. and Botstein, D. (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.) Occasionally, genetic markers and their locations are known from previous studies. More often,

15 however, the markers are simply stretches of DNA that differ among individuals. Examples of genetic linkage maps can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site.

            In another embodiment of the invention, sptm sequences may be used to generate hybridization probes useful in chromosomal mapping of naturally occurring genomic sequences. Either

20 coding or noncoding sequences of sptm may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of an sptm coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes

25 (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

            Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome

30 mapping techniques and genetic map data. (See, e.g., Meyers, supra, pp. 965-968.) Correlation between the location of sptm on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The sptm sequences may also be used to detect polymorphisms that are genetically linked to the inheritance of a particular condition, disease, or disorder.

35   In situ hybridization of chromosomal preparations and genetic mapping techniques, such as

linkage analysis using established chromosomal markers, may be used for extending existing genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of the corresponding human chromosome is not known. These new marker sequences can be mapped to human chromosomes

5   and may provide valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once a disease or syndrome has been crudely correlated by genetic linkage with a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequences of the subject

10   invention may also be used to detect differences in chromosomal architecture due to translocation, inversion, etc., among normal, carrier, or affected individuals.

Once a disease-associated gene is mapped to a chromosomal region, the gene is cloned in order to identify mutations or other alterations (e.g., translocations or inversions) that may be correlated with disease. This process includes a physical map of the chromosomal region containing

15   the disease-gene of interest along with associated markers. A physical map is necessary for determining the nucleotide sequence of and order of marker genes on a particular chromosomal region. Physical mapping techniques are well known in the art and involve the generation of overlapping sets of cloned DNA fragments from a particular organelle, chromosome, or genome. These clones are analyzed to reconstruct and catalog their order. Once the position of a marker is

20   determined, the DNA from that region is obtained by consulting the catalog and selecting clones from that region. The gene of interest is located through positional cloning techniques using hybridization or similar methods.

Diagnostic Uses

25   In various embodiments, embodiments of sptm described herein can be configured to be used to design probes useful in diagnostic assays known to those skilled in the art. Such assays can be configured to be used to diagnose, detect, confirm or quantitate conditions, disorders, or diseases associated with abnormal levels of sptm expression. Labeled probes developed from sptm sequences are added to a sample under hybridizing conditions of desired stringency. In some instances, sptm, or

30   fragments or oligonucleotides derived from sptm, may be used as primers in amplification steps prior to hybridization. The amount of hybridization complex formed is quantified and compared with standards for a selected cell or tissue type. Indication of the presence of the condition, disorder, or disease can be determined by variation of the amount of sptm expression from the assay standard. The amount of variation indicative of the condition can be above or below the standard, can be selected by the

35   medical practioner, can be determined from known patient populations and/or amounts known in the

medical arts and/or associated standards organizations or regulations (e.g. CLIA). Examples of qualitative or quantitative diagnostic assays or methods may include but are not limited to northern, dot blot, or other membrane or dip-stick based technologies or multiple-sample format technologies such as PCR, enzyme-linked immunosorbent assay (ELISA)-like, pin, chip-based assays and the like.

5   The probes described above may also be used to monitor the progress of conditions, disorders, or diseases associated with abnormal levels of sptm expression, or to evaluate the efficacy of a particular therapeutic treatment. The candidate probe may be identified from the sptm that are specific to a given human tissue and have not been observed in GenBank or other genome databases. Such a probe may be used in animal studies, preclinical tests, clinical trials, or in monitoring the

10   treatment of an individual patient. In a typical process, standard expression is established by methods well known in the art for use as a basis of comparison, samples from patients affected by the disorder or disease are combined with the probe to evaluate any deviation from the standard profile, and a therapeutic agent is administered and effects are monitored to generate a treatment profile. Efficacy is evaluated by determining whether the expression progresses toward or returns to the standard

15   normal pattern. Treatment profiles may be generated over a period of several days or several months. Statistical methods well known to those skilled in the art may be use to determine the significance of such therapeutic agents.

The polynucleotides are also useful for identifying individuals from minute biological samples,. for example, by matching the RFLP pattern of a sample's DNA to that of an individual's DNA. The

20   polynucleotides of the present invention can also be used to determine the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, an individual can be identified through a unique set of DNA sequences. Once a unique ID database is established for an individual, positive identification of that individual can be made from

25   extremely small tissue samples.

In a particular aspect, oligonucleotide primers derived from the sptm of the invention may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and

30   fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from sptm are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSCCP, the

35   oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-

throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequences of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

DNA-based identification techniques can be used in forensic technology. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using, e.g., PCR, to identify individuals. (See, e.g., Erlich, H. (1992) PCR Technology, Freeman and Co., New York, NY). Similarly, polynucleotides of the present invention can be used as polymorphic markers.

There is also a need for reagents capable of identifying the source of a particular tissue. Appropriate reagents can comprise, for example, DNA probes or primers prepared from the sequences of the present invention that are specific for particular tissues. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

The polynucleotides of the present invention can also be used as molecular weight markers on nucleic acid gels or Southern blots, as diagnostic probes for the presence of a specific mRNA in a particular cell type, in the creation of subtracted cDNA libraries which aid in the discovery of novel polynucleotides, in selection and synthesis of oligomers for attachment to an array or other support, and as an antigen to elicit an immune response.

Disease Model Systems Using sptm

The polynucleotides encoding SPTM or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330).

Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

5   The polynucleotides encoding SPTM may also be manipulated _in vitro_ in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

10   The polynucleotides encoding SPTM of the invention can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of sptm is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential

15   pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress sptm, resulting, e.g., in the secretion of SPTM in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

Screening Assays

20   SPTM encoded by polynucleotides of the present invention may be used to screen for molecules that bind to or are bound by the encoded polypeptides. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the bound molecule. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

25   Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a ligand or fragment thereof, a natural substrate, or a structural or functional mimetic. (See, Coligan et al., (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or to at least a fragment of the receptor, e.g., the active site. In either case, the molecule can be rationally designed using known techniques.

30   Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing the polypeptide or cell membrane fractions which contain the expressed polypeptide are then contacted with a test compound and binding, stimulation, or inhibition of activity of either the polypeptide or the molecule is analyzed.

35   An assay may simply test binding of a candidate compound to the polypeptide, wherein binding

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is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. Alternatively, the assay may assess binding in the presence of a labeled competitor.

Additionally, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply
5   comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay using, e.g., a monoclonal or polyclonal antibody, can measure polypeptide level in a sample. The antibody can measure polypeptide level by either binding, directly
10   or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of the above assays can be used in a diagnostic or prognostic context. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from
15   suitably manipulated cells or tissues.

Transcript Imaging and Toxicological Testing

Another embodiment relates to the use of sptm to develop a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell
20   type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a
25   particular tissue or cell type. In an embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity pertaining to cell signaling.

Transcript images which profile sptm expression may be generated using transcripts isolated
30   from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect sptm expression _in vivo_, as in the case of a tissue or biopsy sample, or _in vitro_, as in the case of a cell line.

Transcript images which profile sptm expression may also be used in conjunction with _in vitro_ model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of
35   industrial and naturally-occurring environmental compounds. All compounds induce characteristic

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gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E. F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and Anderson, N. L. (2000) Toxicol. Lett. 112-113:467-71, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known

5   toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization

10   procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at

15   http://www.niehs.nih.gov/oc/news/toxchip.htm.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In an embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present

20   invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of SPTM encoded by polynucleotides of the

25   present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by

30   separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, supra). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by

35   staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical

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density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for SPTM to quantify the levels of SPTM expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) Anal. Biochem. 270:103-11; Mendoze, L. G. et al. (1999) Biotechniques 27:778-88). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N. L. and Seilhamer, J. (1997) Electrophoresis 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the SPTM encoded by polynucleotides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the SPTM encoded by polynucleotides of the present invention. The

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amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Transcript images may be used to profile sptm expression in distinct tissue types. This process can be used to determine cell signaling activity in a particular tissue type relative to this activity in a different tissue type. Transcript images may be used to generate a profile of sptm expression characteristic of diseased tissue. Transcript images of tissues before and after treatment may be used for diagnostic purposes, to monitor the progression of disease, and to monitor the efficacy of drug treatments for diseases which affect cell signaling activity.

Transcript images of cell lines can be used to assess cell signaling activity and/or to identify cell lines that lack or misregulate this activity. Such cell lines may then be treated with pharmaceutical agents, and a transcript image following treatment may indicate the efficacy of these agents in restoring desired levels of this activity. A similar approach may be used to assess the toxicity of pharmaceutical agents as reflected by undesirable changes in cell signaling activity. Candidate pharmaceutical agents may be evaluated by comparing their associated transcript images with those of pharmaceutical agents of known effectiveness.

Antisense Molecules

The polynucleotides of the present invention are useful in antisense technology. Antisense technology or therapy relies on the modulation of expression of a target protein through the specific binding of an antisense sequence to a target sequence encoding the target protein or directing its expression. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ; Alama, A. et al. (1997) Pharmacol. Res. 36(3):171-178; Crooke, S.T. (1997) Adv. Pharmacol. 40:1-49; Sharma, H.W. and R. Narayanan (1995) Bioessays 17(12):1055-1063; and Lavrosky, Y. et al. (1997) Biochem. Mol. Med. 62(1):11-22.) An antisense sequence is a polynucleotide sequence capable of specifically hybridizing to at least a portion of the target sequence. Antisense sequences bind to cellular mRNA and/or genomic DNA, affecting translation and/or transcription. Antisense sequences can be DNA, RNA, or nucleic acid mimics and analogs. (See, e.g., Rossi, J.J. et al. (1991) Antisense Res. Dev. 1(3):285-288; Lee, R. et al. (1998) Biochemistry 37(3):900-1010; Pardridge, W.M. et al. (1995) Proc. Natl. Acad. Sci. USA 92(12):5592-5596; and Nielsen, P. E. and Haaima, G. (1997) Chem. Soc. Rev. 96:73-78.) Typically, the binding which results in modulation of expression occurs through hybridization or binding of complementary base pairs. Antisense sequences can also bind to DNA duplexes through specific interactions in the major groove of the double helix.

The polynucleotides of the present invention and fragments thereof can be used as antisense

sequences to modify the expression of the polypeptide encoded by sptm. The antisense sequences can be produced ex vivo, such as by using any of the ABI nucleic acid synthesizer series (Applied Biosystems) or other automated systems known in the art. Antisense sequences can also be produced biologically, such as by transforming an appropriate host cell with an expression vector containing the

5   sequence of interest. (See, e.g., Agrawal, supra.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g.,

10   Slater, J.E., et al. (1998) J. Allergy Clin. Immunol. 102(3):469-475; and Scanlon, K.J., et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) Blood 76:271; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY; Uckert, W. and W. Walther (1994) Pharmacol. Ther. 63(3):323-347.) Other gene delivery

15   mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) Br. Med. Bull. 51(1):217-225; Boado, R.J. et al. (1998) J. Pharm. Sci. 87(11):1308-1315; and Morris, M.C. et al. (1997) Nucleic Acids Res. 25(14):2730-2736.)

Expression

20   In order to express a biologically active SPTM, the nucleotide sequences encoding SPTM or fragments thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding SPTM and appropriate transcriptional and

25   translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, supra, Chapters 4, 8, 16, and 17; and Ausubel, supra, Chapters 9, 10, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding SPTM. These include, but are not limited to, microorganisms such as bacteria transformed

30   with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal (mammalian) cell systems. (See, e.g., Sambrook, supra; Ausubel, 1995, supra, Van Heeke, G.

35   and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Bitter, G.A. et al. (1987) Methods Enzymol.

153:516-544; Scorer, C.A. et al. (1994) Bio/Technology 12:181-184; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105;

5   The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola,

10   M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al., (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

For long term production of recombinant proteins in mammalian systems, stable expression of

15   SPTM in cell lines is preferred. For example, sequences encoding SPTM can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Any number of selection systems may be used to recover transformed cell lines. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.; Wigler, M. et al. (1980) Proc. Natl.

20   Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14; Hartman, S.C. and R.C.Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051; Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Therapeutic Uses of sptm

25   The polynucleotides encoding SPTM of the invention may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al.

30   (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and Somia, N. (1997) Nature 389:239-242)), (ii) express a conditionally

35   lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or

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(iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and

5 protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in sptm expression or regulation causes disease, the expression of sptm from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in sptm

10 are treated by constructing mammalian expression vectors comprising sptm and introducing these vectors by mechanical means into sptm-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and Anderson, W.F. (1993) Annu. Rev. Biochem. 62:191-

15 217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and Récipon, H. (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of sptm include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF,

20 PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). The sptm of the invention may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β-actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and Bujard, H. (1992) Proc. Natl. Acad. Sci. U.S.A. 89:5547-5551; Gossen, M. et al., (1995) Science 268:1766-1769; Rossi, F.M.V. and Blau,

25 H.M. (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding SPTM from a normal individual.

30 Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and Eb, A.J. (1973) Virology 52:456-467), or by electroporation (Neumann, E. et al.

35 (1982) EMBO J. 1:841-845). The introduction of DNA to primary cells involves modification of these

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standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to sptm expression are treated by constructing a retrovirus vector consisting of (i) sptm under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii)

5   appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. U.S.A. 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL)

10   that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and Miller, A.D. (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high

15   transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4+ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997)

20   J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. U.S.A. 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver sptm to cells which have one or more genetic abnormalities with respect to the expression of sptm. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in

25   the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544

30   and Verma, I.M. and Somia, N. (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver sptm to target cells which have one or more genetic abnormalities with respect to the expression of sptm. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing sptm to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of

35   herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent

herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res.169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number

5   5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W. F. et al. 1999 J. Virol. 73:519-532 and Xu, H. et al., (1994) Dev. Biol. 163:152-161, hereby

10 incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to

15 deliver sptm to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and Li, K-J. (1998) Curr. Opin. Biotech. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of capsid

20 proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting sptm into the alphavirus genome in place of the capsid-coding region results in the production of a large number of sptm RNAs and the synthesis of high levels of SPTM in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of

25 Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of sptm into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA

30 transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Antibodies

Anti-SPTM antibodies may be used to analyze protein expression levels. Such antibodies

35 include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, and Fab fragments. For

47

descriptions of and protocols of antibody technologies, see, e.g., Pound J.D. (1998) Immunochemical Protocols, Humana Press, Totowa, NJ.

The amino acid sequence encoded by the sptm of the Sequence Listing may be analyzed by appropriate software (e.g., LASERGENE NAVIGATOR software, DNASTAR) to determine

5   regions of high immunogenicity. The optimal sequences for immunization are selected from the C-terminus, the N-terminus, and those intervening, hydrophilic regions of the polypeptide which are likely to be exposed to the external environment when the polypeptide is in its natural conformation. Analysis used to select appropriate epitopes is also described by Ausubel (1997, supra, Chapter 11.7). Peptides used for antibody induction do not need to have biological activity; however, they should be

10   antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids, and most preferably at least 15 amino acids. A peptide which mimics an antigenic fragment of the natural polypeptide may be fused with another protein such as keyhole limpet hemocyanin (KLH; Sigma, St. Louis MO) for antibody production. A peptide encompassing an antigenic region may be expressed from an sptm, synthesized

15   as described above, or purified from human cells.

Procedures well known in the art may be used for the production of antibodies. Various hosts including mice, goats, and rabbits, may be immunized by injection with a peptide. Depending on the host species, various adjuvants may be used to increase immunological response.

In one procedure, peptides about 15 residues in length may be synthesized using an ABI 431A

20   peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (Ausubel, 1995, supra). Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for antipeptide activity by binding the peptide to plastic, blocking with 1% bovine serum albumin (BSA), reacting with rabbit antisera, washing, and reacting with radioiodinated goat anti-rabbit IgG.

25   Antisera with antipeptide activity are tested for anti-SPTM activity using protocols well known in the art, including ELISA, radioimmunoassay (RIA), and immunoblotting.

In another procedure, isolated and purified peptide may be used to immunize mice (about 100 μg of peptide) or rabbits (about 1 mg of peptide). Subsequently, the peptide is radioiodinated and used to screen the immunized animals' B-lymphocytes for production of antipeptide antibodies. Positive

30   cells are then used to produce hybridomas using standard techniques. About 20 mg of peptide is sufficient for labeling and screening several thousand clones. Hybridomas of interest are detected by screening with radioiodinated peptide to identify those fusions producing peptide-specific monoclonal antibody. In a typical protocol, wells of a multi-well plate (FAST, Becton-Dickinson, Palo Alto, CA) are coated with affinity-purified, specific rabbit-anti-mouse (or suitable anti-species IgG) antibodies at

35   10 mg/ml. The coated wells are blocked with 1% BSA and washed and exposed to supernatants from

hybridomas. After incubation, the wells are exposed to radiolabeled peptide at 1 mg/ml.

Clones producing antibodies bind a quantity of labeled peptide that is detectable above background. Such clones are expanded and subjected to 2 cycles of cloning. Cloned hybridomas are injected into pristane-treated mice to produce ascites, and monoclonal antibody is purified from the

5   ascitic fluid by affinity chromatography on protein A (Amersham Pharmacia Biotech). Several procedures for the production of monoclonal antibodies, including in vitro production, are described in Pound (supra). Monoclonal antibodies with antipeptide activity are tested for anti-SPTM activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

Antibody fragments containing specific binding sites for an epitope may also be generated.

10 For example, such fragments include, but are not limited to, the F(ab')2 fragments produced by pepsin digestion of the antibody molecule, and the Fab fragments generated by reducing the disulfide bridges of the F(ab')2 fragments. Alternatively, construction of Fab expression libraries in filamentous bacteriophage allows rapid and easy identification of monoclonal fragments with desired specificity (Pound, supra, Chaps. 45-47). Antibodies generated against polypeptide encoded by sptm can be used

15 to purify and characterize full-length SPTM protein and its activity, binding partners, etc.

Assays Using Antibodies

Anti-SPTM antibodies may be used in assays to quantify the amount of SPTM found in a particular human cell. Such assays include methods utilizing the antibody and a label to detect

20 expression level under normal or disease conditions. The peptides and antibodies of the invention may be used with or without modification or labeled by joining them, either covalently or noncovalently, with a reporter molecule.

Protocols for detecting and measuring protein expression using either polyclonal or monoclonal antibodies are well known in the art. Examples include ELISA, RIA, and fluorescent activated cell

25 sorting (FACS). Such immunoassays typically involve the formation of complexes between the SPTM and its specific antibody and the measurement of such complexes. These and other assays are described in Pound (supra).

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following embodiments are, therefore,

30 to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

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35 whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, including U.S. Application Ser. No. 60/280,067, U.S. Application Ser. No. 60/280,068, U.S. Application Ser. No.60/291,280, U.S. Application Ser. No. 60/291,849, U.S. Application Ser. No. 60/291,829, U.S. Application Ser. No. 60/299,428, U.S. Application Ser. No. 60/300,001, and U.S.

5   Application Ser. No. 60/299,776, are hereby expressly incorporated by reference herein.

EXAMPLES

I.   Construction of cDNA Libraries

RNA was purchased from CLONTECH Laboratories, Inc. (Palo Alto CA) or isolated from

10   various tissues. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated with either isopropanol or sodium acetate and ethanol, or by other routine methods.

15   Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In most cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega Corporation (Promega), Madison WI), OLIGOTEX latex particles (QIAGEN, Inc. (QIAGEN), Valencia CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other

20   RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Inc., Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene Cloning Systems, Inc. (Stratagene), La Jolla CA) or SUPERSCRIPT plasmid system (Life Technologies), using the recommended procedures or similar

25   methods known in the art. (See, e.g., Ausubel, 1997, supra, Chapters 5.1 through 6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography

30   (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), PCR2-TOPOTA plasmid (Invitrogen), PCMV-ICIS plasmid (Stratagene), pIGEN (Incyte Genomics, Palo Alto CA), pRARE (Incyte Genomics), or

35   pINCY (Incyte Genomics), or derivatives thereof. Recombinant plasmids were transformed into

competent E. coli cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5α, DH10B, or ElectroMAX DH10B from Life Technologies.

II.   Isolation of cDNA Clones

5   Plasmids were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: the Magic or WIZARD Minipreps DNA purification system (Promega); the AGTC Miniprep purification kit (Edge BioSystems, Gaithersburg MD); and the QIAWELL 8, QIAWELL 8 Plus, and QIAWELL 8 Ultra plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit (QIAGEN). Following 10   precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4 °C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format. (Rao, V.B. (1994) Anal. Biochem. 216:1-14.) Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 15   384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Inc. (Molecular Probes), Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III.   Sequencing and Analysis

20   cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 thermal cycler (Applied Biosystems) or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific Corp., Sunnyvale CA) or the MICROLAB 2200 liquid transfer system (Hamilton). cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or 25   supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence 30   analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, Chapter 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

IV.   Assembly and Analysis of Sequences

35   Component sequences from chromatograms were subject to PHRED analysis and assigned a

quality score. The sequences having at least a required quality score were subject to various pre-processing editing pathways to eliminate, e.g., low quality 3' ends, vector and linker sequences, polyA tails, Alu repeats, mitochondrial and ribosomal sequences, bacterial contamination sequences, and sequences smaller than 50 base pairs. In particular, low-information sequences and repetitive

5   elements (e.g., dinucleotide repeats, Alu repeats, etc.) were replaced by "n's", or masked, to prevent spurious matches.

Processed sequences were then subject to assembly procedures in which the sequences were assigned to gene bins (bins). Each sequence could only belong to one bin. Sequences in each gene bin were assembled to produce consensus sequences (templates). Subsequent new sequences were

10 added to existing bins using BLASTN (v.1.4 WashU) and CROSSMATCH. Candidate pairs were identified as all BLAST hits having a quality score greater than or equal to 150. Alignments of at least 82% local identity were accepted into the bin. The component sequences from each bin were assembled using a version of PHRAP. Bins with several overlapping component sequences were assembled using DEEP PHRAP. The orientation (sense or antisense) of each assembled template

15 was determined based on the number and orientation of its component sequences. Template sequences as disclosed in the sequence listing correspond to sense strand sequences (the "forward" reading frames), to the best determination. The complementary (antisense) strands are inherently disclosed herein. The component sequences which were used to assemble each template consensus sequence are listed in Table 3 by their positions along the template nucleotide sequences.

20 Bins were compared against each other and those having local similarity of at least 82% were combined and reassembled. Reassembled bins having templates of insufficient overlap (less than 95% local identity) were re-split. Assembled templates were also subject to analysis by STITCHER/EXON MAPPER algorithms which analyze the probabilities of the presence of splice variants, alternatively spliced exons, splice junctions, differential expression of alternative spliced

25 genes across tissue types or disease states, etc. These resulting bins were subject to several rounds of the above assembly procedures.

Once gene bins were generated based upon sequence alignments, bins were clone joined based upon clone information. If the 5' sequence of one clone was present in one bin and the 3' sequence from the same clone was present in a different bin, it was likely that the two bins actually

30 belonged together in a single bin. The resulting combined bins underwent assembly procedures to regenerate the consensus sequences.

The final assembled templates were subsequently annotated using the following procedure. Template sequences were analyzed using BLASTN (v2.0, NCBI) versus gbpri (GenBank version 128). "Hits" were defined as an exact match having from 95% local identity over 200 base pairs

35 through 100% local identity over 100 base pairs, or a homolog match having an E-value, i.e. a

probability score, of $\leq 1 \times 10^{-8}$. The hits were subject to frameshift FASTx versus GENPEPT (GenBank version 128). (See Table 6). In this analysis, a homolog match was defined as having an E-value of $\leq 1 \times 10^{-8}$. The assembly method used above was described in "System and Methods for Analyzing Biomolecular Sequences," U.S.S.N. 09/276,534, filed March 25, 1999, and the LIFESEQ

5   Gold user manual (Incyte) both incorporated by reference herein.

Following assembly, template sequences were subjected to motif, BLAST, and functional analyses, and categorized in protein hierarchies using methods described in, e.g., "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S. Patent Number 6,023,659; "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845,

10   filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S. Patent Number 5,953,727; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein.

The template sequences were further analyzed by translating each template in all three

15   forward reading frames and searching each translation against the Pfam database of hidden Markov model-based protein families and domains using the HMMER software package (available to the public from Washington University School of Medicine, St. Louis MO). (See also World Wide Web site http://pfam.wustl.edu/ for detailed descriptions of Pfam protein domains and families.)

Additionally, the template sequences were translated in all three forward reading frames, and .

20   each translation was searched against hidden Markov models for signal peptides using the HMMER software package. Construction of hidden Markov models and their usage in sequence analysis has been described. (See, for example, Eddy, S.R. (1996) Curr. Opin. Str. Biol. 6:361-365.) Only those signal peptide hits with a cutoff score of 11 bits or greater are reported. A cutoff score of 11 bits or greater corresponds to at least about 91-94% true-positives in signal peptide prediction. Template

25   sequences were also translated in all three forward reading frames, and each translation was searched against TMHMMER, a program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation (Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA,

30   pp. 175-182.) Regions of templates which, when translated, contain similarity to signal peptide or transmembrane consensus sequences are reported in Table 2.

Template sequences are further analyzed using the bioinformatics tools listed in Table 6, or using sequence analysis software known in the art such as MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR).

35   Template sequences may be further queried against public databases such as the GenBank rodent,

mammalian, vertebrate, prokaryote, and eukaryote databases.

The template sequences were translated to derive the corresponding longest open reading frame as presented by the polypeptide sequences as reported in Table 5. Alternatively, a polypeptide of the invention may begin at any of the methionine residues within the full length translated

5   polypeptide. Polypeptide sequences were subsequently analyzed by querying against the GenBank protein database (GENPEPT, (GenBank version 128)). Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the

10   MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 5 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (GENPEPT) database. Column 1 shows the polypeptide sequence identification number (SEQ ID NO:) for the polypeptide segments of the

15   invention. Column 2 shows the reading frame used in the translation of the polynucleotide sequences encoding the polypeptide segments. Column 3 shows the length of the translated polypeptide segments. Columns 4 and 5 show the start and stop nucleotide positions of the polynucleotide sequences encoding the polypeptide segments. Column 6 shows the GenBank identification number (GI Number) of the nearest GenBank homolog. Column 7 shows the probability score for the match

20   between each polypeptide and its GenBank homolog. Column 8 shows the annotation of the GenBank homolog.

V.   Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a

25   gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is

30   much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

<u>BLAST Score x Percent Identity</u>

5 x minimum {length(Seq. 1), length(Seq. 2)}

The product score takes into account both the degree of similarity between two sequences and the
5   length of the sequence match. The product score is a normalized value between 0 and 100, and is
calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the
product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is
calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair
(HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by
10   gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate
the product score. The product score represents a balance between fractional overlap and quality in a
BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the
entire length of the shorter of the two sequences being compared. A product score of 70 is produced
either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the
15   other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79%
identity and 100% overlap.

Alternatively, polynucleotide sequences encoding SPTM are analyzed with respect to the
tissue sources from which they were derived. Polynucleotide sequences encoding SPTM were
assembled, at least in part, with overlapping Incyte cDNA sequences. Each cDNA sequence is
20   derived from a cDNA library constructed from a human tissue. Each human tissue is classified into
one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive
system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male;
germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas;
respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract.
25   The number of libraries in each category for each polynucleotide sequence encoding SPTM is counted
and divided by the total number of libraries across all categories for each polynucleotide sequence
encoding SPTM. Similarly, each human tissue is classified into one of the following disease/condition
categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled,
and other, and the number of libraries in each category for each polynucleotide sequence encoding
30   SPTM is counted and divided by the total number of libraries across all categories for each
polynucleotide sequence encoding SPTM. The resulting percentages reflect the tissue-specific and
disease-specific expression of cDNA encoding SPTM. Percentage values of tissue-specific
expression are reported in . cDNA sequences and cDNA library/tissue information are found in the
LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

35

VI.   Tissue Distribution Profiling

A tissue distribution profile is determined for each template by compiling the cDNA library tissue classifications of its component cDNA sequences. Each component sequence, is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the
5   following categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. Template sequences, component sequences, and cDNA library/tissue information are found in the LIFESEQ GOLD
10   database (Incyte Genomics, Palo Alto CA).

shows the tissue distribution profile for the templates of the invention. For each template, the three most frequently observed tissue categories are shown in column 2, along with the percentage of component sequences belonging to each category. Only tissue categories with percentage values of ≥10% are shown. A tissue distribution of "widely distributed" in column 2 indicates percentage values
15   of <10% in all tissue categories.

VII.   Transcript Image Analysis

Transcript images are generated as described in Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, incorporated herein by reference.
20

VIII.   Extension of Polynucleotide Sequences and Isolation of a Full-length cDNA

Oligonucleotide primers designed using an sptm of the Sequence Listing are used to extend the nucleic acid sequence. One primer is synthesized to initiate 5' extension of the template, and the other primer, to initiate 3' extension of the template. The initial primers may be designed using OLIGO
25   4.06 software (National Biosciences, Inc. (National Biosciences), Plymouth MN), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68 °C to about 72 °C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations are avoided. Selected human cDNA libraries are used to extend the sequence. If more than one
30   extension is necessary or desired, additional or nested sets of primers are designed.

High fidelity amplification is obtained by PCR using methods well known in the art. PCR is performed in 96-well plates using the PTC-200 thermal cycler (MJ Research). The reaction mix contains DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+}, $(NH_4)_2SO_4$, and ß-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life
35   Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair

PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ are as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times;

5   Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well is determined by dispensing 100 μl PICOGREEN quantitation reagent (0.25% (v/v); Molecular Probes) dissolved in 1X Tris-EDTA (TE) and 0.5 μl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Incorporated (Corning), Corning NY), allowing the DNA to bind to the reagent. The plate is scanned in a FLUOROSKAN II

10   (Labsystems Oy) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μl to 10 μl aliquot of the reaction mixture is analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions are successful in extending the sequence.

The extended nucleotides are desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and

15   sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides are separated on low concentration (0.6 to 0.8%) agarose gels, fragments are excised, and agar digested with AGAR ACE (Promega). Extended clones are religated using T4 ligase (New England Biolabs, Inc., Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction

20   site overhangs, and transfected into competent E. coli cells. Transformed cells are selected on antibiotic-containing media, individual colonies are picked and cultured overnight at 37°C in 384-well plates in LB/2x carbenicillin liquid media.

The cells are lysed, and DNA is amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1:

25   94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA is quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries are reamplified using the same conditions as described above. Samples are diluted with 20% dimethysulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC

30   DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

In like manner, the sptm is used to obtain regulatory sequences (promoters, introns, and enhancers) using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

35

IX.   Labeling of Probes and Southern Hybridization Analyses

Hybridization probes derived from the sptm of the Sequence Listing are employed for
screening cDNAs, mRNAs, or genomic DNA. The labeling of probe nucleotides between 100 and
1000 nucleotides in length is specifically described, but essentially the same procedure may be used

5   with larger cDNA fragments. Probe sequences are labeled at room temperature for 30 minutes using
a T4 polynucleotide kinase, γ^{32}P-ATP, and 0.5X One-Phor-All Plus (Amersham Pharmacia Biotech)
buffer and purified using a ProbeQuant G-50 Microcolumn (Amersham Pharmacia Biotech). The
probe mixture is diluted to 10^7 dpm/μg/ml hybridization buffer and used in a typical membrane-based
hybridization analysis.

10   The DNA is digested with a restriction endonuclease such as Eco RV and is electrophoresed
through a 0.7% agarose gel. The DNA fragments are transferred from the agarose to nylon
membrane (NYTRAN Plus, Schleicher & Schuell, Inc., Keene NH) using procedures specified by the
manufacturer of the membrane. Prehybridization is carried out for three or more hours at 68°C, and
hybridization is carried out overnight at 68°C. To remove non-specific signals, blots are sequentially

15   washed at room temperature under increasingly stringent conditions, up to 0.1x saline sodium citrate
(SSC) and 0.5% sodium dodecyl sulfate. After the blots are placed in a PHOSPHORIMAGER
cassette (Molecular Dynamics) or are exposed to autoradiography film, hybridization patterns of
standard and experimental lanes are compared. Essentially the same procedure is employed when
screening RNA.

20

X.   Chromosome Mapping of sptm

The cDNA sequences which were used to assemble SEQ ID NO:1-567 are compared with
sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other
implementations of the Smith-Waterman algorithm. Sequences from these databases that match SEQ

25   ID NO:1-567 are assembled into clusters of contiguous and overlapping sequences using assembly
algorithms such as PHRAP (Table 6). Radiation hybrid and genetic mapping data available from
public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for
Genome Research (WIGR), and Généthon are used to determine if any of the clustered sequences
have been previously mapped. Inclusion of a mapped sequence in a cluster will result in the

30   assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location.
The genetic map locations of SEQ ID NO:1-567 are described as ranges, or intervals, of human
chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus
of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on
recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to

35   1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of

recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters.

XI.   Microarray Analysis

5   <u>Probe Preparation from Tissue or Cell Samples</u>

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and polyA$^+$ RNA is purified using the oligo (dT) cellulose method. Each polyA$^+$ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/μl oligo-dT primer (21mer), 1X first strand buffer, 0.03 units/μl RNase inhibitor, 500 μM dATP, 500 μM dGTP, 500 μM dTTP, 40 μM dCTP, 40

10   μM dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng polyA$^+$ RNA with GEMBRIGHT kits (Incyte). Specific control polyA$^+$ RNAs are synthesized by <u>in vitro</u> transcription from non-coding yeast genomic DNA (W. Lei, unpublished). As quantitative controls, the control mRNAs at 0.002 ng, 0.02 ng, 0.2 ng, and 2 ng are diluted into reverse transcription reaction at ratios of 1:100,000, 1:10,000,

15   1:1000, 1:100 (w/w) to sample mRNA respectively. The control mRNAs are diluted into reverse transcription reaction at ratios of 1:3, 3:1, 1:10, 10:1, 1:25, 25:1 (w/w) to sample mRNA differential expression patterns. After incubation at 37°C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85°C to the stop the reaction and degrade the RNA. Probes are purified using two

20   successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The probe is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μl 5X SSC/0.2% SDS.

25

<u>Microarray Preparation</u>

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are

30   amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 μg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR

35   Scientific Products Corporation (VWR), West Chester, PA), washed extensively in distilled water, and

coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 μl of the array element DNA, at an average concentration of 100 ng/μl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford, MA) for 30 minutes at 60°C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 μl of probe mixture consisting of 0.2 μg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The probe mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm^2 coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 μl of 5x SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is

typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the probe mix at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two probes from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood, MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot. is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XII.   Complementary Nucleic Acids

Sequences complementary to the sptm are used to detect, decrease, or inhibit expression of the naturally occurring nucleotide. The use of oligonucleotides comprising from about 15 to 30 base pairs is typical in the art. However, smaller or larger sequence fragments can also be used. Appropriate oligonucleotides are designed from the sptm using OLIGO 4.06 software (National Biosciences) or other appropriate programs and are synthesized using methods standard in the art or ordered from a commercial supplier. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent transcription factor binding to the promoter sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding and processing of the transcript.

XIII.   Expression of SPTM

Expression and purification of SPTM is accomplished using bacterial or virus-based

expression systems. For expression of SPTM in bacteria, cDNA is subcloned into an appropriate

vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of

cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*)

hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator

5 regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g.,

BL21(DE3). Antibiotic resistant bacteria express SPTM upon induction with isopropyl beta-D-

thiogalactopyranoside (IPTG). Expression of SPTM in eukaryotic cells is achieved by infecting insect

or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus

(AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is

10 replaced with cDNA encoding SPTM by either homologous recombination or bacterial-mediated

transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong

polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to

infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases.

Infection of the latter requires additional genetic modifications to baculovirus. (See e.g., Engelhard,

15 supra; and Sandig, supra.)

In most expression systems, SPTM is synthesized as a fusion protein with, e.g., glutathione S-

transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step,

affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton

enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized

20 glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia

Biotech). Following purification, the GST moiety can be proteolytically cleaved from SPTM at

specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification

using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak

Company, Rochester NY). 6-His, a stretch of six consecutive histidine residues, enables purification

25 on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in

Ausubel (1995, supra, Chapters 10 and 16). Purified SPTM obtained by these methods can be used

directly in the following activity assay.

XIV. Demonstration of SPTM Activity

30 An assay for SPTM activity measures the expression of SPTM on the cell surface. cDNA

encoding SPTM is subcloned into an appropriate mammalian expression vector suitable for high levels

of cDNA expression. The resulting construct is transfected into a nonhuman cell line such as

NIH3T3. Cell surface proteins are labeled with biotin using methods known in the art.

Immunoprecipitations are performed using SPTM-specific antibodies, and immunoprecipitated samples

35 are analyzed using SDS-PAGE and immunoblotting techniques. The ratio of labeled

immunoprecipitant to unlabeled immunoprecipitant is proportional to the amount of SPTM expressed on the cell surface.

Alternatively, an assay for SPTM activity measures the amount of SPTM in secretory, membrane-bound organelles. Transfected cells as described above are harvested and lysed. The lysate is fractionated using methods known to those of skill in the art, for example, sucrose gradient ultracentrifugation. Such methods allow the isolation of subcellular components such as the Golgi apparatus, ER, small membrane-bound vesicles, and other secretory organelles. Immunoprecipitations from fractionated and total cell lysates are performed using SPTM-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The concentration of SPTM in secretory organelles relative to SPTM in total cell lysate is proportional to the amount of SPTM in transit through the secretory pathway.

XV.   Functional Assays

SPTM function is assessed by expressing sptm at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen Corporation, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 µg of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 µg of an additional plasmid containing sequences encoding a marker protein are co-transfected.

Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; CLONTECH), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties.

. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry,

Oxford, New York NY.

The influence of SPTM on gene expression can be assessed using highly purified populations
of cells transfected with sequences encoding SPTM and either CD64 or CD64-GFP. CD64 and
CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human
5   immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using
magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Inc., Lake
Success NY). mRNA can be purified from the cells using methods well known by those of skill in the
art. Expression of mRNA encoding SPTM and other genes of interest can be analyzed by northern
analysis or microarray techniques.

10

XVI. Production of Antibodies

SPTM substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g.,
Harrington, M.G. (1990) Methods Enzymol. 182:488-495), or other purification techniques, can be
used to immunize rabbits and to produce antibodies using standard protocols.
15   Alternatively, the SPTM amino acid sequence is analyzed using LASERGENE software
(DNASTAR) to determine regions of high immunogenicity, and a corresponding peptide is synthesized
and used to raise antibodies by means known to those of skill in the art. Methods for selection of
appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in
the art. (See, e.g., Ausubel, 1995, supra, Chapter 11.)
20   Typically, peptides 15 residues in length are synthesized using an ABI 431A peptide
synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with
N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g.,
Ausubel, supra.) Rabbits are immunized with the peptide-KLH complex in complete Freund's
adjuvant. Resulting antisera are tested for antipeptide activity by, for example, binding the peptide to
25   plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-
iodinated goat anti-rabbit IgG. Antisera with antipeptide activity are tested for anti-SPTM activity
using protocols well known in the art, including ELISA, RIA, and immunoblotting.

XVII. Purification of Naturally Occurring SPTM Using Specific Antibodies

30   Naturally occurring or recombinant SPTM is substantially purified by immunoaffinity
chromatography using antibodies specific for SPTM. An immunoaffinity column is constructed by
covalently coupling anti-SPTM antibody to an activated chromatographic resin, such as
CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is
blocked and washed according to the manufacturer's instructions.
35   Media containing SPTM are passed over the immunoaffinity column, and the column is

64

washed under conditions that allow the preferential absorbance of SPTM (e.g., high ionic strength

buffers in the presence of detergent). The column is eluted under conditions that disrupt

antibody/SPTM binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as

urea or thiocyanate ion), and SPTM is collected.

5

XVIII. Identification of Molecules Which Interact with SPTM

SPTM, or biologically active fragments thereof, are labeled with ^{125}I Bolton-Hunter reagent.

(See, e.g., Bolton, A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules

previously arrayed in the wells of a multi-well plate are incubated with the labeled SPTM, washed,

10   and any wells with labeled SPTM complex are assayed. Data obtained using different concentrations

of SPTM are used to calculate values for the number, affinity, and association of SPTM with the

candidate molecules.

Alternatively, molecules interacting with SPTM are analyzed using the yeast two-hybrid

system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially

15   available kits based on the two-hybrid system, such as the MATCHMAKER system (CLONTECH).

SPTM may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT)

which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions

between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S.

Patent No. 6,057,101).

20

All publications and patents mentioned in the above specification are herein incorporated by

reference. Various modifications and variations of the described method and system of the invention

will be apparent to those skilled in the art without departing from the scope and spirit of the invention.

Although the invention has been described in connection with specific embodiments, it should be

25   understood that the invention as claimed should not be unduly limited to such specific embodiments.

Indeed, various modifications of the above-described modes for carrying out the invention which are

obvious to those skilled in the field of molecular biology or related fields are intended to be within the

scope of the following claims.

30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
1	LG:1041015.22:2001MAR30	568	LG:1041015.22.orf1:2001MAR30
2	LG:106877.10:2001MAR30	569	LG:106877.10.orf3:2001MAR30
3	LG:1138554.16:2001MAR30	570	LG:1138554.16.orf2:2001MAR30
4	LG:1383277.7:2001MAR30	571	LG:1383277.7.orf3:2001MAR30
5	LG:1397614.15:2001MAR30	572	LG:1397614.15.orf1:2001MAR30
6	LG:1399315.8:2001MAR30	573	LG:1399315.8.orf1:2001MAR30
7	LG:198782.1:2001MAR30	574	LG:198782.1.orf2a:2001MAR30
7	LG:198782.1:2001MAR30	575	LG:198782.1.orf2b:2001MAR30
7	LG:198782.1:2001MAR30	576	LG:198782.1.orf3:2001MAR30
8	LG:236046.1:2001MAR30	577	LG:236046.1.orf2:2001MAR30
9	LG:332122.6:2001MAR30	578	LG:332122.6.orf3:2001MAR30
10	LG:345320.16:2001MAR30	579	LG:345320.16.orf1:2001MAR30
11	LG:350827.10:2001MAR30	580	LG:350827.10.orf3:2001MAR30
12	LG:399901.5:2001MAR30	581	LG:399901.5.orf3:2001MAR30
13	LG:404563.1:2001MAR30	582	LG:404563.1.orf2:2001MAR30
14	LG:977812.15:2001MAR30	583	LG:977812.15.orf2:2001MAR30
15	LG:983810.1:2001MAR30	584	LG:983810.1.orf1:2001MAR30
16	LG:984488.1:2001MAR30	585	LG:984488.1.orf1:2001MAR30
17	LG:011606.1:2001MAR30	586	LG:011606.1.orf1:2001MAR30
18	LG:025465.5:2001MAR30	587	LG:025465.5.orf1:2001MAR30
19	LG:025724.10:2001MAR30	588	LG:025724.10.orf3:2001MAR30
20	LG:1095426.1:2001MAR30	589	LG:1095426.1.orf3:2001MAR30
21	LG:1132418.1:2001MAR30	590	LG:1132418.1.orf2:2001MAR30
22	LG:1377900.14:2001MAR30	591	LG:1377900.14.orf3:2001MAR30
23	LG:1383812.1:2001MAR30	592	LG:1383812.1.orf2:2001MAR30
24	LG:1468687.1:2001MAR30	593	LG:1468687.1.orf3:2001MAR30
25	LG:1505513.1:2001MAR30	594	LG:1505513.1.orf1:2001MAR30
26	LG:178823.9:2001MAR30	595	LG:178823.9.orf2:2001MAR30
27	LG:198342.3:2001MAR30	596	LG:198342.3.orf3:2001MAR30
28	LG:210672.1:2001MAR30	597	LG:210672.1.orf1:2001MAR30
29	LG:212823.8:2001MAR30	598	LG:212823.8.orf1:2001MAR30
30	LG:220495.9:2001MAR30	599	LG:220495.9.orf2:2001MAR30
31	LG:238262.1:2001MAR30	600	LG:238262.1.orf3:2001MAR30
32	LG:239410.21:2001MAR30	601	LG:239410.21.orf2:2001MAR30
33	LG:245854.7:2001MAR30	602	LG:245854.7.orf3:2001MAR30
34	LG:294697.1:2001MAR30	603	LG:294697.1.orf3:2001MAR30
35	LG:345884.1:2001MAR30	604	LG:345884.1.orf1:2001MAR30
36	LG:400095.15:2001MAR30	605	LG:400095.15.orf1:2001MAR30
37	LG:402180.1:2001MAR30	606	LG:402180.1.orf3:2001MAR30
38	LG:403401.1:2001MAR30	607	LG:403401.1.orf3:2001MAR30
39	LG:411327.29:2001MAR30	608	LG:411327.29.orf1:2001MAR30
40	LG:417464.10:2001MAR30	609	LG:417464.10.orf2:2001MAR30
41	LG:481997.1:2001MAR30	610	LG:481997.1.orf1:2001MAR30
42	LG:979304.7:2001MAR30	611	LG:979304.7.orf3:2001MAR30
43	LG:997964.1:2001MAR30	612	LG:997964.1.orf3:2001MAR30
44	LG:998845.1:2001MAR30	613	LG:998845.1.orf2:2001MAR30
45	LG:000014.1:2001MAR30	614	LG:000014.1.orf1:2001MAR30
46	LG:000290.9:2001MAR30	615	LG:000290.9.orf1:2001MAR30
47	LG:001923.1:2001MAR30	616	LG:001923.1.orf3a:2001MAR30
47	LG:001923.1:2001MAR30	617	LG:001923.1.orf3b:2001MAR30
48	LG:008606.21:2001MAR30	618	LG:008606.21.orf3:2001MAR30
49	LG:009699.32:2001MAR30	619	LG:009699.32.orf3:2001MAR30
50	LG:016723.6:2001MAR30	620	LG:016723.6.orf1:2001MAR30
51	LG:017126.5:2001MAR30	621	LG:017126.5.orf2:2001MAR30 .

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
52	LG:019362.10:2001MAR30	622	LG:019362.10.orf1:2001MAR30
53	LG:022183.1:2001MAR30	623	LG:022183.1.orf2:2001MAR30
54	LG:028493.1:2001MAR30	624	LG:028493.1.orf3:2001MAR30
55	LG:034197.1:2001MAR30	625	LG:034197.1.orf2:2001MAR30
56	LG:054096.31:2001MAR30	626	LG:054096.31.orf1:2001MAR30
57	LG:054807.3:2001MAR30	627	LG:054807.3.orf2:2001MAR30
58	LG:065873.12:2001MAR30	628	LG:065873.12.orf2:2001MAR30
59	LG:083814.6:2001MAR30	629	LG:083814.6.orf1:2001MAR30
59	LG:083814.6:2001MAR30	630	LG:083814.6.orf2:2001MAR30
60	LG:093477.1:2001MAR30	631	LG:093477.1.orf3:2001MAR30
61	LG:099572.12:2001MAR30	632	LG:099572.12.orf1:2001MAR30
62	LG:100396.31:2001MAR30	633	LG:100396.31.orf3:2001MAR30
63	LG:1026903.5:2001MAR30	634	LG:1026903.5.orf2:2001MAR30
63	LG:1026903.5:2001MAR30	635	LG:1026903.5.orf3:2001MAR30
64	LG:1060168.6:2001MAR30	636	LG:1060168.6.orf1:2001MAR30
65	LG:1086906.41:2001MAR30	637	LG:1086906.41.orf1:2001MAR30
66	LG:1089326.18:2001MAR30	638	LG:1089326.18.orf2:2001MAR30
67	LG:1090862.32:2001MAR30	639	LG:1090862.32.orf3:2001MAR30
68	LG:1091941.41:2001MAR30	640	LG:1091941.41.orf3:2001MAR30
69	LG:1093386.8:2001MAR30	641	LG:1093386.8.orf2:2001MAR30
70	LG:1094187.33:2001MAR30	642	LG:1094187.33.orf3:2001MAR30
71	LG:1098692.18:2001MAR30	643	LG:1098692.18.orf2:2001MAR30
72	LG:1173104.22:2001MAR30	644	LG:1173104.22.orf3:2001MAR30
73	LG:1215335.7:2001MAR30	645	LG:1215335.7.orf1:2001MAR30
74	LG:1256753.1:2001MAR30	646	LG:1256753.1.orf2:2001MAR30
75	LG:1326702.10:2001MAR30	647	LG:1326702.10.orf2:2001MAR30
76	LG:1327239.15:2001MAR30	648	LG:1327239.15.orf2:2001MAR30
77	LG:1327867.15:2001MAR30	649	LG:1327867.15.orf2:2001MAR30
78	LG:1383232.1:2001MAR30	650	LG:1383232.1.orf1:2001MAR30
79	LG:1383368.40:2001MAR30	651	LG:1383368.40.orf2:2001MAR30
80	LG:1384477.1:2001MAR30	652	LG:1384477.1.orf2:2001MAR30
81	LG:1390822.1:2001MAR30	653	LG:1390822.1.orf1:2001MAR30
82	LG:1398274.13:2001MAR30	654	LG:1398274.13.orf3:2001MAR30
83	LG:1398646.1:2001MAR30	655	LG:1398646.1.orf2:2001MAR30
84	LG:1398905.1:2001MAR30	656	LG:1398905.1.orf1:2001MAR30
84	LG:1398905.1:2001MAR30	657	LG:1398905.1.orf2:2001MAR30
85	LG:1399785.1:2001MAR30	658	LG:1399785.1.orf1:2001MAR30
86	LG:1446193.10:2001MAR30	659	LG:1446193.10.orf1:2001MAR30
87	LG:1446210.8:2001MAR30	660	LG:1446210.8.orf1:2001MAR30
88	LG:1450054.6:2001MAR30	661	LG:1450054.6.orf2:2001MAR30
89	LG:1452516.4:2001MAR30	662	LG:1452516.4.orf3:2001MAR30
90	LG:1455293.7:2001MAR30	663	LG:1455293.7.orf2:2001MAR30
91	LG:1498113.1:2001MAR30	664	LG:1498113.1.orf1:2001MAR30
92	LG:1500042.1:2001MAR30	665	LG:1500042.1.orf1:2001MAR30
93	LG:1500434.4:2001MAR30	666	LG:1500434.4.orf3:2001MAR30
94	LG:1501102.4:2001MAR30	667	LG:1501102.4.orf3:2001MAR30
95	LG:1501768.2:2001MAR30	668	LG:1501768.2.orf1:2001MAR30
96	LG:1502155.6:2001MAR30	669	LG:1502155.6.orf1:2001MAR30
97	LG:1512304.2:2001MAR30	670	LG:1512304.2.orf3:2001MAR30
98	LG:1512931.11:2001MAR30	671	LG:1512931.11.orf3:2001MAR30
99	LG:155076.18:2001MAR30	672	LG:155076.18.orf3:2001MAR30
100	LG:159111.41:2001MAR30	673	LG:159111.41.orf3:2001MAR30
101	LG:170604.1:2001MAR30	674	LG:170604.1.orf3:2001MAR30
102	LG:190477.4:2001MAR30	675	LG:190477.4.orf3:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
103	LG:198087.8:2001MAR30	676	LG:198087.8.orf2:2001MAR30
104	LG:198743.2:2001MAR30	677	LG:198743.2.orf3:2001MAR30
105	LG:199194.1:2001MAR30	678	LG:199194.1.orf2:2001MAR30
106	LG:200727.6:2001MAR30	679	LG:200727.6.orf2:2001MAR30
107	LG:201572.20:2001MAR30	680	LG:201572.20.orf1:2001MAR30
108	LG:201669.25:2001MAR30	681	LG:201669.25.orf3:2001MAR30
109	LG:208588.4:2001MAR30	682	LG:208588.4.orf1:2001MAR30
110	LG:210412.29:2001MAR30	683	LG:210412.29.orf1:2001MAR30
111	LG:215051.15:2001MAR30	684	LG:215051.15.orf1:2001MAR30
112	LG:215475.21:2001MAR30	685	LG:215475.21.orf1:2001MAR30
113	LG:224523.1:2001MAR30	686	LG:224523.1.orf1:2001MAR30
114	LG:228186.1:2001MAR30	687	LG:228186.1.orf2:2001MAR30
115	LG:233138.2:2001MAR30	688	LG:233138.2.orf2:2001MAR30
116	LG:234811.10:2001MAR30	689	LG:234811.10.orf2:2001MAR30
117	LG:236092.1:2001MAR30	690	LG:236092.1.orf2:2001MAR30
118	LG:236098.12:2001MAR30	691	LG:236098.12.orf1:2001MAR30
119	LG:236697.15:2001MAR30	692	LG:236697.15.orf1:2001MAR30
120	LG:237503.21:2001MAR30	693	LG:237503.21.orf3:2001MAR30
121	LG:238023.7:2001MAR30	694	LG:238023.7.orf2:2001MAR30
122	LG:238209.1:2001MAR30	695	LG:238209.1.orf2:2001MAR30
123	LG:238456.10:2001MAR30	696	LG:238456.10.orf3:2001MAR30
124	LG:239245.1:2001MAR30	697	LG:239245.1.orf3:2001MAR30
125	LG:239579.8:2001MAR30	698	LG:239579.8.orf3:2001MAR30
126	LG:239601.22:2001MAR30	699	LG:239601.22.orf1:2001MAR30
126	LG:239601.22:2001MAR30	700	LG:239601.22.orf3:2001MAR30
127	LG:240121.1:2001MAR30	701	LG:240121.1.orf3:2001MAR30
128	LG:241110.2:2001MAR30	702	LG:241110.2.orf3:2001MAR30
129	LG:244948.4:2001MAR30	703	LG:244948.4.orf3:2001MAR30
130	LG:245378.6:2001MAR30	704	LG:245378.6.orf3:2001MAR30
131	LG:248203.9:2001MAR30	705	LG:248203.9.orf1:2001MAR30
132	LG:249247.1:2001MAR30	706	LG:249247.1.orf3:2001MAR30
133	LG:267153.16:2001MAR30	707	LG:267153.16.orf2:2001MAR30
134	LG:291759.5:2001MAR30	708	LG:291759.5.orf2:2001MAR30
135	LG:298102.1:2001MAR30	709	LG:298102.1.orf1:2001MAR30
136	LG:308891.1:2001MAR30	710	LG:308891.1.orf2:2001MAR30
137	LG:312668.4:2001MAR30	711	LG:312668.4.orf1:2001MAR30
138	LG:331642.6:2001MAR30	712	LG:331642.6.orf2:2001MAR30
139	LG:331851.12:2001MAR30	713	LG:331851.12.orf3:2001MAR30
140	LG:332414.5:2001MAR30	714	LG:332414.5.orf2:2001MAR30
141	LG:332730.12:2001MAR30	715	LG:332730.12.orf2:2001MAR30
142	LG:333062.22:2001MAR30	716	LG:333062.22.orf2:2001MAR30
143	LG:335705.2:2001MAR30	717	LG:335705.2.orf2:2001MAR30
144	LG:337930.16:2001MAR30	718	LG:337930.16.orf2:2001MAR30
145	LG:346481.15:2001MAR30	719	LG:346481.15.orf1:2001MAR30
146	LG:349164.1:2001MAR30	720	LG:349164.1.orf3:2001MAR30
147	LG:350957.5:2001MAR30	721	LG:350957.5.orf1:2001MAR30
148	LG:383512.8:2001MAR30	722	LG:383512.8.orf1:2001MAR30
149	LG:401163.10:2001MAR30	723	LG:401163.10.orf1:2001MAR30
150	LG:402133.1:2001MAR30	724	LG:402133.1.orf1:2001MAR30
151	LG:405820.1:2001MAR30	725	LG:405820.1.orf2:2001MAR30
152	LG:405846.1:2001MAR30	726	LG:405846.1.orf3:2001MAR30
153	LG:407401.2:2001MAR30	727	LG:407401.2.orf2:2001MAR30
154	LG:408448.10:2001MAR30	728	LG:408448.10.orf3:2001MAR30
155	LG:408854.13:2001MAR30	729	LG:408854.13.orf2:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
156	LG:411150.14:2001MAR30	730	LG:411150.14.orf2:2001MAR30
157	LG:411466.1:2001MAR30	731	LG:411466.1.orf2:2001MAR30
158	LG:413969.68:2001MAR30	732	LG:413969.68.orf1:2001MAR30
159	LG:419641.35:2001MAR30	733	LG:419641.35.orf1:2001MAR30
160	LG:428206.7:2001MAR30	734	LG:428206.7.orf2:2001MAR30
161	LG:430059.1:2001MAR30	735	LG:430059.1.orf3:2001MAR30
162	LG:448040.3:2001MAR30	736	LG:448040.3.orf2:2001MAR30
163	LG:451274.1:2001MAR30	737	LG:451274.1.orf3:2001MAR30
164	LG:456110.1:2001MAR30	738	LG:456110.1.orf1:2001MAR30
165	LG:456954.1:2001MAR30	739	LG:456954.1.orf3:2001MAR30
166	LG:474942.12:2001MAR30	740	LG:474942.12.orf3:2001MAR30
167	LG:475119.14:2001MAR30	741	LG:475119.14.orf1:2001MAR30
168	LG:479908.77:2001MAR30	742	LG:479908.77.orf3:2001MAR30
169	LG:480127.47:2001MAR30	743	LG:480127.47.orf3:2001MAR30
170	LG:481154.12:2001MAR30	744	LG:481154.12.orf1:2001MAR30
171	LG:481414.6:2001MAR30	745	LG:481414.6.orf2:2001MAR30
172	LG:481941.1:2001MAR30	746	LG:481941.1.orf3:2001MAR30
173	LG:887216.4:2001MAR30	747	LG:887216.4.orf3:2001MAR30
174	LG:899402.3:2001MAR30	748	LG:899402.3.orf1:2001MAR30
175	LG:899894.2:2001MAR30	749	LG:899894.2.orf3:2001MAR30
176	LG:977908.1:2001MAR30	750	LG:977908.1.orf3:2001MAR30
177	LG:977929.1:2001MAR30	751	LG:977929.1.orf1:2001MAR30
178	LG:978008.14:2001MAR30	752	LG:978008.14.orf3:2001MAR30
179	LG:979054.18:2001MAR30	753	LG:979054.18.orf1:2001MAR30
180	LG:979185.10:2001MAR30	754	LG:979185.10.orf1:2001MAR30
181	LG:983654.1:2001MAR30	755	LG:983654.1.orf2:2001MAR30
182	LG:985092.12:2001MAR30	756	LG:985092.12.orf3:2001MAR30
183	LG:987396.8:2001MAR30	757	LG:987396.8.orf2:2001MAR30
184	LG:987418.10:2001MAR30	758	LG:987418.10.orf2:2001MAR30
184	LG:987418.10:2001MAR30	759	LG:987418.10.orf3:2001MAR30
185	LG:997203.25:2001MAR30	760	LG:997203.25.orf3:2001MAR30
186	LG:997477.8:2001MAR30	761	LG:997477.8.orf3:2001MAR30
187	LG:998855.4:2001MAR30	762	LG:998855.4.orf1:2001MAR30
188	LG:999093.1:2001MAR30	763	LG:999093.1.orf2:2001MAR30
189	LG:999183.1:2001MAR30	764	LG:999183.1.orf3:2001MAR30
190	LI:1032972.1:2001MAY17	765	LI:1032972.1.orf1:2001MAY17
191	LI:170666.6:2001MAY17	766	LI:170666.6.orf2:2001MAY17
192	LI:197048.10:2001MAY17	767	LI:197048.10.orf3:2001MAY17
193	LI:228655.5:2001MAY17	768	LI:228655.5.orf3:2001MAY17
194	LI:229789.6:2001MAY17	769	LI:229789.6.orf3:2001MAY17
195	LI:231500.8:2001MAY17	770	LI:231500.8.orf1:2001MAY17
196	LI:253851.26:2001MAY17	771	LI:253851.26.orf3:2001MAY17
197	LI:373302.1:2001MAY17	772	LI:373302.1.orf1:2001MAY17
198	LI:405707.12:2001MAY17	773	LI:405707.12.orf2:2001MAY17
199	LI:411441.8:2001MAY17	774	LI:411441.8.orf3:2001MAY17
200	LI:758193.3:2001MAY17	775	LI:758193.3.orf2:2001MAY17
201	LI:1028562.3:2001MAY17	776	LI:1028562.3.orf2:2001MAY17
202	LI:104650.7:2001MAY17	777	LI:104650.7.orf3:2001MAY17
203	LI:1094557.4:2001MAY17	778	LI:1094557.4.orf3:2001MAY17
204	LI:1143528.4:2001MAY17	779	LI:1143528.4.orf2:2001MAY17
205	LI:1172210.7:2001MAY17	780	LI:1172210.7.orf2:2001MAY17
206	LI:1178659.14:2001MAY17	781	LI:1178659.14.orf1:2001MAY17
207	LI:1983726.3:2001MAY17	782	LI:1983726.3.orf3:2001MAY17
208	LI:2051495.3:2001MAY17	783	LI:2051495.3.orf2:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
209	LI:2117629.1:2001MAY17	784	LI:2117629.1.orf3:2001MAY17
210	LI:2118007.3:2001MAY17	785	LI:2118007.3.orf3:2001MAY17
211	LI:2118292.9:2001MAY17	786	LI:2118292.9.orf1:2001MAY17
212	LI:2118733.7:2001MAY17	787	LI:2118733.7.orf1:2001MAY17
213	LI:212702.3:2001MAY17	788	LI:212702.3.orf1:2001MAY17
214	LI:2207871.10:2001MAY17	789	LI:2207871.10.orf2:2001MAY17
215	LI:2207876.5:2001MAY17	790	LI:2207876.5.orf1:2001MAY17
215	LI:2207876.5:2001MAY17	791	LI:2207876.5.orf2:2001MAY17
216	LI:2208743.1:2001MAY17	792	LI:2208743.1.orf3:2001MAY17
217	LI:2208744.1:2001MAY17	793	LI:2208744.1.orf2:2001MAY17
218	LI:230905.3:2001MAY17	794	LI:230905.3.orf2:2001MAY17
219	LI:235233.95:2001MAY17	795	LI:235233.95.orf3:2001MAY17
220	LI:235359.24:2001MAY17	796	LI:235359.24.orf3:2001MAY17
221	LI:238365.6:2001MAY17	797	LI:238365.6.orf2:2001MAY17
222	LI:260259.23:2001MAY17	798	LI:260259.23.orf2:2001MAY17
223	LI:321069.2:2001MAY17	799	LI:321069.2.orf1:2001MAY17
224	LI:331499.8:2001MAY17	800	LI:331499.8.orf1:2001MAY17
225	LI:332176.8:2001MAY17	801	LI:332176.8.orf2:2001MAY17
226	LI:333952.7:2001MAY17	802	LI:333952.7.orf1:2001MAY17
227	LI:338428.2:2001MAY17	803	LI:338428.2.orf3:2001MAY17
228	LI:343869.2:2001MAY17	804	LI:343869.2.orf3:2001MAY17
229	LI:363532.1:2001MAY17	805	LI:363532.1.orf1:2001MAY17
230	LI:398153.37:2001MAY17	806	LI:398153.37.orf3:2001MAY17
231	LI:416650.1:2001MAY17	807	LI:416650.1.orf3:2001MAY17
232	LI:444767.32:2001MAY17	808	LI:444767.32.orf2:2001MAY17
233	LI:759073.1:2001MAY17	809	LI:759073.1.orf1:2001MAY17
234	LI:759902.4:2001MAY17	810	LI:759902.4.orf3:2001MAY17
235	LI:762268.1:2001MAY17	811	LI:762268.1.orf1:2001MAY17
236	LI:813699.1:2001MAY17	812	LI:813699.1.orf3:2001MAY17
237	LI:024142.16:2001MAY17	813	LI:024142.16.orf2:2001MAY17
238	LI:1018424.4:2001MAY17	814	LI:1018424.4.orf2:2001MAY17
239	LI:1085250.6:2001MAY17	815	LI:1085250.6.orf1:2001MAY17
240	LI:179233.63:2001MAY17	816	LI:179233.63.orf2:2001MAY17
241	LI:2207125.3:2001MAY17	817	LI:2207125.3.orf3:2001MAY17
242	LI:235153.44:2001MAY17	818	LI:235153.44.orf1:2001MAY17
243	LI:007101.10:2001MAY17	819	LI:007101.10.orf1:2001MAY17
244	LI:008541.2:2001MAY17	820	LI:008541.2.orf3:2001MAY17
245	LI:009658.13:2001MAY17	821	LI:009658.13.orf1:2001MAY17
246	LI:020012.14:2001MAY17	822	LI:020012.14.orf3:2001MAY17
247	LI:020691.1:2001MAY17	823	LI:020691.1.orf1:2001MAY17
248	LI:021188.12:2001MAY17	824	LI:021188.12.orf2:2001MAY17
249	LI:021324.4:2001MAY17	825	LI:021324.4.orf3:2001MAY17
250	LI:021834.15:2001MAY17	826	LI:021834.15.orf1:2001MAY17
251	LI:024841.1:2001MAY17	827	LI:024841.1.orf1:2001MAY17
252	LI:025724.12:2001MAY17	828	LI:025724.12.orf2:2001MAY17
253	LI:029328.2:2001MAY17	829	LI:029328.2.orf2:2001MAY17
254	LI:032171.5:2001MAY17	830	LI:032171.5.orf2:2001MAY17
255	LI:035055.1:2001MAY17	831	LI:035055.1.orf2a:2001MAY17
255	LI:035055.1:2001MAY17	832	LI:035055.1.orf2b:2001MAY17
256	LI:036747.17:2001MAY17	833	LI:036747.17.orf2:2001MAY17
257	LI:044301.2:2001MAY17	834	LI:044301.2.orf3:2001MAY17
258	LI:061585.10:2001MAY17	835	LI:061585.10.orf3:2001MAY17
259	LI:066742.21:2001MAY17	836	LI:066742.21.orf2:2001MAY17
260	LI:075492.206:2001MAY17	837	LI:075492.206.orf2:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
261	LI:090782.3:2001MAY17	838	LI:090782.3.orf1:2001MAY17
262	LI:1031308.1:2001MAY17	839	LI:1031308.1.orf2:2001MAY17
263	LI:1054377.1:2001MAY17	840	LI:1054377.1.orf2:2001MAY17
264	LI:1072074.10:2001MAY17	841	LI:1072074.10.orf2:2001MAY17
265	LI:1072889.15:2001MAY17	842	LI:1072889.15.orf3:2001MAY17
266	LI:1077480.1:2001MAY17	843	LI:1077480.1.orf3:2001MAY17
267	LI:1079555.1:2001MAY17	844	LI:1079555.1.orf2:2001MAY17
268	LI:1084992.28:2001MAY17	845	LI:1084992.28.orf2:2001MAY17
269	LI:1085472.5:2001MAY17	846	LI:1085472.5.orf1:2001MAY17
270	LI:1086800.7:2001MAY17	847	LI:1086800.7.orf2:2001MAY17
271	LI:1089871.9:2001MAY17	848	LI:1089871.9.orf2:2001MAY17
272	LI:110297.6:2001MAY17	849	LI:110297.6.orf2:2001MAY17
273	LI:1143463.8:2001MAY17	850	LI:1143463.8.orf1:2001MAY17
274	LI:1144466.1:2001MAY17	851	LI:1144466.1.orf2:2001MAY17
275	LI:1170624.2:2001MAY17	852	LI:1170624.2.orf2:2001MAY17
276	LI:1171602.39:2001MAY17	853	LI:1171602.39.orf2:2001MAY17
277	LI:1182361.3:2001MAY17	854	LI:1182361.3.orf1:2001MAY17
278	LI:1188194.15:2001MAY17	855	LI:1188194.15.orf1:2001MAY17
279	LI:1189195.7:2001MAY17	856	LI:1189195.7.orf3:2001MAY17
280	LI:1190092.13:2001MAY17	857	LI:1190092.13.orf3:2001MAY17
281	LI:1190318.4:2001MAY17	858	LI:1190318.4.orf2:2001MAY17
282	LI:144233.1:2001MAY17	859	LI:144233.1.orf3:2001MAY17
283	LI:154608.1:2001MAY17	860	LI:154608.1.orf2:2001MAY17
284	LI:170101.1:2001MAY17	861	LI:170101.1.orf2:2001MAY17
285	LI:180043.1:2001MAY17	862	LI:180043.1.orf1:2001MAY17
286	LI:193050.1:2001MAY17	863	LI:193050.1.orf2:2001MAY17
287	LI:197477.31:2001MAY17	864	LI:197477.31.orf1:2001MAY17
288	LI:199639.12:2001MAY17	865	LI:199639.12.orf1:2001MAY17
289	LI:200058.6:2001MAY17	866	LI:200058.6.orf3:2001MAY17
290	LI:201374.23:2001MAY17	867	LI:201374.23.orf2:2001MAY17
291	LI:201824.1:2001MAY17	868	LI:201824.1.orf2:2001MAY17
292	LI:201989.11:2001MAY17	869	LI:201989.11.orf2:2001MAY17
293	LI:2035159.1:2001MAY17	870	LI:2035159.1.orf3:2001MAY17
294	LI:204818.10:2001MAY17	871	LI:204818.10.orf1:2001MAY17
295	LI:2048337.1:2001MAY17	872	LI:2048337.1.orf3:2001MAY17
296	LI:2049697.4:2001MAY17	873	LI:2049697.4.orf3:2001MAY17
297	LI:2050808.19:2001MAY17	874	LI:2050808.19.orf2:2001MAY17
298	LI:209773.25:2001MAY17	875	LI:209773.25.orf3:2001MAY17
299	LI:2117881.32:2001MAY17	876	LI:2117881.32.orf2:2001MAY17
300	LI:2118140.9:2001MAY17	877	LI:2118140.9.orf1:2001MAY17
301	LI:2118151.15:2001MAY17	878	LI:2118151.15.orf2:2001MAY17
302	LI:2118324.9:2001MAY17	879	LI:2118324.9.orf2:2001MAY17
303	LI:2118368.12:2001MAY17	880	LI:2118368.12.orf2:2001MAY17
304	LI:2119448.5:2001MAY17	881	LI:2119448.5.orf3:2001MAY17
305	LI:212023.7:2001MAY17	882	LI:212023.7.orf2:2001MAY17
306	LI:2120556.1:2001MAY17	883	LI:2120556.1.orf2:2001MAY17
307	LI:2121577.3:2001MAY17	884	LI:2121577.3.orf3:2001MAY17
308	LI:2123395.11:2001MAY17	885	LI:2123395.11.orf3:2001MAY17
309	LI:2123452.9:2001MAY17	886	LI:2123452.9.orf2:2001MAY17
310	LI:2164109.1:2001MAY17	887	LI:2164109.1.orf3:2001MAY17
311	LI:2168320.1:2001MAY17	888	LI:2168320.1.orf1:2001MAY17
312	LI:2173577.1:2001MAY17	889	LI:2173577.1.orf1:2001MAY17
313	LI:2179256.1:2001MAY17	890	LI:2179256.1.orf1:2001MAY17
314	LI:2180388.1:2001MAY17	891	LI:2180388.1.orf1:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
315	LI:2199713.8:2001MAY17	892	LI:2199713.8.orf1:2001MAY17
316	LI:2200587.2:2001MAY17	893	LI:2200587.2.orf1:2001MAY17
317	LI:2200761.12:2001MAY17	894	LI:2200761.12.orf2:2001MAY17
318	LI:2203624.1:2001MAY17	895	LI:2203624.1.orf2:2001MAY17
319	LI:220495.9:2001MAY17	896	LI:220495.9.orf2:2001MAY17
320	LI:2205532.1:2001MAY17	897	LI:2205532.1.orf3:2001MAY17
321	LI:2206277.1:2001MAY17	898	LI:2206277.1.orf3:2001MAY17
322	LI:2207765.8:2001MAY17	899	LI:2207765.8.orf3:2001MAY17
323	LI:2208404.4:2001MAY17	900	LI:2208404.4.orf2:2001MAY17
324	LI:2208715.3:2001MAY17	901	LI:2208715.3.orf1:2001MAY17
325	LI:2208766.2:2001MAY17	902	LI:2208766.2.orf3:2001MAY17
326	LI:2209636.3:2001MAY17	903	LI:2209636.3.orf1:2001MAY17
327	LI:221864.68:2001MAY17	904	LI:221864.68.orf1:2001MAY17
328	LI:229267.1:2001MAY17	905	LI:229267.1.orf3:2001MAY17
329	LI:229648.2:2001MAY17	906	LI:229648.2.orf1:2001MAY17
330	LI:231016.1:2001MAY17	907	LI:231016.1.orf3:2001MAY17
331	LI:231140.5:2001MAY17	908	LI:231140.5.orf1:2001MAY17
332	LI:231695.14:2001MAY17	909	LI:231695.14.orf3:2001MAY17
333	LI:232846.24:2001MAY17	910	LI:232846.24.orf3:2001MAY17
334	LI:233411.11:2001MAY17	911	LI:233411.11.orf3:2001MAY17
335	LI:233545.13:2001MAY17	912	LI:233545.13.orf3:2001MAY17
336	LI:234671.101:2001MAY17	913	LI:234671.101.orf3:2001MAY17
337	LI:236098.14:2001MAY17	914	LI:236098.14.orf3:2001MAY17
338	LI:236196.15:2001MAY17	915	LI:236196.15.orf1:2001MAY17
339	LI:237086.1:2001MAY17	916	LI:237086.1.orf2:2001MAY17
340	LI:238585.30:2001MAY17	917	LI:238585.30.orf2:2001MAY17
341	LI:238672.6:2001MAY17	918	LI:238672.6.orf2:2001MAY17
342	LI:239579.9:2001MAY17	919	LI:239579.9.orf2:2001MAY17
343	LI:239720.1:2001MAY17	920	LI:239720.1.orf3:2001MAY17
344	LI:240037.6:2001MAY17	921	LI:240037.6.orf2:2001MAY17
345	LI:243900.7:2001MAY17	922	LI:243900.7.orf3:2001MAY17
346	LI:244378.1:2001MAY17	923	LI:244378.1.orf2:2001MAY17
347	LI:245500.3:2001MAY17	924	LI:245500.3.orf1:2001MAY17
348	LI:245982.24:2001MAY17	925	LI:245982.24.orf2:2001MAY17
349	LI:246054.1:2001MAY17	926	LI:246054.1.orf3:2001MAY17
350	LI:256051.229:2001MAY17	927	LI:256051.229.orf3:2001MAY17
351	LI:260629.7:2001MAY17	928	LI:260629.7.orf1:2001MAY17
352	LI:272723.1:2001MAY17	929	LI:272723.1.orf3a:2001MAY17
352	LI:272723.1:2001MAY17	930	LI:272723.1.orf3b:2001MAY17
353	LI:272766.1:2001MAY17	931	LI:272766.1.orf2:2001MAY17
354	LI:275726.1:2001MAY17	932	LI:275726.1.orf2:2001MAY17
355	LI:276815.1:2001MAY17	933	LI:276815.1.orf2:2001MAY17
356	LI:283562.5:2001MAY17	934	LI:283562.5.orf3:2001MAY17
357	LI:289066.15:2001MAY17	935	LI:289066.15.orf3:2001MAY17
358	LI:331040.17:2001MAY17	936	LI:331040.17.orf1:2001MAY17
359	LI:332414.5:2001MAY17	937	LI:332414.5.orf1:2001MAY17
360	LI:332730.16:2001MAY17	938	LI:332730.16.orf2:2001MAY17
361	LI:333849.21:2001MAY17	939	LI:333849.21.orf3:2001MAY17
362	LI:337038.15:2001MAY17	940	LI:337038.15.orf1:2001MAY17
363	LI:337606.6:2001MAY17	941	LI:337606.6.orf2:2001MAY17
364	LI:338032.10:2001MAY17	942	LI:338032.10.orf2:2001MAY17
365	LI:339265.16:2001MAY17	943	LI:339265.16.orf3:2001MAY17
366	LI:344646.4:2001MAY17	944	LI:344646.4.orf3:2001MAY17
367	LI:347393.7:2001MAY17	945	LI:347393.7.orf2:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
368	LI:348107.36:2001MAY17	946	LI:348107.36.orf3:2001MAY17
369	LI:351120.6:2001MAY17	947	LI:351120.6.orf3:2001MAY17
370	LI:358762.41:2001MAY17	948	LI:358762.41.orf3:2001MAY17
371	LI:363003.48:2001MAY17	949	LI:363003.48.orf2:2001MAY17
372	LI:370899.6:2001MAY17	950	LI:370899.6.orf1:2001MAY17
373	LI:376470.1:2001MAY17	951	LI:376470.1.orf2:2001MAY17
374	LI:400961.18:2001MAY17	952	LI:400961.18.orf1:2001MAY17
375	LI:404482.20:2001MAY17	953	LI:404482.20.orf3:2001MAY17
376	LI:405985.1:2001MAY17	954	LI:405985.1.orf2:2001MAY17
377	LI:406389.1:2001MAY17	955	LI:406389.1.orf2:2001MAY17
378	LI:406833.1:2001MAY17	956	LI:406833.1.orf2:2001MAY17
379	LI:407921.3:2001MAY17	957	LI:407921.3.orf1:2001MAY17
380	LI:409078.54:2001MAY17	958	LI:409078.54.orf3:2001MAY17
381	LI:423601.6:2001MAY17	959	LI:423601.6.orf3:2001MAY17
382	LI:425024.5:2001MAY17	960	LI:425024.5.orf1:2001MAY17
383	LI:427909.29:2001MAY17	961	LI:427909.29.orf1:2001MAY17
384	LI:428198.20:2001MAY17	962	LI:428198.20.orf3:2001MAY17
385	LI:429738.6:2001MAY17	963	LI:429738.6.orf3:2001MAY17
386	LI:449437.1:2001MAY17	964	LI:449437.1.orf1:2001MAY17
387	LI:459269.25:2001MAY17	965	LI:459269.25.orf1:2001MAY17
388	LI:464206.1:2001MAY17	966	LI:464206.1.orf3:2001MAY17
389	LI:465821.2:2001MAY17	967	LI:465821.2.orf1:2001MAY17
390	LI:474414.28:2001MAY17	968	LI:474414.28.orf1:2001MAY17
391	LI:474435.14:2001MAY17	969	LI:474435.14.orf2:2001MAY17
392	LI:474458.11:2001MAY17	970	LI:474458.11.orf3:2001MAY17
393	LI:477127.18:2001MAY17	971	LI:477127.18.orf3:2001MAY17
394	LI:480375.55:2001MAY17	972	LI:480375.55.orf3:2001MAY17
395	LI:480467.24:2001MAY17	973	LI:480467.24.orf2:2001MAY17
396	LI:480587.1:2001MAY17	974	LI:480587.1.orf3:2001MAY17
397	LI:480798.13:2001MAY17	975	LI:480798.13.orf2:2001MAY17
398	LI:481203.14:2001MAY17	976	LI:481203.14.orf1:2001MAY17
399	LI:481237.11:2001MAY17	977	LI:481237.11.orf1:2001MAY17
400	LI:481368.12:2001MAY17	978	LI:481368.12.orf3:2001MAY17
401	LI:482301.8:2001MAY17	979	LI:482301.8.orf3:2001MAY17
402	LI:482482.29:2001MAY17	980	LI:482482.29.orf1:2001MAY17
403	LI:758877.26:2001MAY17	981	LI:758877.26.orf3:2001MAY17
404	LI:791042.1:2001MAY17	982	LI:791042.1.orf3:2001MAY17
405	LI:808999.26:2001MAY17	983	LI:808999.26.orf3:2001MAY17
406	LI:815715.10:2001MAY17	984	LI:815715.10.orf1:2001MAY17
407	LI:902980.16:2001MAY17	985	LI:902980.16.orf3:2001MAY17
408	LI:903196.25:2001MAY17	986	LI:903196.25.orf2:2001MAY17
409	LI:903914.10:2001MAY17	987	LI:903914.10.orf2:2001MAY17
410	LG:006764.2:2001JUN22	988	LG:006764.2.orf2:2001JUN22
411	LG:014704.8:2001JUN22	989	LG:014704.8.orf3:2001JUN22
412	LG:1447607.7:2001JUN22	990	LG:1447607.7.orf1:2001JUN22
413	LG:1455032.3:2001JUN22	991	LG:1455032.3.orf2:2001JUN22
414	LG:1501898.18:2001JUN22	992	LG:1501898.18.orf1:2001JUN22
415	LG:1502692.5:2001JUN22	993	LG:1502692.5.orf2:2001JUN22
416	LG:208949.8:2001JUN22	994	LG:208949.8.orf2:2001JUN22
417	LG:240501.10:2001JUN22	995	LG:240501.10.orf3:2001JUN22
418	LG:329228.27:2001JUN22	996	LG:329228.27.orf2:2001JUN22
419	LG:337056.11:2001JUN22	997	LG:337056.11.orf2:2001JUN22
420	LG:346663.9:2001JUN22	998	LG:346663.9.orf3:2001JUN22
421	LG:7685586.2:2001JUN22	999	LG:7685586.2.orf3:2001JUN22

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
422	LG:407730.13:2001JUN22	1000	LG:407730.13.orf1:2001JUN22
423	LG:025465.5:2001JUN22	1001	LG:025465.5.orf3:2001JUN22
424	LG:054509.14:2001JUN22	1002	LG:054509.14.orf3:2001JUN22
425	LG:1067876.1:2001JUN22	1003	LG:1067876.1.orf1:2001JUN22
426	LG:1327699.55:2001JUN22	1004	LG:1327699.55.orf3:2001JUN22
427	LG:1482904.10:2001JUN22	1005	LG:1482904.10.orf3:2001JUN22
428	LG:222317.4:2001JUN22	1006	LG:222317.4.orf2:2001JUN22
429	LG:332701.3:2001JUN22	1007	LG:332701.3.orf1:2001JUN22
430	LG:369881.5:2001JUN22	1008	LG:369881.5.orf1:2001JUN22
431	LG:404381.2:2001JUN22	1009	.LG:404381.2.orf2:2001JUN22
432	LG:405709.2:2001JUN22	1010	LG:405709.2.orf2:2001JUN22
433	LG:406664.17:2001JUN22	1011	LG:406664.17.orf3:2001JUN22
434	LG:7670681.1:2001JUN22	1012	LG:7670681.1.orf1:2001JUN22
435	LG:7687404.1:2001JUN22	1013	LG:7687404.1.orf2:2001JUN22
436	LG:7690030.24:2001JUN22	1014	LG:7690030.24.orf3:2001JUN22
437	LG:7690229.3:2001JUN22	1015	LG:7690229.3.orf1:2001JUN22
438	LG:7690533.16:2001JUN22	1016	LG:7690533.16.orf3:2001JUN22
439	LG:7691131.2:2001JUN22	1017	LG:7691131.2.orf3:2001JUN22
440	LG:7692559.6:2001JUN22	1018	LG:7692559.6.orf3:2001JUN22
441	LG:7684866.10:2001JUN22	1019	LG:7684866.10.orf2:2001JUN22
442	LG:002106.5:2001JUN22	1020	LG:002106.5.orf1:2001JUN22
443	LG:004064.1:2001JUN22	1021	LG:004064.1.orf2:2001JUN22
444	LG:007916.8:2001JUN22	1022	LG:007916.8.orf2:2001JUN22
445	LG:014719.14:2001JUN22	1023	LG:014719.14.orf3:2001JUN22
446	LG:021763.31:2001JUN22	1024	LG:021763.31.orf3:2001JUN22
447	LG:025397.1:2001JUN22	1025	LG:025397.1.orf3:2001JUN22
448	LG:029880.20:2001JUN22	1026	LG:029880.20.orf2:2001JUN22
449	LG:040422.37:2001JUN22	1027	LG:040422.37.orf1:2001JUN22
450	LG:065935.11:2001JUN22	1028	LG:065935.11.orf2:2001JUN22
451	LG:074381.1:2001JUN22	1029	LG:074381.1.orf2:2001JUN22
452	LG:083814.6:2001JUN22	1030	LG:083814.6.orf3:2001JUN22
453	LG:090985.1:2001JUN22	1031	LG:090985.1.orf2:2001JUN22
454	LG:093750.2:2001JUN22	1032	LG:093750.2.orf3:2001JUN22
455	LG:1013708.26:2001JUN22	1033	LG:1013708.26.orf1:2001JUN22
456	LG:1022283.8:2001JUN22	1034	LG:1022283.8.orf1:2001JUN22
457	LG:1034386.1:2001JUN22	1035	LG:1034386.1.orf3:2001JUN22
458	LG:1045617.36:2001JUN22	1036	LG:1045617.36.orf1:2001JUN22
459	LG:1063303.1:2001JUN22	1037	LG:1063303.1.orf1:2001JUN22
460	LG:1094200.1:2001JUN22	1038	LG:1094200.1.orf1:2001JUN22
461	LG:1099249.19:2001JUN22	1039	LG:1099249.19.orf3:2001JUN22
462	LG:110667.1:2001JUN22	1040	LG:110667.1.orf1:2001JUN22
463	LG:1132386.20:2001JUN22	1041	LG:1132386.20.orf2:2001JUN22
464	LG:116015.2:2001JUN22	1042	LG:116015.2.orf1:2001JUN22
465	LG:1173104.15:2001JUN22	1043	LG:1173104.15.orf3:2001JUN22
466	LG:1285109.14:2001JUN22	1044	LG:1285109.14.orf3:2001JUN22
467	LG:131477.11:2001JUN22	1045	LG:131477.11.orf3:2001JUN22
468	LG:1333618.1:2001JUN22	1046	LG:1333618.1.orf2:2001JUN22
469	LG:1347760.16:2001JUN22	1047	LG:1347760.16.orf1:2001JUN22
470	LG:1383039.369:2001JUN22	1048	LG:1383039.369.orf3:2001JUN22
471	LG:1383313.3:2001JUN22	1049	LG:1383313.3.orf3:2001JUN22
472	LG:1384075.8:2001JUN22	1050	LG:1384075.8.orf2:2001JUN22
473	LG:1384155.1:2001JUN22	1051	LG:1384155.1.orf1:2001JUN22
474	LG:1385280.12:2001JUN22	1052	LG:1385280.12.orf3:2001JUN22
475	LG:1390535.25:2001JUN22	1053	LG:1390535.25.orf3:2001JUN22

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
476	LG:1397047.1:2001JUN22	1054	LG:1397047.1.orf3:2001JUN22
477	LG:1398646.15:2001JUN22	1055	LG:1398646.15.orf2:2001JUN22
478	LG:1446193.10:2001JUN22	1056	LG:1446193.10.orf1:2001JUN22
479	LG:1446405.14:2001JUN22	1057	LG:1446405.14.orf2:2001JUN22
480	LG:1448148.1:2001JUN22	1058	LG:1448148.1.orf1:2001JUN22
481	LG:1452619.13:2001JUN22	1059	LG:1452619.13.orf1:2001JUN22
482	LG:1452783.22:2001JUN22	1060	LG:1452783.22.orf3:2001JUN22
483	LG:1453417.5:2001JUN22	1061	LG:1453417.5.orf3:2001JUN22
484	LG:1455222.23:2001JUN22	1062	LG:1455222.23.orf1:2001JUN22
485	LG:149121.8:2001JUN22	1063	LG:149121.8.orf1:2001JUN22
486	LG:1500175.18:2001JUN22	1064	LG:1500175.18.orf3:2001JUN22
487	LG:1500434.6:2001JUN22	1065	LG:1500434.6.orf2:2001JUN22
488	LG:1501550.19:2001JUN22	1066	LG:1501550.19.orf1:2001JUN22
489	LG:1501923.26:2001JUN22	1067	LG:1501923.26.orf2:2001JUN22
490	LG:150960.9:2001JUN22	1068	LG:150960.9.orf2:2001JUN22
491	LG:182744.29:2001JUN22	1069	LG:182744.29.orf1:2001JUN22
492	LG:197166.1:2001JUN22	1070	LG:197166.1.orf1:2001JUN22
493	LG:197455.5:2001JUN22	1071	LG:197455.5.orf2:2001JUN22
494	LG:198251.8:2001JUN22	1072	LG:198251.8.orf2:2001JUN22
495	LG:200149.3:2001JUN22	1073	LG:200149.3.orf1:2001JUN22
496	LG:203483.3:2001JUN22	1074	LG:203483.3.orf2:2001JUN22
497	LG:209701.7:2001JUN22	1075	LG:209701.7.orf1:2001JUN22
498	LG:210614.1:2001JUN22	1076	LG:210614.1.orf1:2001JUN22
499	LG:210672.1:2001JUN22	1077	LG:210672.1.orf1:2001JUN22
500	LG:215051.10:2001JUN22	1078	LG:215051.10.orf3:2001JUN22
501	LG:218989.3:2001JUN22	1079	LG:218989.3.orf2:2001JUN22
502	LG:228107.11:2001JUN22	1080	LG:228107.11.orf3:2001JUN22
503	LG:231016.1:2001JUN22	1081	LG:231016.1.orf2:2001JUN22
504	LG:235943.60:2001JUN22	1082	LG:235943.60.orf1:2001JUN22
505	LG:235970.14:2001JUN22	1083	LG:235970.14.orf2:2001JUN22
506	LG:236697.15:2001JUN22	1084	LG:236697.15.orf1:2001JUN22
507	LG:238576.3:2001JUN22	1085	LG:238576.3.orf2:2001JUN22
508	LG:238602.2:2001JUN22	1086	LG:238602.2.orf1:2001JUN22
509	LG:241291.46:2001JUN22	1087	LG:241291.46.orf1:2001JUN22
510	LG:241742.1:2001JUN22	1088	LG:241742.1.orf3:2001JUN22
511	LG:244520.33:2001JUN22	1089	LG:244520.33.orf2:2001JUN22
512	LG:247556.1:2001JUN22	1090	LG:247556.1.orf1:2001JUN22
513	LG:247792.5:2001JUN22	1091	LG:247792.5.orf3:2001JUN22
514	LG:253580.6:2001JUN22	1092	LG:253580.6.orf3:2001JUN22
515	LG:291759.5:2001JUN22	1093	LG:291759.5.orf3:2001JUN22
516	LG:298226.1:2001JUN22	1094	LG:298226.1.orf1:2001JUN22
517	LG:306342.1:2001JUN22	1095	LG:306342.1.orf2:2001JUN22
518	LG:327144.5:2001JUN22	1096	LG:327144.5.orf2:2001JUN22
519	LG:331499.8:2001JUN22	1097	LG:331499.8.orf3:2001JUN22
520	LG:331582.12:2001JUN22	1098	LG:331582.12.orf2:2001JUN22
521	LG:333017.12:2001JUN22	1099	LG:333017.12.orf2:2001JUN22
522	LG:334438.8:2001JUN22	1100	LG:334438.8.orf2:2001JUN22
523	LG:337835.7:2001JUN22	1101	LG:337835.7.orf3:2001JUN22
524	LG:346536.12:2001JUN22	1102	LG:346536.12.orf2:2001JUN22
525	LG:348117.5:2001JUN22	1103	LG:348117.5.orf1:2001JUN22
526	LG:350407.22:2001JUN22	1104	LG:350407.22.orf3:2001JUN22
527	LG:373219.13:2001JUN22	1105	LG:373219.13.orf2:2001JUN22
528	LG:375048.15:2001JUN22	1106	LG:375048.15.orf3:2001JUN22
529	LG:400114.3:2001JUN22	1107	LG:400114.3.orf3:2001JUN22

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
530	LG:400652.1:2001JUN22	1108	LG:400652.1.orf1:2001JUN22
531	LG:401313.10:2001JUN22	1109	LG:401313.10.orf1:2001JUN22
532	LG:406389.1:2001JUN22	1110	LG:406389.1.orf2:2001JUN22
533	LG:406595.2:2001JUN22	1111	LG:406595.2.orf1:2001JUN22
534	LG:410628.21:2001JUN22	1112	LG:410628.21.orf2:2001JUN22
535	LG:413583.15:2001JUN22	1113	LG:413583.15.orf3:2001JUN22
536	LG:419641.35:2001JUN22	1114	LG:419641.35.orf3:2001JUN22
537	LG:420759.4:2001JUN22	1115	LG:420759.4.orf1:2001JUN22
538	LG:425448.18:2001JUN22	1116	LG:425448.18.orf1:2001JUN22
539	LG:435717.5:2001JUN22	1117	LG:435717.5.orf1:2001JUN22
540	LG:441159.31:2001JUN22	1118	LG:441159.31.orf1:2001JUN22
541	LG:461375.2:2001JUN22	1119	LG:461375.2.orf1:2001JUN22
542	LG:474674.34:2001JUN22	1120	LG:474674.34.orf3:2001JUN22
543	LG:481414.8:2001JUN22	1121	LG:481414.8.orf1:2001JUN22
544	LG:7669276.1:2001JUN22	1122	LG:7669276.1.orf2:2001JUN22
545	LG:7677848.1:2001JUN22	1123	LG:7677848.1.orf3:2001JUN22
546	LG:7684981.3:2001JUN22	1124	LG:7684981.3.orf3:2001JUN22
547	LG:7685048.6:2001JUN22	1125	LG:7685048.6.orf2:2001JUN22
548	LG:7688302.1:2001JUN22	1126	LG:7688302.1.orf3:2001JUN22
549	LG:7690463.3:2001JUN22	1127	LG:7690463.3.orf1:2001JUN22
550	LG:7691479.5:2001JUN22	1128	LG:7691479.5.orf1:2001JUN22
551	LG:7691527.4:2001JUN22	1129	LG:7691527.4.orf1:2001JUN22
552	LG:7691663.1:2001JUN22	1130	LG:7691663.1.orf2:2001JUN22
553	LG:7691854.1:2001JUN22	1131	LG:7691854.1.orf2:2001JUN22
554	LG:7692235.2:2001JUN22	1132	LG:7692235.2.orf2:2001JUN22
555	LG:7692239.1:2001JUN22	1133	LG:7692239.1.orf1:2001JUN22
556	LG:7692575.1:2001JUN22	1134	LG:7692575.1.orf1:2001JUN22
557	LG:7692742.1:2001JUN22	1135	LG:7692742.1.orf1:2001JUN22
558	LG:7693942.1:2001JUN22	1136	LG:7693942.1.orf3:2001JUN22
559	LG:899248.22:2001JUN22	1137	LG:899248.22.orf1:2001JUN22
560	LG:979051.25:2001JUN22	1138	LG:979051.25.orf2:2001JUN22
561	LG:979054.18:2001JUN22	1139	LG:979054.18.orf2:2001JUN22
562	LG:979415.1:2001JUN22	1140	LG:979415.1.orf1:2001JUN22
562	LG:979415.1:2001JUN22	1141	LG:979415.1.orf3:2001JUN22
563	LG:980685.1:2001JUN22	1142	LG:980685.1.orf3:2001JUN22
564	LG:981272.6:2001JUN22	1143	LG:981272.6.orf1:2001JUN22
565	LG:982723.4:2001JUN22	1144	LG:982723.4.orf3:2001JUN22
566	LG:982915.8:2001JUN22	1145	LG:982915.8.orf2:2001JUN22
567	LG:987785.10:2001JUN22	1146	LG:987785.10.orf2:2001JUN22

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
1	LG:1041015.22:2001MAR30	1	19	forward 1	TM	Non-Cytosolic
1	LG:1041015.22:2001MAR30	20	42	forward 1	TM	Transmembrane
1	LG:1041015.22:2001MAR30	43	54	forward 1	TM	Cytosolic
1	LG:1041015.22:2001MAR30	55	77	forward 1	TM	Transmembrane
1	LG:1041015.22:2001MAR30	78	290	forward 1	TM	Non-Cytosolic
1	LG:1041015.22:2001MAR30	1	60	forward 2	TM	Cytosolic
1	LG:1041015.22:2001MAR30	61	83	forward 2	TM	Transmembrane
1	LG:1041015.22:2001MAR30	84	290	forward 2	TM	Non-Cytosolic
2	LG:106877.10:2001MAR30	1	78	forward 1	TM	Non-Cytosolic
2	LG:106877.10:2001MAR30	79	101	forward 1	TM	Transmembrane
2	LG:106877.10:2001MAR30	102	127	forward 1	TM	Cytosolic
2	LG:106877.10:2001MAR30	128	150	forward 1	TM	Transmembrane
2	LG:106877.10:2001MAR30	151	952	forward 1	TM	Non-Cytosolic
2	LG:106877.10:2001MAR30	1	71	forward 3	TM	Non-Cytosolic
2	LG:106877.10:2001MAR30	72	94	forward 3	TM	Transmembrane
2	LG:106877.10:2001MAR30	95	177	forward 3	TM	Cytosolic
2	LG:106877.10:2001MAR30	178	200	forward 3	TM	Transmembrane
2	LG:106877.10:2001MAR30	201	742	forward 3	TM	Non-Cytosolic
2	LG:106877.10:2001MAR30	743	765	forward 3	TM	Transmembrane
2	LG:106877.10:2001MAR30	766	952	forward 3	TM	Cytosolic
3	LG:1138554.16:2001MAR30	1	227	forward 3	TM	Non-Cytosolic
3	LG:1138554.16:2001MAR30	228	250	forward 3	TM	Transmembrane
3	LG:1138554.16:2001MAR30	251	256	forward 3	TM	Cytosolic
3	LG:1138554.16:2001MAR30	257	279	forward 3	TM	Transmembrane
3	LG:1138554.16:2001MAR30	280	293	forward 3	TM	Non-Cytosolic
3	LG:1138554.16:2001MAR30	294	316	forward 3	TM	Transmembrane
3	LG:1138554.16:2001MAR30	317	332	forward 3	TM	Cytosolic
4	LG:1383277.7:2001MAR30	1	44	forward 1	TM	Cytosolic
4	LG:1383277.7:2001MAR30	45	67	forward 1	TM	Transmembrane
4	LG:1383277.7:2001MAR30	68	155	forward 1	TM	Non-Cytosolic
4	LG:1383277.7:2001MAR30	156	178	forward 1	, TM	Transmembrane
4	LG:1383277.7:2001MAR30	179	198	forward 1	TM	Cytosolic
4	LG:1383277.7:2001MAR30	199	218	forward 1	TM	Transmembrane
4	LG:1383277.7:2001MAR30	219	221	forward 1	TM	Non-Cytosolic
4	LG:1383277.7:2001MAR30	1	52	forward 2	TM	Non-Cytosolic
4	LG:1383277.7:2001MAR30	53	75	forward 2	TM	Transmembrane
4	LG:1383277.7:2001MAR30	76	221	forward 2	TM	Cytosolic
4	LG:1383277.7:2001MAR30	1	67	forward 3	TM	Cytosolic
4	LG:1383277.7:2001MAR30	68	90	forward 3	TM	Transmembrane
4	LG:1383277.7:2001MAR30	91	93	forward 3	TM	Non-Cytosolic
4	LG:1383277.7:2001MAR30	94	113	forward 3	TM	Transmembrane
4	LG:1383277.7:2001MAR30	114	153	forward 3	TM	Cytosolic
4	LG:1383277.7:2001MAR30	154	176	forward 3	TM	Transmembrane
4	LG:1383277.7:2001MAR30	177	198	forward 3	TM	Non-Cytosolic
4	LG:1383277.7:2001MAR30	199	218	forward 3	TM	Transmembrane
4	LG:1383277.7:2001MAR30	219	220	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	1	1	forward 1	TM	Cytosolic
5	LG:1397614.15:2001MAR30	2	21	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	22	35	forward 1	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	36	58	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	59	193	forward 1	TM	Cytosolic
5	LG:1397614.15:2001MAR30	194	216	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	217	225	forward 1	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	226	243	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
5	LG:1397614.15:2001MAR30	244	259	forward 1	TM	Cytosolic
5	LG:1397614.15:2001MAR30	260	282	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	283	458	forward 1	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	459	481	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	482	534	forward 1	TM	Cytosolic
5	LG:1397614.15:2001MAR30	535	557	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	558	566	forward 1	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	567	589	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	590	644	forward 1	TM	Cytosolic
5	LG:1397614.15:2001MAR30	1	43	forward 2	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	44	66	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	67	97	forward 2	TM	Cytosolic
5	LG:1397614.15:2001MAR30	98	120	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	121	195	forward 2	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	196	218	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	219	260	forward 2	TM	Cytosolic
5	LG:1397614.15:2001MAR30	261	283	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	284	342	forward 2	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	343	365	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	366	457	forward 2	TM	Cytosolic
5	LG:1397614.15:2001MAR30	458	480	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	481	499	forward 2	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	500	522	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	523	644	forward 2	TM	Cytosolic
5	LG:1397614.15:2001MAR30	1	1	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	2	19	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	20	33	forward 3	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	34	56	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	57	195	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	196	218	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	219	263	forward 3	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	264	286	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	287	292	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	293	315	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	316	324	forward 3	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	325	347	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	348	396	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	397	416	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	417	457	forward 3	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	458	480	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	481	533	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	534	556	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	557	565	forward 3	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	566	588	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	589	644	forward 3	TM	Cytosolic
6	LG:1399315.8:2001MAR30	1	612	forward 2	TM	Non-Cytosolic
6	LG:1399315.8:2001MAR30	613	635	forward 2	TM	Transmembrane
6	LG:1399315.8:2001MAR30	636	742	forward 2	TM	Cytosolic
6	LG:1399315.8:2001MAR30	743	760	forward 2	TM	Transmembrane
6	LG:1399315.8:2001MAR30	761	987	forward 2	TM	Non-Cytosolic
6	LG:1399315.8:2001MAR30	1	243	forward 3	TM	Non-Cytosolic
6	LG:1399315.8:2001MAR30	244	261	forward 3	TM	Transmembrane
6	LG:1399315.8:2001MAR30	262	292	forward 3	TM	Cytosolic
6	LG:1399315.8:2001MAR30	293	315	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
6	LG:1399315.8:2001MAR30	316	986	forward 3	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	1	735	forward 1	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	736	758	forward 1	TM	Transmembrane
7	LG:198782.1:2001MAR30	759	770	forward 1	TM	Cytosolic
7	LG:198782.1:2001MAR30	771	793	forward 1	TM	Transmembrane
7	LG:198782.1:2001MAR30	794	851	forward 1	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	1	27	forward 2	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	28	50	forward 2	TM	Transmembrane
7	LG:198782.1:2001MAR30	51	377	forward 2	TM	Cytosolic
7	LG:198782.1:2001MAR30	378	400	forward 2	TM	Transmembrane
7	LG:198782.1:2001MAR30	401	404	forward 2	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	405	424	forward 2	TM	Transmembrane
7	LG:198782.1:2001MAR30	425	769	forward 2	TM	Cytosolic
7	LG:198782.1:2001MAR30	770	792	forward 2	TM	Transmembrane
7	LG:198782.1:2001MAR30	793	801	forward 2	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	802	819	forward 2	TM	Transmembrane
7	LG:198782.1:2001MAR30	820	850	forward 2	TM	Cytosolic
7	LG:198782.1:2001MAR30	1	33	forward 3	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	34	51	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	52	380	forward 3	TM	Cytosolic
7	LG:198782.1:2001MAR30	381	403	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	404	406	forward 3	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	407	424	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	425	436	forward 3	TM	Cytosolic
7	LG:198782.1:2001MAR30	437	459	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	460	541	forward 3	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	542	564	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	565	770	forward 3	TM	Cytosolic
7	LG:198782.1:2001MAR30	771	793	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	794	802	forward 3	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	803	822	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	823	850	forward 3	TM	Cytosolic
8	LG:236046.1:2001MAR30	1	160	forward 1	TM	Non-Cytosolic
8	LG:236046.1:2001MAR30	161	183	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	184	203	forward 1	TM	Cytosolic
8	LG:236046.1:2001MAR30	204	226	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	227	235	forward 1	TM	Non-Cytosolic
8	LG:236046.1:2001MAR30	236	253	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	254	273	forward 1	TM	Cytosolic
8	LG:236046.1:2001MAR30	274	296	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	297	367	forward 1	TM	Non-Cytosolic
8	LG:236046.1:2001MAR30	368	390	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	391	396	forward 1	TM	Cytosolic
8	LG:236046.1:2001MAR30	397	416	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	417	848	forward 1	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	1	389	forward 1	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	390	412	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	413	447	forward 1	TM	Cytosolic
9	LG:332122.6:2001MAR30	448	470	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	471	557	forward 1	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	558	575	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	576	655	forward 1	TM	Cytosolic
9	LG:332122.6:2001MAR30	656	678	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	679	681	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
9	LG:332122.6:2001MAR30	682	701	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	702	758	forward 1	TM	Cytosolic
9	LG:332122.6:2001MAR30	759	778	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	779	797	forward 1	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	798	817	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	818	837	forward 1	TM	Cytosolic
9	LG:332122.6:2001MAR30	1	66	forward 2	TM	Cytosolic
9	LG:332122.6:2001MAR30	67	84	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	85	120	forward 2	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	121	140	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	141	235	forward 2	TM	Cytosolic
9	LG:332122.6:2001MAR30	236	255	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	256	269	forward 2	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	270	289	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	290	347	forward 2	TM	Cytosolic
9	LG:332122.6:2001MAR30	348	370	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	371	396	forward 2	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	397	419	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	420	431	forward 2	TM	Cytosolic
9	LG:332122.6:2001MAR30	432	451	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	452	465	forward 2	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	466	488	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	489	554	forward 2	TM	Cytosolic
9	LG:332122.6:2001MAR30	555	574	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	575	837	forward 2	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	1	231	forward 3	TM	Cytosolic
9	LG:332122.6:2001MAR30	232	254	forward 3	TM	Transmembrane
9	LG:332122.6:2001MAR30	255	268	forward 3	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	269	286	forward 3	TM	Transmembrane
9	LG:332122.6:2001MAR30	287	328	forward 3	TM	Cytosolic
9	LG:332122.6:2001MAR30	329	351	forward 3	TM	Transmembrane
9	LG:332122.6:2001MAR30	352	393	forward 3	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	394	416	forward 3	TM	Transmembrane
9	LG:332122.6:2001MAR30	417	428	forward 3	TM	Cytosolic
9	LG:332122.6:2001MAR30	429	451	forward 3	TM	Transmembrane
9	LG:332122.6:2001MAR30	452	836	forward 3	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	1	82	forward 1	TM	Cytosolic
10	LG:345320.16:2001MAR30	83	105	forward 1	TM	Transmembrane
10	LG:345320.16:2001MAR30	106	114	forward 1	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	115	137	forward 1	TM	Transmembrane
10	LG:345320.16:2001MAR30	138	290	forward 1	TM	Cytosolic
10	LG:345320.16:2001MAR30	291	313	forward 1	TM	Transmembrane
10	LG:345320.16:2001MAR30	314	327	forward 1	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	328	350	forward 1	TM	Transmembrane
10	LG:345320.16:2001MAR30	351	424	forward 1	TM	Cytosolic
10	LG:345320.16:2001MAR30	425	447	forward 1	TM	Transmembrane
10	LG:345320.16:2001MAR30	448	764	forward 1	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	1	98	forward 2	TM	Cytosolic
10	LG:345320.16:2001MAR30	99	121	forward 2	TM	Transmembrane
10	LG:345320.16:2001MAR30	122	159	forward 2	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	160	182	forward 2	TM	Transmembrane
10	LG:345320.16:2001MAR30	183	188	forward 2	TM	Cytosolic
10	LG:345320.16:2001MAR30	189	211	forward 2	TM	Transmembrane
10	LG:345320.16:2001MAR30	212	331	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
5	LG:1397614.15:2001MAR30	244	259	forward 1	TM	Cytosolic
5	LG:1397614.15:2001MAR30	260	282	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	283	458	forward 1	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	459	481	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	482	534	forward 1	TM	Cytosolic
5	LG:1397614.15:2001MAR30	535	557	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	558	566	forward 1	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	567	589	forward 1	TM	Transmembrane
5	LG:1397614.15:2001MAR30	590	644	forward 1	TM	Cytosolic
5	LG:1397614.15:2001MAR30	1	43	forward 2	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	44	66	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	67	97	forward 2	TM	Cytosolic
5	LG:1397614.15:2001MAR30	98	120	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	121	195	forward 2	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	196	218	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	219	260	forward 2	TM	Cytosolic
5	LG:1397614.15:2001MAR30	261	283	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	284	342	forward 2	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	343	365	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	366	457	forward 2	TM	Cytosolic
5	LG:1397614.15:2001MAR30	458	480	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	481	499	forward 2	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	500	522	forward 2	TM	Transmembrane
5	LG:1397614.15:2001MAR30	523	644	forward 2	TM	Cytosolic
5	LG:1397614.15:2001MAR30	1	1	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	2	19	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	20	33	forward 3	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	34	56	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	57	195	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	196	218	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	219	263	forward 3	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	264	286	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	287	292	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	293	315	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	316	324	forward 3	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	325	347	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	348	396	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	397	416	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	417	457	forward 3	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	458	480	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	481	533	forward 3	TM	Cytosolic
5	LG:1397614.15:2001MAR30	534	556	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	557	565	forward 3	TM	Non-Cytosolic
5	LG:1397614.15:2001MAR30	566	588	forward 3	TM	Transmembrane
5	LG:1397614.15:2001MAR30	589	644	forward 3	TM	Cytosolic
6	LG:1399315.8:2001MAR30	1	612	forward 2	TM	Non-Cytosolic
6	LG:1399315.8:2001MAR30	613	635	forward 2	TM	Transmembrane
6	LG:1399315.8:2001MAR30	636	742	forward 2	TM	Cytosolic
6	LG:1399315.8:2001MAR30	743	760	forward 2	TM	Transmembrane
6	LG:1399315.8:2001MAR30	761	987	forward 2	TM	Non-Cytosolic
6	LG:1399315.8:2001MAR30	1	243	forward 3	TM	Non-Cytosolic
6	LG:1399315.8:2001MAR30	244	261	forward 3	TM	Transmembrane
6	LG:1399315.8:2001MAR30	262	292	forward 3	TM	Cytosolic
6	LG:1399315.8:2001MAR30	293	315	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
6	LG:1399315.8:2001MAR30	316	986	forward 3	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	1	735	forward 1	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	736	758	forward 1	TM	Transmembrane
7	LG:198782.1:2001MAR30	759	770	forward 1	TM	Cytosolic
7	LG:198782.1:2001MAR30	771	793	forward 1	TM	Transmembrane
7	LG:198782.1:2001MAR30	794	851	forward 1	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	1	27	forward 2	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	28	50	forward 2	TM	Transmembrane
7	LG:198782.1:2001MAR30	51	377	forward 2	TM	Cytosolic
7	LG:198782.1:2001MAR30	378	400	forward 2	TM	Transmembrane
7	LG:198782.1:2001MAR30	401	404	forward 2	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	405	424	forward 2	TM	Transmembrane
7	LG:198782.1:2001MAR30	425	769	forward 2	TM	Cytosolic
7	LG:198782.1:2001MAR30	770	792	forward 2	TM	Transmembrane
7	LG:198782.1:2001MAR30	793	801	forward 2	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	802	819	forward 2	TM	Transmembrane
7	LG:198782.1:2001MAR30	820	850	forward 2	TM	Cytosolic
7	LG:198782.1:2001MAR30	1	33	forward 3	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	34	51	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	52	380	forward 3	TM	Cytosolic
7	LG:198782.1:2001MAR30	381	403	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	404	406	forward 3	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	407	424	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	425	436	forward 3	TM	Cytosolic
7	LG:198782.1:2001MAR30	437	459	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	460	541	forward 3	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	542	564	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	565	770	forward 3	TM	Cytosolic
7	LG:198782.1:2001MAR30	771	793	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	794	802	forward 3	TM	Non-Cytosolic
7	LG:198782.1:2001MAR30	803	822	forward 3	TM	Transmembrane
7	LG:198782.1:2001MAR30	823	850	forward 3	TM	Cytosolic
8	LG:236046.1:2001MAR30	1	160	forward 1	TM	Non-Cytosolic
8	LG:236046.1:2001MAR30	161	183	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	184	203	forward 1	TM	Cytosolic
8	LG:236046.1:2001MAR30	204	226	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	227	235	forward 1	TM	Non-Cytosolic
8	LG:236046.1:2001MAR30	236	253	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	254	273	forward 1	TM	Cytosolic
8	LG:236046.1:2001MAR30	274	296	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	297	367	forward 1	TM	Non-Cytosolic
8	LG:236046.1:2001MAR30	368	390	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	391	396	forward 1	TM	Cytosolic
8	LG:236046.1:2001MAR30	397	416	forward 1	TM	Transmembrane
8	LG:236046.1:2001MAR30	417	848	forward 1	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	1	389	forward 1	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	390	412	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	413	447	forward 1	TM	Cytosolic
9	LG:332122.6:2001MAR30	448	470	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	471	557	forward 1	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	558	575	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	576	655	forward 1	TM	Cytosolic
9	LG:332122.6:2001MAR30	656	678	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	679	681	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
9	LG:332122.6:2001MAR30	682	701	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	702	758	forward 1	TM	Cytosolic
9	LG:332122.6:2001MAR30	759	778	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	779	797	forward 1	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	798	817	forward 1	TM	Transmembrane
9	LG:332122.6:2001MAR30	818	837	forward 1	TM	Cytosolic
9	LG:332122.6:2001MAR30	1	66	forward 2	TM	Cytosolic
9	LG:332122.6:2001MAR30	67	84	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	85	120	forward 2	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	121	140	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	141	235	forward 2	TM	Cytosolic
9	LG:332122.6:2001MAR30	236	255	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	256	269	forward 2	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	270	289	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	290	347	forward 2	TM	Cytosolic
9	LG:332122.6:2001MAR30	348	370	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	371	396	forward 2	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	397	419	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	420	431	forward 2	TM	Cytosolic
9	LG:332122.6:2001MAR30	432	451	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	452	465	forward 2	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	466	488	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	489	554	forward 2	TM	Cytosolic
9	LG:332122.6:2001MAR30	555	574	forward 2	TM	Transmembrane
9	LG:332122.6:2001MAR30	575	837	forward 2	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	1	231	forward 3	TM	Cytosolic
9	LG:332122.6:2001MAR30	232	254	forward 3	TM	Transmembrane
9	LG:332122.6:2001MAR30	255	268	forward 3	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	269	286	forward 3	TM	Transmembrane
9	LG:332122.6:2001MAR30	287	328	forward 3	TM	Cytosolic
9	LG:332122.6:2001MAR30	329	351	forward 3	TM	Transmembrane
9	LG:332122.6:2001MAR30	352	393	forward 3	TM	Non-Cytosolic
9	LG:332122.6:2001MAR30	394	416	forward 3	TM	Transmembrane
9	LG:332122.6:2001MAR30	417	428	forward 3	TM	Cytosolic
9	LG:332122.6:2001MAR30	429	451	forward 3	TM	Transmembrane
9	LG:332122.6:2001MAR30	452	836	forward 3	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	1	82	forward 1	TM	Cytosolic
10	LG:345320.16:2001MAR30	83	105	forward 1	TM	Transmembrane
10	LG:345320.16:2001MAR30	106	114	forward 1	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	115	137	forward 1	TM	Transmembrane
10	LG:345320.16:2001MAR30	138	290	forward 1	TM	Cytosolic
10	LG:345320.16:2001MAR30	291	313	forward 1	TM	Transmembrane
10	LG:345320.16:2001MAR30	314	327	forward 1	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	328	350	forward 1	TM	Transmembrane
10	LG:345320.16:2001MAR30	351	424	forward 1	TM	Cytosolic
10	LG:345320.16:2001MAR30	425	447	forward 1	TM	Transmembrane
10	LG:345320.16:2001MAR30	448	764	forward 1	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	1	98	forward 2	TM	Cytosolic
10	LG:345320.16:2001MAR30	99	121	forward 2	TM	Transmembrane
10	LG:345320.16:2001MAR30	122	159	forward 2	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	160	182	forward 2	TM	Transmembrane
10	LG:345320.16:2001MAR30	183	188	forward 2	TM	Cytosolic
10	LG:345320.16:2001MAR30	189	211	forward 2	TM	Transmembrane
10	LG:345320.16:2001MAR30	212	331	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
10	LG:345320.16:2001MAR30	332	354	forward 2	TM	Transmembrane
10	LG:345320.16:2001MAR30	355	447	forward 2	TM	Cytosolic
10	LG:345320.16:2001MAR30	448	470	forward 2	TM	Transmembrane
10	LG:345320.16:2001MAR30	471	764	forward 2	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	1	88	forward 3	TM	Cytosolic
10	LG:345320.16:2001MAR30	89	111	forward 3	TM	Transmembrane
10	LG:345320.16:2001MAR30	112	114	forward 3	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	115	137	forward 3	TM	Transmembrane
10	LG:345320.16:2001MAR30	138	172	forward 3	TM	Cytosolic
10	LG:345320.16:2001MAR30	173	195	forward 3	TM	Transmembrane
10	LG:345320.16:2001MAR30	196	330	forward 3	TM	Non-Cytosolic
10	LG:345320.16:2001MAR30	331	353	forward 3	TM	Transmembrane
10	LG:345320.16:2001MAR30	354	438	forward 3	TM	Cytosolic
10	LG:345320.16:2001MAR30	439	461	forward 3	TM	Transmembrane
10	LG:345320.16:2001MAR30	462	764	forward 3	TM	Non-Cytosolic
11	LG:350827.10:2001MAR30	1	9	forward 2	TM	Non-Cytosolic
11	LG:350827.10:2001MAR30	10	32	forward 2	TM	Transmembrane
11	LG:350827.10:2001MAR30	33	82	forward 2	TM	Cytosolic
11	LG:350827.10:2001MAR30	83	105	forward 2	TM	Transmembrane
11	LG:350827.10:2001MAR30	106	109	forward 2	TM	Non-Cytosolic
11	LG:350827.10:2001MAR30	110	129	forward 2	TM	Transmembrane
11	LG:350827.10:2001MAR30	130	149	forward 2	TM	Cytosolic
11	LG:350827.10:2001MAR30	150	172	forward 2	TM	Transmembrane
11	LG:350827.10:2001MAR30	173	181	forward 2	TM	Non-Cytosolic
11	LG:350827.10:2001MAR30	182	204	forward 2	TM	Transmembrane
11	LG:350827.10:2001MAR30	205	273	forward 2	TM	Cytosolic
11	LG:350827.10:2001MAR30	274	296	forward 2	TM	Transmembrane
11	LG:350827.10:2001MAR30	297	352	forward 2	TM	Non-Cytosolic
11	LG:350827.10:2001MAR30	1	9	forward 3	TM	Non-Cytosolic
11	LG:350827.10:2001MAR30	10	32	forward 3	TM	Transmembrane
11	LG:350827.10:2001MAR30	33	140	forward 3	TM	Cytosolic
11	LG:350827.10:2001MAR30	141	163	forward 3	TM	Transmembrane
11	LG:350827.10:2001MAR30	164	177	forward 3	TM	Non-Cytosolic
11	LG:350827.10:2001MAR30	178	197	forward 3	TM	Transmembrane
11	LG:350827.10:2001MAR30	198	351	forward 3	TM	Cytosolic
12	LG:399901.5:2001MAR30	1	308	forward 1	TM	Non-Cytosolic
12	LG:399901.5:2001MAR30	309	331	forward 1	TM	Transmembrane
12	LG:399901.5:2001MAR30	332	343	forward 1	TM	Cytosolic
12	LG:399901.5:2001MAR30	344	366	forward 1	TM	Transmembrane
12	LG:399901.5:2001MAR30	367	376	forward 1	TM	Non-Cytosolic
13	LG:404563.1:2001MAR30	1	351	forward 1	TM	Non-Cytosolic
13	LG:404563.1:2001MAR30	352	374	forward 1	TM	Transmembrane
13	LG:404563.1:2001MAR30	375	662	forward 1	TM	Cytosolic
13	LG:404563.1:2001MAR30	663	685	forward 1	TM	Transmembrane
13	LG:404563.1:2001MAR30	686	1103	forward 1	TM	Non-Cytosolic
13	LG:404563.1:2001MAR30	1	33	forward 2	TM	Cytosolic
13	LG:404563.1:2001MAR30	34	51	forward 2	TM	Transmembrane
13	LG:404563.1:2001MAR30	52	894	forward 2	TM	Non-Cytosolic
13	LG:404563.1:2001MAR30	895	917	forward 2	TM	Transmembrane
13	LG:404563.1:2001MAR30	918	999	forward 2	TM	Cytosolic
13	LG:404563.1:2001MAR30	1000	1022	forward 2	TM	Transmembrane
13	LG:404563.1:2001MAR30	1023	1102	forward 2	TM	Non-Cytosolic
13	LG:404563.1:2001MAR30	1	896	forward 3	TM	Non-Cytosolic
13	LG:404563.1:2001MAR30	897	919	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
13	LG:404563.1:2001MAR30	920	996	forward 3	TM	Cytosolic
13	LG:404563.1:2001MAR30	997	1014	forward 3	TM	Transmembrane
13	LG:404563.1:2001MAR30	1015	1102	forward 3	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	1	23	forward 1	TM	Cytosolic
14	LG:977812.15:2001MAR30	24	43	forward 1	TM	Transmembrane
14	LG:977812.15:2001MAR30	44	52	forward 1	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	53	75	forward 1	TM	Transmembrane
14	LG:977812.15:2001MAR30	76	94	forward 1	TM	Cytosolic
14	LG:977812.15:2001MAR30	95	112	forward 1	TM	Transmembrane
14	LG:977812.15:2001MAR30	113	115	forward 1	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	116	138	forward 1	TM	Transmembrane
14	LG:977812.15:2001MAR30	139	158	forward 1	TM	Cytosolic
14	LG:977812.15:2001MAR30	159	177	forward 1	TM	Transmembrane
14	LG:977812.15:2001MAR30	178	210	forward 1	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	211	228	forward 1	TM	Transmembrane
14	LG:977812.15:2001MAR30	229	247	forward 1	TM	Cytosolic
14	LG:977812.15:2001MAR30	248	270	forward 1	TM	Transmembrane
14	LG:977812.15:2001MAR30	271	284	forward 1	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	285	307	forward 1	TM	Transmembrane
14	LG:977812.15:2001MAR30	308	339	forward 1	TM	Cytosolic
14	LG:977812.15:2001MAR30	340	357	forward 1	TM	Transmembrane
14	LG:977812.15:2001MAR30	358	446	forward 1	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	447	466	forward 1	TM	Transmembrane
14	LG:977812.15:2001MAR30	467	482	forward 1	TM	Cytosolic
14	LG:977812.15:2001MAR30	1	89	forward 2	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	90	107	forward 2	TM	Transmembrane
14	LG:977812.15:2001MAR30	108	113	forward 2	TM	Cytosolic
14	LG:977812.15:2001MAR30	114	136	forward 2	TM	Transmembrane
14	LG:977812.15:2001MAR30	137	150	forward 2	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	151	173	forward 2	TM	Transmembrane
14	LG:977812.15:2001MAR30	174	259	forward 2	TM	Cytosolic
14	LG:977812.15:2001MAR30	260	282	forward 2	TM	Transmembrane
14	LG:977812.15:2001MAR30	283	333	forward 2	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	334	356	forward 2	TM	Transmembrane
14	LG:977812.15:2001MAR30	357	417	forward 2	TM	Cytosolic
14	LG:977812.15:2001MAR30	418	440	forward 2	TM	Transmembrane
14	LG:977812.15:2001MAR30	441	449	forward 2	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	450	467	forward 2	TM	Transmembrane
14	LG:977812.15:2001MAR30	468	481	forward 2	TM	Cytosolic
14	LG:977812.15:2001MAR30	1	93	forward 3	TM	Cytosolic
14	LG:977812.15:2001MAR30	94	116	forward 3	TM	Transmembrane
14	LG:977812.15:2001MAR30	117	125	forward 3	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	126	148	forward 3	TM	Transmembrane
14	LG:977812.15:2001MAR30	149	154	forward 3	TM	Cytosolic
14	LG:977812.15:2001MAR30	155	174	forward 3	TM	Transmembrane
14	LG:977812.15:2001MAR30	175	209	forward 3	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	210	227	forward 3	TM	Transmembrane
14	LG:977812.15:2001MAR30	228	246	forward 3	TM	Cytosolic
14	LG:977812.15:2001MAR30	247	269	forward 3	TM	Transmembrane
14	LG:977812.15:2001MAR30	270	283	forward 3	TM	Non-Cytosolic
14	LG:977812.15:2001MAR30	284	306	forward 3	TM	Transmembrane
14	LG:977812.15:2001MAR30	307	337	forward 3	TM	Cytosolic
14	LG:977812.15:2001MAR30	338	355	forward 3	TM	Transmembrane
14	LG:977812.15:2001MAR30	356	381	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
14	LG:977812.15:2001MAR30	382	404	forward 3	TM	Transmembrane
14	LG:977812.15:2001MAR30	405	446	forward 3	TM	Cytosolic
14	LG:977812.15:2001MAR30	447	469	forward 3	TM	Transmembrane
14	LG:977812.15:2001MAR30	470	481	forward 3	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	1	86	forward 1	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	87	109	forward 1	TM	Transmembrane
15	LG:983810.1:2001MAR30	110	115	forward 1	TM	Cytosolic
15	LG:983810.1:2001MAR30	116	138	forward 1	TM	Transmembrane
15	LG:983810.1:2001MAR30	139	380	forward 1	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	381	403	forward 1	TM	Transmembrane
15	LG:983810.1:2001MAR30	404	451	forward 1	TM	Cytosolic
15	LG:983810.1:2001MAR30	452	474	forward 1	TM	Transmembrane
15	LG:983810.1:2001MAR30	475	493	forward 1	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	494	516	forward 1	TM	Transmembrane
15	LG:983810.1:2001MAR30	517	528	forward 1	TM	Cytosolic
15	LG:983810.1:2001MAR30	529	551	forward 1	TM	Transmembrane
15	LG:983810.1:2001MAR30	552	615	forward 1	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	616	638	forward 1	TM	Transmembrane
15	LG:983810.1:2001MAR30	639	650	forward 1	TM	Cytosolic
15	LG:983810.1:2001MAR30	651	673	forward 1	TM	Transmembrane
15	LG:983810.1:2001MAR30	674	773	forward 1	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	1	93	forward 2	TM	Cytosolic
15	LG:983810.1:2001MAR30	94	116	forward 2	TM	Transmembrane
15	LG:983810.1:2001MAR30	117	331	forward 2	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	332	351	forward 2	TM	Transmembrane
15	LG:983810.1:2001MAR30	352	455	forward 2	TM	Cytosolic
15	LG:983810.1:2001MAR30	456	478	forward 2	TM	Transmembrane
15	LG:983810.1:2001MAR30	479	521	forward 2	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	522	541	forward 2	TM	Transmembrane
15	LG:983810.1:2001MAR30	542	553	forward 2	TM	Cytosolic
15	LG:983810.1:2001MAR30	554	571	forward 2	TM	Transmembrane
15	LG:983810.1:2001MAR30	572	613	forward 2	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	614	636	forward 2	TM	Transmembrane
15	LG:983810.1:2001MAR30	637	642	forward 2	TM	Cytosolic
15	LG:983810.1:2001MAR30	643	665	forward 2	TM	Transmembrane
15	LG:983810.1:2001MAR30	666	684	forward 2	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	685	707	forward 2	TM	Transmembrane
15	LG:983810.1:2001MAR30	708	772	forward 2	TM	Cytosolic
15	LG:983810.1:2001MAR30	1	94	forward 3	TM	Non-Cytosolic
15	LG:983810.1:2001MAR30	95	117	forward 3	TM	Transmembrane
15	LG:983810.1:2001MAR30	118	123	forward 3	TM	Cytosolic
15	LG:983810.1:2001MAR30	124	146	forward 3	TM	Transmembrane
15	LG:983810.1:2001MAR30	147	772	forward 3	TM	Non-Cytosolic
16	LG:984488.1:2001MAR30	1	12	forward 1	TM	Cytosolic
16	LG:984488.1:2001MAR30	13	35	forward 1	TM	Transmembrane
16	LG:984488.1:2001MAR30	36	54	forward 1	TM	Non-Cytosolic
16	LG:984488.1:2001MAR30	55	77	forward 1	TM	Transmembrane
16	LG:984488.1:2001MAR30	78	218	forward 1	TM	Cytosolic
16	LG:984488.1:2001MAR30	1	14	forward 3	TM	Non-Cytosolic
16	LG:984488.1:2001MAR30	15	37	forward 3	TM	Transmembrane
16.	LG:984488.1:2001MAR30	38	218	forward 3	TM	Cytosolic
17	LG:011606.1:2001MAR30	1	92	forward 3	TM	Cytosolic
17	LG:011606.1:2001MAR30	93	115	forward 3	TM	Transmembrane
17	LG:011606.1:2001MAR30	116	129	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
17	LG:011606.1:2001MAR30	130	152	forward 3	TM	Transmembrane
17	LG:011606.1:2001MAR30	153	400	forward 3	TM	Cytosolic
18	LG:025465.5:2001MAR30	1	374	forward 2	TM	Non-Cytosolic
18	LG:025465.5:2001MAR30	375	397	forward 2	TM	Transmembrane
18	LG:025465.5:2001MAR30	398	453	forward 2	TM	Cytosolic
18	LG:025465.5:2001MAR30	454	476	forward 2	TM	Transmembrane
18	LG:025465.5:2001MAR30	477	661	forward 2	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	1	92	forward 1	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	93	115	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	116	403	forward 1	TM	Cytosolic
19	LG:025724.10:2001MAR30	404	426	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	427	638	forward 1	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	639	656	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	657	662	forward 1	TM	Cytosolic
19	LG:025724.10:2001MAR30	663	685	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	686	694	forward 1	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	695	717	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	718	728	forward 1	TM	Cytosolic
19	LG:025724.10:2001MAR30	729	748	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	749	762	forward 1	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	763	785	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	786	805	forward 1	TM	Cytosolic
19	LG:025724.10:2001MAR30	806	828	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	829	831	forward 1	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	832	854	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	855	860	forward 1	TM	Cytosolic
19	LG:025724.10:2001MAR30	861	883	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	884	929	forward 1	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	930	952	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	953	993	forward 1	TM	Cytosolic
19	LG:025724.10:2001MAR30	994	1016	forward 1	TM	Transmembrane
19	LG:025724.10:2001MAR30	1017	1151	forward 1	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	1	683	forward 2	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	684	703	forward 2	TM	Transmembrane
19	LG:025724.10:2001MAR30	704	714	forward 2	TM	Cytosolic
19	LG:025724.10:2001MAR30	715	732	forward 2	TM	Transmembrane
19	LG:025724.10:2001MAR30	733	746	forward 2	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	747	769	forward 2	TM	Transmembrane
19	LG:025724.10:2001MAR30	770	845	forward 2	TM	Cytosolic
19	LG:025724.10:2001MAR30	846	868	forward 2	TM	Transmembrane
19	LG:025724.10:2001MAR30	869	934	forward 2	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	935	957	forward 2	TM	Transmembrane
19	LG:025724.10:2001MAR30	958	968	forward 2	TM	Cytosolic
19	LG:025724.10:2001MAR30	969	991	forward 2	TM	Transmembrane
19	LG:025724.10:2001MAR30	992	1024	forward 2	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	1025	1047	forward 2	TM	Transmembrane
19	LG:025724.10:2001MAR30	1048	1151	forward 2	TM	Cytosolic
19	LG:025724.10:2001MAR30	1	9	forward 3	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	10	28	forward 3	TM	Transmembrane
19	LG:025724.10:2001MAR30	29	74	forward 3	TM	Cytosolic
19	LG:025724.10:2001MAR30	75	97	forward 3	TM	Transmembrane
19	LG:025724.10:2001MAR30	98	396	forward 3	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	397	419	forward 3	TM	Transmembrane
19	LG:025724.10:2001MAR30	420	635	forward 3	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
19	LG:025724.10:2001MAR30	636	653	forward 3	TM	Transmembrane
19	LG:025724.10:2001MAR30	654	680	forward 3	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	681	703	forward 3	TM	Transmembrane
19	LG:025724.10:2001MAR30	704	871	forward 3	TM	Cytosolic
19	LG:025724.10:2001MAR30	872	889	forward 3	TM	Transmembrane
19	LG:025724.10:2001MAR30	890	968	forward 3	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	969	991	forward 3	TM	Transmembrane
19	LG:025724.10:2001MAR30	992	1083	forward 3	TM	Cytosolic
19	LG:025724.10:2001MAR30	1084	1106	forward 3	TM	Transmembrane
19	LG:025724.10:2001MAR30	1107	1115	forward 3	TM	Non-Cytosolic
19	LG:025724.10:2001MAR30	1116	1135	forward 3	TM	Transmembrane
19	LG:025724.10:2001MAR30	1136	1151	forward 3	TM	Cytosolic
20	LG:1095426.1:2001MAR30	1	168	forward 1	TM	Non-Cytosolic
20	LG:1095426.1:2001MAR30	169	191	forward 1	TM	Transmembrane
20	LG:1095426.1:2001MAR30	192	202	forward 1	TM	Cytosolic
20	LG:1095426.1:2001MAR30	203	225	forward 1	TM	Transmembrane
20	LG:1095426.1:2001MAR30	226	883	forward 1	TM	Non-Cytosolic
20	LG:1095426.1:2001MAR30	1	119	forward 3	TM	Cytosolic
20	LG:1095426.1:2001MAR30	120	142	forward 3	TM	Transmembrane
20	LG:1095426.1:2001MAR30	143	882	forward 3	TM	Non-Cytosolic
21	LG:1132418.1:2001MAR30	1	141	forward 3	TM	Cytosolic
21	LG:1132418.1:2001MAR30	142	164	forward 3	TM	Transmembrane
21	LG:1132418.1:2001MAR30	165	260	forward 3	TM	Non-Cytosolic
22	LG:1377900.14:2001MAR30	1	157	forward 1	TM	Cytosolic
22	LG:1377900.14:2001MAR30	158	180	forward 1	TM	Transmembrane
22	LG:1377900.14:2001MAR30	181	199	forward 1	TM	Non-Cytosolic
22	LG:1377900.14:2001MAR30	200	222	forward 1	TM	Transmembrane
22	LG:1377900.14:2001MAR30	223	230	forward 1	TM	Cytosolic
23	LG:1383812.1:2001MAR30	1	83	forward 2	TM	Non-Cytosolic
23	LG:1383812.1:2001MAR30	84	106	forward 2	TM	Transmembrane
23	LG:1383812.1:2001MAR30	107	125	forward 2	TM	Cytosolic
23	LG:1383812.1:2001MAR30	126	143	forward 2	TM	Transmembrane
23	LG:1383812.1:2001MAR30	144	152	forward 2	TM	Non-Cytosolic
23	LG:1383812.1:2001MAR30	153	170	forward 2	TM	Transmembrane
23	LG:1383812.1:2001MAR30	171	176	forward 2	TM	Cytosolic
23	LG:1383812.1:2001MAR30	177	196	forward 2	TM	Transmembrane
23	LG:1383812.1:2001MAR30	197	200	forward 2	TM	Non-Cytosolic
23	LG:1383812.1:2001MAR30	201	218	forward 2	TM	Transmembrane
23	LG:1383812.1:2001MAR30	219	224	forward 2	TM	Cytosolic
23	LG:1383812.1:2001MAR30	225	247	forward 2	TM	Transmembrane
23	LG:1383812.1:2001MAR30	248	732	forward 2	TM	Non-Cytosolic
24	LG:1468687.1:2001MAR30	1	48	forward 1	TM	Non-Cytosolic
24	LG:1468687.1:2001MAR30	49	71	forward 1	TM	Transmembrane
24	LG:1468687.1:2001MAR30	72	152	forward 1	TM	Cytosolic
25	LG:1505513.1:2001MAR30	1	14	forward 1	TM	Non-Cytosolic
25	LG:1505513.1:2001MAR30	15	37	forward 1	TM	Transmembrane
25	LG:1505513.1:2001MAR30	38	110	forward 1	TM	Cytosolic
25	LG:1505513.1:2001MAR30	111	133	forward 1	TM	Transmembrane
25	LG:1505513.1:2001MAR30	134	152	forward 1	TM	Non-Cytosolic
25	LG:1505513.1:2001MAR30	153	172	forward 1	TM	Transmembrane
25	LG:1505513.1:2001MAR30	173	344	forward 1	TM	Cytosolic
25	LG:1505513.1:2001MAR30	1	12	forward 2	TM	Cytosolic
25	LG:1505513.1:2001MAR30	13	35	forward 2	TM	Transmembrane
25	LG:1505513.1:2001MAR30	36	49	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
25	LG:1505513.1:2001MAR30	50	72	forward 2	TM	Transmembrane
25	LG:1505513.1:2001MAR30	73	110	forward 2	TM	Cytosolic
25	LG:1505513.1:2001MAR30	111	133	forward 2	TM	Transmembrane
25	LG:1505513.1:2001MAR30	134	343	forward 2	TM	Non-Cytosolic
25	LG:1505513.1:2001MAR30	1	14	forward 3	TM	Non-Cytosolic
25	LG:1505513.1:2001MAR30	15	37	forward 3	TM	Transmembrane
25	LG:1505513.1:2001MAR30	38	108	forward 3	TM	Cytosolic
25	LG:1505513.1:2001MAR30	109	126	forward 3	TM	Transmembrane
25	LG:1505513.1:2001MAR30	127	343	forward 3	TM	Non-Cytosolic
26	LG:178823.9:2001MAR30	1	262	forward 1	TM	Non-Cytosolic
26	LG:178823.9:2001MAR30	263	281	forward 1	TM	Transmembrane
26	LG:178823.9:2001MAR30	282	292	forward 1	TM	Cytosolic
26	LG:178823.9:2001MAR30	293	312	forward 1	TM	Transmembrane
26	LG:178823.9:2001MAR30	313	316	forward 1	TM	Non-Cytosolic
26	LG:178823.9:2001MAR30	317	334	forward 1	TM	Transmembrane
26	LG:178823.9:2001MAR30	335	346	forward 1	TM	Cytosolic
26	LG:178823.9:2001MAR30	347	369	forward 1	TM	Transmembrane
26	LG:178823.9:2001MAR30	370	398	forward 1	TM	Non-Cytosolic
26	LG:178823.9:2001MAR30	1	90	forward 2	TM	Cytosolic
26	LG:178823.9:2001MAR30	91	113	forward 2	TM	Transmembrane
26	LG:178823.9:2001MAR30	114	127	forward 2	TM	Non-Cytosolic
26	LG:178823.9:2001MAR30	128	150	forward 2	TM	Transmembrane
26	LG:178823.9:2001MAR30	151	296	forward 2	TM	Cytosolic
26	LG:178823.9:2001MAR30	297	319	forward 2	TM	Transmembrane
26	LG:178823.9:2001MAR30	320	333	forward 2	TM	Non-Cytosolic
26	LG:178823.9:2001MAR30	334	351	forward 2	TM	Transmembrane
26	LG:178823.9:2001MAR30	352	398	forward 2	TM	Cytosolic
27	LG:198342.3:2001MAR30	1	1418	forward 3	TM	Non-Cytosolic
27	LG:198342.3:2001MAR30	1419	1441	forward 3	TM	Transmembrane
27	LG:198342.3:2001MAR30	1442	1545	forward 3	TM	Cytosolic
27	LG:198342.3:2001MAR30	1546	1568	forward 3	TM	Transmembrane
27	LG:198342.3:2001MAR30	1569	1597	forward 3	TM	Non-Cytosolic
28	LG:210672.1:2001MAR30	1	397	forward 1	TM	Cytosolic
28	LG:210672.1:2001MAR30	398	420	forward 1	TM	Transmembrane
28	LG:210672.1:2001MAR30	421	468	forward 1	TM	Non-Cytosolic
28	LG:210672.1:2001MAR30	469	491	forward 1	TM	Transmembrane
28	LG:210672.1:2001MAR30	492	585	forward 1	TM	Cytosolic
28	LG:210672.1:2001MAR30	1	76	forward 2	TM	Cytosolic
28	LG:210672.1:2001MAR30	77	99	forward 2	TM	Transmembrane
28	LG:210672.1:2001MAR30	100	102	forward 2	TM	Non-Cytosolic
28	LG:210672.1:2001MAR30	103	125	forward 2	TM	Transmembrane
28	LG:210672.1:2001MAR30	126	402	forward 2	TM	Cytosolic
28	LG:210672.1:2001MAR30	403	425	forward 2	TM	Transmembrane
28	LG:210672.1:2001MAR30	426	585	forward 2	TM	Non-Cytosolic
29	LG:212823.8:2001MAR30	1	58	forward 1	TM	Non-Cytosolic
29	LG:212823.8:2001MAR30	59	81	forward 1	TM	Transmembrane
29	LG:212823.8:2001MAR30	82	100	forward 1	TM	Cytosolic
29	LG:212823.8:2001MAR30	101	123	forward 1	TM	Transmembrane
29	LG:212823.8:2001MAR30	124	569	forward 1	TM	Non-Cytosolic
29	LG:212823.8:2001MAR30	570	588	forward 1	TM	Transmembrane
29	LG:212823.8:2001MAR30	589	594	forward 1	TM	Cytosolic
29	LG:212823.8:2001MAR30	595	617	forward 1	TM	Transmembrane
29	LG:212823.8:2001MAR30	618	835	forward 1	TM	Non-Cytosolic
29	LG:212823.8:2001MAR30	1	37	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
29	LG:212823.8:2001MAR30	38	60	forward 2	TM	Transmembrane
29	LG:212823.8:2001MAR30	61	64	forward 2	TM	Non-Cytosolic
29	LG:212823.8:2001MAR30	65	82	forward 2	TM	Transmembrane
29	LG:212823.8:2001MAR30	83	88	forward 2	TM	Cytosolic
29	LG:212823.8:2001MAR30	89	111	forward 2	TM	Transmembrane
29	LG:212823.8:2001MAR30	112	835	forward 2	TM	Non-Cytosolic
29	LG:212823.8:2001MAR30	1	9	forward 3	TM	Non-Cytosolic
29	LG:212823.8:2001MAR30	10	32	forward 3	TM	Transmembrane
29	LG:212823.8:2001MAR30	33	51	forward 3	TM	Cytosolic
29	LG:212823.8:2001MAR30	52	74	forward 3	TM	Transmembrane
29	LG:212823.8:2001MAR30	75	587	forward 3	TM	Non-Cytosolic
29	LG:212823.8:2001MAR30	588	610	forward 3	TM	Transmembrane
29	LG:212823.8:2001MAR30	611	834	forward 3	TM	Cytosolic
30	LG:220495.9:2001MAR30	1	14	forward 1	TM	Non-Cytosolic
30	LG:220495.9:2001MAR30	15	37	forward 1	TM	Transmembrane
30	LG:220495.9:2001MAR30	38	446	forward 1	TM	Cytosolic
30	LG:220495.9:2001MAR30	447	465	forward 1	TM	Transmembrane
30	LG:220495.9:2001MAR30	466	484	forward 1	TM	Non-Cytosolic
30	LG:220495.9:2001MAR30	485	507	forward 1	TM	Transmembrane
30	LG:220495.9:2001MAR30	508	567	forward 1	TM	Cytosolic
30	LG:220495.9:2001MAR30	568	590	forward 1	TM	Transmembrane
30	LG:220495.9:2001MAR30	591	599	forward 1	TM	Non-Cytosolic
30	LG:220495.9:2001MAR30	600	622	forward 1	TM	Transmembrane
30	LG:220495.9:2001MAR30	623	737	forward 1	TM	Cytosolic
30	LG:220495.9:2001MAR30	1	40	forward 2	TM	Non-Cytosolic
30	LG:220495.9:2001MAR30	41	63	forward 2	TM	Transmembrane
30	LG:220495.9:2001MAR30	64	163	forward 2	TM	Cytosolic
30	LG:220495.9:2001MAR30	164	183	forward 2	TM	Transmembrane
30	LG:220495.9:2001MAR30	184	192	forward 2	TM	Non-Cytosolic
30	LG:220495.9:2001MAR30	193	210	forward 2	TM	Transmembrane
30	LG:220495.9:2001MAR30	211	247	forward 2	TM	Cytosolic
30	LG:220495.9:2001MAR30	248	270	forward 2	TM	Transmembrane
30	LG:220495.9:2001MAR30	271	284	forward 2	TM	Non-Cytosolic
30	LG:220495.9:2001MAR30	285	307	forward 2	TM	Transmembrane
30	LG:220495.9:2001MAR30	308	486	forward 2	TM	Cytosolic
30	LG:220495.9:2001MAR30	487	509	forward 2	TM	Transmembrane
30	LG:220495.9:2001MAR30	510	737	forward 2	TM	Non-Cytosolic
31	LG:238262.1:2001MAR30	1	327	forward 1	TM	Cytosolic
31	LG:238262.1:2001MAR30	328	350	forward 1	TM	Transmembrane
31	LG:238262.1:2001MAR30	351	369	forward 1	TM	Non-Cytosolic
31	LG:238262.1:2001MAR30	370	392	forward 1	TM	Transmembrane
31	LG:238262.1:2001MAR30	393	405	forward 1	TM	Cytosolic
31	LG:238262.1:2001MAR30	1	334	forward 3	TM	Non-Cytosolic
31	LG:238262.1:2001MAR30	335	357	forward 3	TM	Transmembrane
31	LG:238262.1:2001MAR30	358	404	forward 3	TM	Cytosolic
32	LG:239410.21:2001MAR30	1	816	forward 1	TM	Non-Cytosolic
32	LG:239410.21:2001MAR30	817	834	forward 1	TM	Transmembrane
32	LG:239410.21:2001MAR30	835	963	forward 1	TM	Cytosolic
32	LG:239410.21:2001MAR30	1	139	forward 2	TM	Non-Cytosolic
32	LG:239410.21:2001MAR30	140	162	forward 2	TM	Transmembrane
32	LG:239410.21:2001MAR30	163	163	forward 2	TM	Cytosolic
32	LG:239410.21:2001MAR30	164	186	forward 2	TM	Transmembrane
32	LG:239410.21:2001MAR30	187	219	forward 2	TM	Non-Cytosolic
32	LG:239410.21:2001MAR30	220	242	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
32	LG:239410.21:2001MAR30	243	267	forward 2	TM	Cytosolic
32	LG:239410.21:2001MAR30	268	290	forward 2	TM	Transmembrane
32	LG:239410.21:2001MAR30	291	365	forward 2	TM	Non-Cytosolic
32	LG:239410.21:2001MAR30	366	388	forward 2	TM	Transmembrane
32	LG:239410.21:2001MAR30	389	408	forward 2	TM	Cytosolic
32	LG:239410.21:2001MAR30	409	431	forward 2	TM	Transmembrane
32	LG:239410.21:2001MAR30	432	470	forward 2	TM	Non-Cytosolic
32	LG:239410.21:2001MAR30	471	493	forward 2	TM	Transmembrane
32	LG:239410.21:2001MAR30	494	508	forward 2	TM	Cytosolic
32	LG:239410.21:2001MAR30	509	531	forward 2	TM	Transmembrane
32	LG:239410.21:2001MAR30	532	550	forward 2	TM	Non-Cytosolic
32	LG:239410.21:2001MAR30	551	573	forward 2	TM	Transmembrane
32	LG:239410.21:2001MAR30	574	963	forward 2	TM	Cytosolic
33	LG:245854.7:2001MAR30	1	68	forward 3	TM	Cytosolic
33	LG:245854.7:2001MAR30	69	88	forward 3	TM	Transmembrane
33	LG:245854.7:2001MAR30	89	1346	forward 3	TM	Non-Cytosolic
34	LG:294697.1:2001MAR30	1	61	forward 1	TM	Cytosolic
34	LG:294697.1:2001MAR30	62	84	forward 1	TM	Transmembrane
34	LG:294697.1:2001MAR30	85	225	forward 1	TM	Non-Cytosolic
34	LG:294697.1:2001MAR30	1	85	forward 3	TM	Cytosolic
34	LG:294697.1:2001MAR30	86	105	forward 3	TM	Transmembrane
34	LG:294697.1:2001MAR30	106	178	forward 3	TM	Non-Cytosolic
34	LG:294697.1:2001MAR30	179	201	forward 3	TM	Transmembrane
34	LG:294697.1:2001MAR30	202	224	forward 3	TM	Cytosolic
35	LG:345884.1:2001MAR30	1	28	forward 1	TM	Cytosolic
35	LG:345884.1:2001MAR30	29	51	forward 1	TM	Transmembrane
35	LG:345884.1:2001MAR30	52	192	forward 1	TM	Non-Cytosolic
36	LG:400095.15:2001MAR30	1	970	forward 1	TM	Non-Cytosolic
36	LG:400095.15:2001MAR30	971	993	forward 1	TM	Transmembrane
36	LG:400095.15:2001MAR30	994	997	forward 1	TM	Cytosolic
36	LG:400095.15:2001MAR30	998	1015	forward 1	TM	Transmembrane
36	LG:400095.15:2001MAR30	1016	1018	forward 1	TM	Non-Cytosolic
36	LG:400095.15:2001MAR30	1019	1036	forward 1	TM	Transmembrane
36	LG:400095.15:2001MAR30	1037	1062	forward 1	TM	Cytosolic
37	LG:402180.1:2001MAR30	1	162	forward 1	TM	Cytosolic
37	LG:402180.1:2001MAR30	163	185	forward 1	TM	Transmembrane
37	LG:402180.1:2001MAR30	186	204	forward 1	TM	Non-Cytosolic
37	LG:402180.1:2001MAR30	205	227	forward 1	TM	Transmembrane
37	LG:402180.1:2001MAR30	228	283	forward 1	TM	Cytosolic
37	LG:402180.1:2001MAR30	284	306	forward 1	TM	Transmembrane
37	LG:402180.1:2001MAR30	307	325	forward 1	TM	Non-Cytosolic
37	LG:402180.1:2001MAR30	326	348	forward 1	TM	Transmembrane
37	LG:402180.1:2001MAR30	349	560	forward 1	TM	Cytosolic
37	LG:402180.1:2001MAR30	561	583	forward 1	TM	Transmembrane
37	LG:402180.1:2001MAR30	584	614	forward 1	TM	Non-Cytosolic
37	LG:402180.1:2001MAR30	615	637	forward 1	TM	Transmembrane
37	LG:402180.1:2001MAR30	638	658	forward 1	TM	Cytosolic
37	LG:402180.1:2001MAR30	1	318	forward 2	TM	Non-Cytosolic
37	LG:402180.1:2001MAR30	319	341	forward 2	TM	Transmembrane
37	LG:402180.1:2001MAR30	342	562	forward 2	TM	Cytosolic
37	LG:402180.1:2001MAR30	563	585	forward 2	TM	Transmembrane
37	LG:402180.1:2001MAR30	586	658	forward 2	TM	Non-Cytosolic
38	LG:403401.1:2001MAR30	1	176	forward 1	TM	Cytosolic
38	LG:403401.1:2001MAR30	177	199	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
38	LG:403401.1:2001MAR30	200	218	forward 1	TM	Non-Cytosolic
38	LG:403401.1:2001MAR30	219	238	forward 1	TM	Transmembrane
38	LG:403401.1:2001MAR30	239	250	forward 1	TM	Cytosolic
38	LG:403401.1:2001MAR30	251	273	forward 1	TM	Transmembrane
38	LG:403401.1:2001MAR30	274	350	forward 1	TM	Non-Cytosolic
38	LG:403401.1:2001MAR30	1	14	forward 2	TM	Non-Cytosolic
38	LG:403401.1:2001MAR30	15	37	forward 2	TM	Transmembrane
38	LG:403401.1:2001MAR30	38	176	forward 2	TM	Cytosolic
38	LG:403401.1:2001MAR30	177	199	forward 2	TM	Transmembrane
38	LG:403401.1:2001MAR30	200	213	forward 2	TM	Non-Cytosolic
38	LG:403401.1:2001MAR30	214	236	forward 2	TM	Transmembrane
38	LG:403401.1:2001MAR30	237	350	forward 2	TM	Cytosolic
38	LG:403401.1:2001MAR30	1	138	forward 3	TM	Cytosolic
38	LG:403401.1:2001MAR30	139	161	forward 3	TM	Transmembrane
38	LG:403401.1:2001MAR30	162	192	forward 3	TM	Non-Cytosolic
38	LG:403401.1:2001MAR30	193	215	forward 3	TM	Transmembrane
38	LG:403401.1:2001MAR30	216	226	forward 3	TM	Cytosolic
38	LG:403401.1:2001MAR30	227	249	forward 3	TM	Transmembrane
38	LG:403401.1:2001MAR30	250	350	forward 3	TM	Non-Cytosolic
39	LG:411327.29:2001MAR30	1	97	forward 1	TM	Cytosolic
39	LG:411327.29:2001MAR30	98	120	forward 1	TM	Transmembrane
39	LG:411327.29:2001MAR30	121	371	forward 1	TM	Non-Cytosolic
40	LG:417464.10:2001MAR30	1	19	forward 1	TM	Non-Cytosolic
40	LG:417464.10:2001MAR30	20	42	forward 1	TM	Transmembrane
40	LG:417464.10:2001MAR30	43	298	forward 1	TM	Cytosolic
40	LG:417464.10:2001MAR30	299	321	forward 1	TM	Transmembrane
40	LG:417464.10:2001MAR30	322	340	forward 1	TM	Non-Cytosolic
40	LG:417464.10:2001MAR30	341	363	forward 1	TM	Transmembrane
40	LG:417464.10:2001MAR30	364	418	forward 1	TM	Cytosolic
40	LG:417464.10:2001MAR30	1	287	forward 2	TM	Non-Cytosolic
40	LG:417464.10:2001MAR30	288	310	forward 2	TM	Transmembrane
40	LG:417464.10:2001MAR30	311	330	forward 2	TM	Cytosolic
40	LG:417464.10:2001MAR30	331	353	forward 2	TM	Transmembrane
40	LG:417464.10:2001MAR30	354	367	forward 2	TM	Non-Cytosolic
40	LG:417464.10:2001MAR30	368	390	forward 2	TM	Transmembrane
40	LG:417464.10:2001MAR30	391	418	forward 2	TM	Cytosolic
40	LG:417464.10:2001MAR30	1	1	forward 3	TM	Cytosolic
40	LG:417464.10:2001MAR30	2	24	forward 3	TM	Transmembrane
40	LG:417464.10:2001MAR30	25	95	forward 3	TM	Non-Cytosolic
40	LG:417464.10:2001MAR30	96	118	forward 3	TM	Transmembrane
40	LG:417464.10:2001MAR30	119	328	forward 3	TM	Cytosolic
40	LG:417464.10:2001MAR30	329	351	forward 3	TM	Transmembrane
40	LG:417464.10:2001MAR30	352	417	forward 3	TM	Non-Cytosolic
41	LG:481997.1:2001MAR30	1	82	forward 1	TM	Cytosolic
41	LG:481997.1:2001MAR30	83	105	forward 1	TM	Transmembrane
41	LG:481997.1:2001MAR30	106	152	forward 1	TM	Non-Cytosolic
41	LG:481997.1:2001MAR30	153	175	forward 1	TM	Transmembrane
41	LG:481997.1:2001MAR30	176	253	forward 1	TM	Cytosolic
41	LG:481997.1:2001MAR30	254	276	forward 1	TM	Transmembrane
41	LG:481997.1:2001MAR30	277	279	forward 1	TM	Non-Cytosolic
41	LG:481997.1:2001MAR30	280	302	forward 1	TM	Transmembrane
41	LG:481997.1:2001MAR30	303	383	forward 1	TM	Cytosolic
41	LG:481997.1:2001MAR30	1	81	forward 3	TM	Cytosolic
41	LG:481997.1:2001MAR30	82	104	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
41	LG:481997.1:2001MAR30	105	382	forward 3	TM	Non-Cytosolic
42	LG:979304.7:2001MAR30	1	319	forward 2	TM	Non-Cytosolic
42	LG:979304.7:2001MAR30	320	342	forward 2	TM	Transmembrane
42	LG:979304.7:2001MAR30	343	354	forward 2	TM	Cytosolic
42	LG:979304.7:2001MAR30	355	377	forward 2	TM	Transmembrane
42	LG:979304.7:2001MAR30	378	391	forward 2	TM	Non-Cytosolic
42	LG:979304.7:2001MAR30	392	414	forward 2	TM	Transmembrane
42	LG:979304.7:2001MAR30	415	426	forward 2	TM	Cytosolic
43	LG:997964.1:2001MAR30	21	110	forward 3	SP	
43	LG:997964.1:2001MAR30	1	356	forward 3	TM	Cytosolic
43	LG:997964.1:2001MAR30	357	379	forward 3	TM	Transmembrane
43	LG:997964.1:2001MAR30	380	1082	forward 3	TM	Non-Cytosolic
44	LG:998845.1:2001MAR30	1	66	forward 2	TM	Non-Cytosolic
44	LG:998845.1:2001MAR30	67	89	forward 2	TM	Transmembrane
44	LG:998845.1:2001MAR30	90	281	forward 2	TM	Cytosolic
44	LG:998845.1:2001MAR30	1	67	forward 3	TM	Non-Cytosolic
44	LG:998845.1:2001MAR30	68	90	forward 3	TM	Transmembrane
44	LG:998845.1:2001MAR30	91	102	forward 3	TM	Cytosolic
44	LG:998845.1:2001MAR30	103	125	forward 3	TM	Transmembrane
44	LG:998845.1:2001MAR30	126	185	forward 3	TM	Non-Cytosolic
44	LG:998845.1:2001MAR30	186	208	forward 3	TM	Transmembrane
44	LG:998845.1:2001MAR30	209	281	forward 3	TM	Cytosolic
45	LG:000014.1:2001MAR30	1	92	forward 1	TM	Cytosolic
45	LG:000014.1:2001MAR30	93	115	forward 1	TM	Transmembrane
45	LG:000014.1:2001MAR30	116	156	forward 1	TM	Non-Cytosolic
45	LG:000014.1:2001MAR30	157	179	forward 1	TM	Transmembrane
45	LG:000014.1:2001MAR30	180	198	forward 1	TM	Cytosolic
45	LG:000014.1:2001MAR30	199	221	forward 1	TM	Transmembrane
45	LG:000014.1:2001MAR30	222	300	forward 1	TM	Non-Cytosolic
45	LG:000014.1:2001MAR30	301	323	forward 1	TM	Transmembrane
45	LG:000014.1:2001MAR30	324	327	forward 1	TM	Cytosolic
45	LG:000014.1:2001MAR30	328	347	forward 1	TM	Transmembrane
45	LG:000014.1:2001MAR30	348	363	forward 1	TM	Non-Cytosolic
45	LG:000014.1:2001MAR30	1	183	forward 2	TM	Non-Cytosolic
45	LG:000014.1:2001MAR30	184	206	forward 2	TM	Transmembrane
45	LG:000014.1:2001MAR30	207	276	forward 2	TM	Cytosolic
45	LG:000014.1:2001MAR30	277	296	forward 2	TM	Transmembrane
45	LG:000014.1:2001MAR30	297	363	forward 2	TM	Non-Cytosolic
45	LG:000014.1:2001MAR30	1	94	forward 3	TM	Cytosolic
45	LG:000014.1:2001MAR30	95	117	forward 3	TM	Transmembrane
45	LG:000014.1:2001MAR30	118	120	forward 3	TM	Non-Cytosolic
45	LG:000014.1:2001MAR30	121	140	forward 3	TM	Transmembrane
45	LG:000014.1:2001MAR30	141	160	forward 3	TM	Cytosolic
45	LG:000014.1:2001MAR30	161	183	forward 3	TM	Transmembrane
45	LG:000014.1:2001MAR30	184	363	forward 3	TM	Non-Cytosolic
46	LG:000290.9:2001MAR30	1	559	forward 2	TM	Non-Cytosolic
46	LG:000290.9:2001MAR30	560	582	forward 2	TM	Transmembrane
46	LG:000290.9:2001MAR30	583	617	forward 2	TM	Cytosolic
47	LG:001923.1:2001MAR30	1	109	forward 1	TM	Cytosolic
47	LG:001923.1:2001MAR30	110	132	forward 1	TM	Transmembrane
47	LG:001923.1:2001MAR30	133	141	forward 1	TM	Non-Cytosolic
47	LG:001923.1:2001MAR30	142	164	forward 1	TM	Transmembrane
47	LG:001923.1:2001MAR30	165	176	forward 1	TM	Cytosolic
47	LG:001923.1:2001MAR30	177	199	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
47	LG:001923.1:2001MAR30	200	265	forward 1	TM	Non-Cytosolic
47	LG:001923.1:2001MAR30	266	288	forward 1	TM	Transmembrane
47	LG:001923.1:2001MAR30	289	461	forward 1	TM	Cytosolic
47	LG:001923.1:2001MAR30	462	484	forward 1	TM	Transmembrane
47	LG:001923.1:2001MAR30	485	503	forward 1	TM	Non-Cytosolic
47	LG:001923.1:2001MAR30	504	526	forward 1	TM	Transmembrane
47	LG:001923.1:2001MAR30	527	532	forward 1	TM	Cytosolic
47	LG:001923.1:2001MAR30	533	555	forward 1	TM	Transmembrane
47	LG:001923.1:2001MAR30	556	590	forward 1	TM	Non-Cytosolic
47	LG:001923.1:2001MAR30	1	135	forward 3	TM	Non-Cytosolic
47	LG:001923.1:2001MAR30	136	158	forward 3	TM	Transmembrane
47	LG:001923.1:2001MAR30	159	164	forward 3	TM	Cytosolic
47	LG:001923.1:2001MAR30	165	187	forward 3	TM	Transmembrane
47	LG:001923.1:2001MAR30	188	201	forward 3	TM	Non-Cytosolic
47	LG:001923.1:2001MAR30	202	221	forward 3	TM	Transmembrane
47	LG:001923.1:2001MAR30	222	241	forward 3	TM	Cytosolic
47	LG:001923.1:2001MAR30	242	264	forward 3	TM	Transmembrane
47	LG:001923.1:2001MAR30	265	589	forward 3	TM	Non-Cytosolic
48	LG:008606.21:2001MAR30	1	160	forward 1	TM	Cytosolic
48	LG:008606.21:2001MAR30	161	183	forward 1	TM	Transmembrane
48	LG:008606.21:2001MAR30	184	202	forward 1	TM	Non-Cytosolic
48	LG:008606.21:2001MAR30	203	225	forward 1	TM	Transmembrane
48	LG:008606.21:2001MAR30	226	401	forward 1	TM	Cytosolic
48	LG:008606.21:2001MAR30	402	424	forward 1	TM	Transmembrane
48	LG:008606.21:2001MAR30	425	443	forward 1	TM	Non-Cytosolic
48	LG:008606.21:2001MAR30	444	466	forward 1	TM	Transmembrane
48	LG:008606.21:2001MAR30	467	668	forward 1	TM	Cytosolic
48	LG:008606.21:2001MAR30	1	404	forward 2	TM	Non-Cytosolic
48	LG:008606.21:2001MAR30	405	427	forward 2	TM	Transmembrane
48	LG:008606.21:2001MAR30	428	439	forward 2	TM	Cytosolic
48	LG:008606.21:2001MAR30	440	462	forward 2	TM	Transmembrane
48	LG:008606.21:2001MAR30	463	667	forward 2	TM	Non-Cytosolic
48	LG:008606.21:2001MAR30	1	169	forward 3	TM	Cytosolic
48	LG:008606.21:2001MAR30	170	192	forward 3	TM	Transmembrane
48	LG:008606.21:2001MAR30	193	201	forward 3	TM	Non-Cytosolic
48	LG:008606.21:2001MAR30	202	224	forward 3	TM	Transmembrane
48	LG:008606.21:2001MAR30	225	230	forward 3	TM	Cytosolic
48	LG:008606.21:2001MAR30	231	253	forward 3	TM	Transmembrane
48	LG:008606.21:2001MAR30	254	410	forward 3	TM	Non-Cytosolic
48	LG:008606.21:2001MAR30	411	433	forward 3	TM	Transmembrane
48	LG:008606.21:2001MAR30	434	439	forward 3	TM	Cytosolic
48	LG:008606.21:2001MAR30	440	462	forward 3	TM	Transmembrane
48	LG:008606.21:2001MAR30	463	667	forward 3	TM	Non-Cytosolic
49	LG:009699.32:2001MAR30	1	6	forward 1	TM	Cytosolic
49	LG:009699.32:2001MAR30	7	25	forward 1	TM	Transmembrane
49	LG:009699.32:2001MAR30	26	127	forward 1	TM	Non-Cytosolic
49	LG:009699.32:2001MAR30	128	150	forward 1	TM	Transmembrane
49	LG:009699.32:2001MAR30	151	180	forward 1	TM	Cytosolic
49	LG:009699.32:2001MAR30	1	128	forward 2	TM	Non-Cytosolic
49	LG:009699.32:2001MAR30	129	151	forward 2	TM	Transmembrane
49	LG:009699.32:2001MAR30	152	180	forward 2	TM	Cytosolic
50	LG:016723.6:2001MAR30	1	187	forward 1	TM	Cytosolic
50	LG:016723.6:2001MAR30	188	205	forward 1	TM	Transmembrane
50	LG:016723.6:2001MAR30	206	276	forward 1	TM	Non-Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
51	LG:017126.5:2001MAR30	1	310	forward 1	TM	Cytosolic
51	LG:017126.5:2001MAR30	311	333	forward 1	TM	Transmembrane
51	LG:017126.5:2001MAR30	334	360	forward 1	TM	Non-Cytosolic
51	LG:017126.5:2001MAR30	361	383	forward 1	TM	Transmembrane
51	LG:017126.5:2001MAR30	384	413	forward 1	TM	Cytosolic
51	LG:017126.5:2001MAR30	414	433	forward 1	TM	Transmembrane
51	LG:017126.5:2001MAR30	434	952	forward 1	TM	Non-Cytosolic
52	LG:019362.10:2001MAR30	1	20	forward 1	TM	Cytosolic
52	LG:019362.10:2001MAR30	21	40	forward 1	TM	Transmembrane
52	LG:019362.10:2001MAR30	41	49	forward 1	TM	Non-Cytosolic
52	LG:019362.10:2001MAR30	50	72	forward 1	TM	Transmembrane
52	LG:019362.10:2001MAR30	73	304	forward 1	TM	Cytosolic
52	LG:019362.10:2001MAR30	305	323	forward 1	TM	Transmembrane
52	LG:019362.10:2001MAR30	324	337	forward 1	TM	Non-Cytosolic
52	LG:019362.10:2001MAR30	338	357	forward 1	TM	Transmembrane
52	LG:019362.10:2001MAR30	358	377	forward 1	TM	Cytosolic
52	LG:019362.10:2001MAR30	378	400	forward 1	TM	Transmembrane
52	LG:019362.10:2001MAR30	401	494	forward 1	TM	Non-Cytosolic
52	LG:019362.10:2001MAR30	495	514	forward 1	TM	Transmembrane
52	LG:019362.10:2001MAR30	515	534	forward 1	TM	Cytosolic
52	LG:019362.10:2001MAR30	535	557	forward 1	TM	Transmembrane
52	LG:019362.10:2001MAR30	558	572	forward 1	TM	Non-Cytosolic
52	LG:019362.10:2001MAR30	1	47	forward 2	TM	Non-Cytosolic
52	LG:019362.10:2001MAR30	48	70	forward 2	TM	Transmembrane
52	LG:019362.10:2001MAR30	71	377	forward 2	TM	Cytosolic
52	LG:019362.10:2001MAR30	378	397	forward 2	TM	Transmembrane
52	LG:019362.10:2001MAR30	398	463	forward 2	TM	Non-Cytosolic
52	LG:019362.10:2001MAR30	464	483	forward 2	TM	Transmembrane
52	LG:019362.10:2001MAR30	484	495	forward 2	TM	Cytosolic
52	LG:019362.10:2001MAR30	496	518	forward 2	TM	Transmembrane
52	LG:019362.10:2001MAR30	519	546	forward 2	TM	Non-Cytosolic
52	LG:019362.10:2001MAR30	547	569	forward 2	TM	Transmembrane
52	LG:019362.10:2001MAR30	570	571	forward 2	TM	Cytosolic
53	LG:022183.1:2001MAR30	1	19	forward 2	TM	Cytosolic
53	LG:022183.1:2001MAR30	20	42	forward 2	TM	Transmembrane
53	LG:022183.1:2001MAR30	43	272	forward 2	TM	Non-Cytosolic
54	LG:028493.1:2001MAR30	1	521	forward 3	TM	Non-Cytosolic
54	LG:028493.1:2001MAR30	522	544	forward 3	TM	Transmembrane
54	LG:028493.1:2001MAR30	545	689	forward 3	TM	Cytosolic
55	LG:034197.1:2001MAR30	1	12	forward 3	TM	Cytosolic
55	LG:034197.1:2001MAR30	13	35	forward 3	TM	Transmembrane
55	LG:034197.1:2001MAR30	36	139	forward 3	TM	Non-Cytosolic
55	LG:034197.1:2001MAR30	140	162	forward 3	TM	Transmembrane
55	LG:034197.1:2001MAR30	163	192	forward 3	TM	Cytosolic
56	LG:054096.31:2001MAR30	1	723	forward 1	TM	Non-Cytosolic
56	LG:054096.31:2001MAR30	724	746	forward 1	TM	Transmembrane
56	LG:054096.31:2001MAR30	747	752	forward 1	TM	Cytosolic
56	LG:054096.31:2001MAR30	753	775	forward 1	TM	Transmembrane
56	LG:054096.31:2001MAR30	776	789	forward 1	TM	Non-Cytosolic
56	LG:054096.31:2001MAR30	790	812	forward 1	TM	Transmembrane
56	LG:054096.31:2001MAR30	813	844	forward 1	TM	Cytosolic
57	LG:054807.3:2001MAR30	1	253	forward 1	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	254	276	forward 1	TM	Transmembrane
57	LG:054807.3:2001MAR30	277	330	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
57	LG:054807.3:2001MAR30	331	350	forward 1	TM	Transmembrane
57	LG:054807.3:2001MAR30	351	353	forward 1	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	354	373	forward 1	TM	Transmembrane
57	LG:054807.3:2001MAR30	374	385	forward 1	TM	Cytosolic
57	LG:054807.3:2001MAR30	386	408	forward 1	TM	Transmembrane
57	LG:054807.3:2001MAR30	409	458	forward 1	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	459	481	forward 1	TM	Transmembrane
57	LG:054807.3:2001MAR30	482	551	forward 1	TM	Cytosolic
57	LG:054807.3:2001MAR30	552	574	forward 1	TM	Transmembrane
57	LG:054807.3:2001MAR30	575	577	forward 1	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	578	600	forward 1	TM	Transmembrane
57	LG:054807.3:2001MAR30	601	694	forward 1	TM	Cytosolic
57	LG:054807.3:2001MAR30	695	717	forward 1	TM	Transmembrane
57	LG:054807.3:2001MAR30	718	815	forward 1	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	1	426	forward 2	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	427	449	forward 2	TM	Transmembrane
57	LG:054807.3:2001MAR30	450	461	forward 2	TM	Cytosolic
57	LG:054807.3:2001MAR30	462	484	forward 2	TM	Transmembrane
57	LG:054807.3:2001MAR30	485	692	forward 2	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	693	710	forward 2	TM	Transmembrane
57	LG:054807.3:2001MAR30	711	751	forward 2	TM	Cytosolic
57	LG:054807.3:2001MAR30	752	774	forward 2	TM	Transmembrane
57	LG:054807.3:2001MAR30	775	788	forward 2	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	789	808	forward 2	TM	Transmembrane
57	LG:054807.3:2001MAR30	809	814	forward 2	TM	Cytosolic
57	LG:054807.3:2001MAR30	1	177	forward 3	TM	Cytosolic
57	LG:054807.3:2001MAR30	178	197	forward 3	TM	Transmembrane
57	LG:054807.3:2001MAR30	198	247	forward 3	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	248	270	forward 3	TM	Transmembrane
57	LG:054807.3:2001MAR30	271	327	forward 3	TM	Cytosolic
57	LG:054807.3:2001MAR30	328	350	forward 3	TM	Transmembrane
57	LG:054807.3:2001MAR30	351	433	forward 3	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	434	456	forward 3	TM	Transmembrane
57	LG:054807.3:2001MAR30	457	462	forward 3	TM	Cytosolic
57	LG:054807.3:2001MAR30	463	485	forward 3	TM	Transmembrane
57	LG:054807.3:2001MAR30	486	489	forward 3	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	490	512	forward 3	TM	Transmembrane
57	LG:054807.3:2001MAR30	513	550	forward 3	TM	Cytosolic
57	LG:054807.3:2001MAR30	551	573	forward 3	TM	Transmembrane
57	LG:054807.3:2001MAR30	574	576	forward 3	TM	Non-Cytosolic
57	LG:054807.3:2001MAR30	577	596	forward 3	TM	Transmembrane
57	LG:054807.3:2001MAR30	597	692	forward 3	TM	Cytosolic
57	LG:054807.3:2001MAR30	693	712	forward 3	TM	Transmembrane
57	LG:054807.3:2001MAR30	713	814	forward 3	TM	Non-Cytosolic
58	LG:065873.12:2001MAR30	1	38	forward 1	TM	Cytosolic
58	LG:065873.12:2001MAR30	39	58	forward 1	TM	Transmembrane
58	LG:065873.12:2001MAR30	59	925	forward 1	TM	Non-Cytosolic
58	LG:065873.12:2001MAR30	1	19	forward 3	TM	Cytosolic
58	LG:065873.12:2001MAR30	20	42	forward 3	TM	Transmembrane
58	LG:065873.12:2001MAR30	43	867	forward 3	TM	Non-Cytosolic
58	LG:065873.12:2001MAR30	868	890	forward 3	TM	Transmembrane
58	LG:065873.12:2001MAR30	891	924	forward 3	TM	Cytosolic
59	LG:083814.6:2001MAR30	1	660	forward 1	TM	Non-Cytosolic
59	LG:083814.6:2001MAR30	661	680	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
59	LG:083814.6:2001MAR30	681	714	forward 1	TM	Cytosolic
59	LG:083814.6:2001MAR30	715	733	forward 1	TM	Transmembrane
59	LG:083814.6:2001MAR30	734	741	forward 1	TM	Non-Cytosolic
59	LG:083814.6:2001MAR30	1	681	forward 3	TM	Non-Cytosolic
59	LG:083814.6:2001MAR30	682	701	forward 3	TM	Transmembrane
59	LG:083814.6:2001MAR30	702	712	forward 3	TM	Cytosolic
59	LG:083814.6:2001MAR30	713	730	forward 3	TM	Transmembrane
59	LG:083814.6:2001MAR30	731	740	forward 3	TM	Non-Cytosolic
60	LG:093477.1:2001MAR30	1	12	forward 2	TM	Cytosolic
60	LG:093477.1:2001MAR30	13	35	forward 2	TM	Transmembrane
60	LG:093477.1:2001MAR30	36	291	forward 2	TM	Non-Cytosolic
60	LG:093477.1:2001MAR30	1	6	forward 3	TM	Cytosolic
60	LG:093477.1:2001MAR30	7	29	forward 3	TM	Transmembrane
60	LG:093477.1:2001MAR30	30	291	forward 3	TM	Non-Cytosolic
61	LG:099572.12:2001MAR30	1	803	forward 2	TM	Non-Cytosolic
61	LG:099572.12:2001MAR30	804	826	forward 2	TM	Transmembrane
61	LG:099572.12:2001MAR30	827	960	forward 2	TM	Cytosolic
61	LG:099572.12:2001MAR30	961	975	forward 2	TM	Transmembrane
61	LG:099572.12:2001MAR30	976	984	forward 2	TM	Non-Cytosolic
61	LG:099572.12:2001MAR30	985	1007	forward 2	TM	Transmembrane
61	LG:099572.12:2001MAR30	1008	1043	forward 2	TM	Cytosolic
61	LG:099572.12:2001MAR30	1044	1066	forward 2	TM	Transmembrane
61	LG:099572.12:2001MAR30	1067	1510	forward 2	TM	Non-Cytosolic
61	LG:099572.12:2001MAR30	1511	1533	forward 2	TM	Transmembrane
61	LG:099572.12:2001MAR30	1534	1546	forward 2	TM	Cytosolic
61	LG:099572.12:2001MAR30	1	1008	forward 3	TM	Non-Cytosolic
61	LG:099572.12:2001MAR30	1009	1031	forward 3	TM	Transmembrane
61	LG:099572.12:2001MAR30	1032	1089	forward 3	TM	Cytosolic
61	LG:099572.12:2001MAR30	1090	1112	forward 3	TM	Transmembrane
61	LG:099572.12:2001MAR30	1113	1546	forward 3	TM	Non-Cytosolic
62	LG:100396.31:2001MAR30	1	247	forward 1	TM	Non-Cytosolic
62	LG:100396.31:2001MAR30	248	265	forward 1	TM	Transmembrane
62	LG:100396.31:2001MAR30	266	318	forward 1	TM	Cytosolic
62	LG:100396.31:2001MAR30	319	338	forward 1	TM	Transmembrane
62	LG:100396.31:2001MAR30	339	373	forward 1	TM	Non-Cytosolic
62	LG:100396.31:2001MAR30	374	393	forward 1	TM	Transmembrane
62	LG:100396.31:2001MAR30	394	394	forward 1	TM	Cytosolic
62	LG:100396.31:2001MAR30	1	361	forward 2	TM	Non-Cytosolic
62	LG:100396.31:2001MAR30	362	393	forward 2	TM	Transmembrane
62	LG:100396.31:2001MAR30	394	394	forward 2	TM	Cytosolic
63	LG:1026903.5:2001MAR30	1	84	forward 1	TM	Cytosolic
63	LG:1026903.5:2001MAR30	85	107	forward 1	TM	Transmembrane
63	LG:1026903.5:2001MAR30	108	452	forward 1	TM	Non-Cytosolic
64	LG:1060168.6:2001MAR30	1	147	forward 1	TM	Cytosolic
65	LG:1086906.41:2001MAR30	1	417	forward 2	TM	Non-Cytosolic
65	LG:1086906.41:2001MAR30	418	435	forward 2	TM	Transmembrane
65	LG:1086906.41:2001MAR30	436	551	forward 2	TM	Cytosolic
65	LG:1086906.41:2001MAR30	1	412	forward 3	TM	Non-Cytosolic
65	LG:1086906.41:2001MAR30	413	435	forward 3	TM	Transmembrane
65	LG:1086906.41:2001MAR30	436	551	forward 3	TM	Cytosolic
66	LG:1089326.18:2001MAR30	1	73	forward 2	TM	Cytosolic
66	LG:1089326.18:2001MAR30	74	96	forward 2	TM	Transmembrane
66	LG:1089326.18:2001MAR30	97	807	forward 2	TM	Non-Cytosolic
67	LG:1090862.32:2001MAR30	1	47	forward 3	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
67	LG:1090862.32:2001MAR30	48	70	forward 3	TM	Transmembrane
67	LG:1090862.32:2001MAR30	71	568	forward 3	TM	Non-Cytosolic
68	LG:1091941.41:2001MAR30	1	6	forward 1	TM	Cytosolic
68	LG:1091941.41:2001MAR30	7	29	forward 1	TM	Transmembrane
68	LG:1091941.41:2001MAR30	30	260	forward 1	TM	Non-Cytosolic
69	LG:1093386.8:2001MAR30	1	22	forward 1	TM	Non-Cytosolic
69	LG:1093386.8:2001MAR30	23	42	forward 1	TM	Transmembrane
69	LG:1093386.8:2001MAR30	43	254	forward 1	TM	Cytosolic
69	LG:1093386.8:2001MAR30	255	274	forward 1	TM	Transmembrane
69	LG:1093386.8:2001MAR30	275	612	forward 1	TM	Non-Cytosolic
69	LG:1093386.8:2001MAR30	613	635	forward 1	TM	Transmembrane
69	LG:1093386.8:2001MAR30	636	647	forward 1	TM	Cytosolic
69	LG:1093386.8:2001MAR30	648	670	forward 1	TM	Transmembrane
69	LG:1093386.8:2001MAR30	671	680	forward 1	TM	Non-Cytosolic
69	LG:1093386.8:2001MAR30	1	123	forward 2	TM	Non-Cytosolic
69	LG:1093386.8:2001MAR30	124	146	forward 2	TM	Transmembrane
69	LG:1093386.8:2001MAR30	147	597	forward 2	TM	Cytosolic
69	LG:1093386.8:2001MAR30	598	620	forward 2	TM	Transmembrane
69	LG:1093386.8:2001MAR30	621	642	forward 2	TM	Non-Cytosolic
69	LG:1093386.8:2001MAR30	643	665	forward 2	TM	Transmembrane
69	LG:1093386.8:2001MAR30	666	679	forward 2	TM	Cytosolic
69	LG:1093386.8:2001MAR30	1	252	forward 3	TM	Non-Cytosolic
69	LG:1093386.8:2001MAR30	253	275	forward 3	TM	Transmembrane
69	LG:1093386.8:2001MAR30	276	294	forward 3	TM	Cytosolic
69	LG:1093386.8:2001MAR30	295	317	forward 3	TM	Transmembrane
69	LG:1093386.8:2001MAR30	318	596	forward 3	TM	Non-Cytosolic
69	LG:1093386.8:2001MAR30	597	619	forward 3	TM	Transmembrane
69	LG:1093386.8:2001MAR30	620	639	forward 3	TM	Cytosolic
69	LG:1093386.8:2001MAR30	640	662	forward 3	TM	Transmembrane
69	LG:1093386.8:2001MAR30	663	679	forward 3	TM	Non-Cytosolic
70	LG:1094187.33:2001MAR30	1	128	forward 1	TM	Cytosolic
70	LG:1094187.33:2001MAR30	129	151	forward 1	TM	Transmembrane
70	LG:1094187.33:2001MAR30	152	154	forward 1	TM	Non-Cytosolic
70	LG:1094187.33:2001MAR30	155	177	forward 1	TM	Transmembrane
70	LG:1094187.33:2001MAR30	178	373	forward 1	TM	Cytosolic
70	LG:1094187.33:2001MAR30	374	396	forward 1	TM	Transmembrane
70	LG:1094187.33:2001MAR30	397	415	forward 1	TM	Non-Cytosolic
70	LG:1094187.33:2001MAR30	416	438	forward 1	TM	Transmembrane
70	LG:1094187.33:2001MAR30	439	472	forward 1	TM	Cytosolic
70	LG:1094187.33:2001MAR30	1	126	forward 2	TM	Cytosolic
70	LG:1094187.33:2001MAR30	127	149	forward 2	TM	Transmembrane
70	LG:1094187.33:2001MAR30	150	181	forward 2	TM	Non-Cytosolic
70	LG:1094187.33:2001MAR30	182	199	forward 2	TM	Transmembrane
70	LG:1094187.33:2001MAR30	200	372	forward 2	TM	Cytosolic
70	LG:1094187.33:2001MAR30	373	395	forward 2	TM	Transmembrane
70	LG:1094187.33:2001MAR30	396	421	forward 2	TM	Non-Cytosolic
70	LG:1094187.33:2001MAR30	422	444	forward 2	TM	Transmembrane
70	LG:1094187.33:2001MAR30	445	471	forward 2	TM	Cytosolic
70	LG:1094187.33:2001MAR30	1	129	forward 3	TM	Non-Cytosolic
70	LG:1094187.33:2001MAR30	130	149	forward 3	TM	Transmembrane
70	LG:1094187.33:2001MAR30	150	150	forward 3	TM	Cytosolic
70	LG:1094187.33:2001MAR30	151	170	forward 3	TM	Transmembrane
70	LG:1094187.33:2001MAR30	171	179	forward 3	TM	Non-Cytosolic
70	LG:1094187.33:2001MAR30	180	197	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
70	LG:1094187.33:2001MAR30	198	355	forward 3	TM	Cytosolic
70	LG:1094187.33:2001MAR30	356	375	forward 3	TM	Transmembrane
70	LG:1094187.33:2001MAR30	376	404	forward 3	TM	Non-Cytosolic
70	LG:1094187.33:2001MAR30	405	427	forward 3	TM	Transmembrane
70	LG:1094187.33:2001MAR30	428	439	forward 3	TM	Cytosolic
70	LG:1094187.33:2001MAR30	440	462	forward 3	TM	Transmembrane
70	LG:1094187.33:2001MAR30	463	471	forward 3	TM	Non-Cytosolic
71	LG:1098692.18:2001MAR30	1	37	forward 2	TM	Non-Cytosolic
71	LG:1098692.18:2001MAR30	38	57	forward 2	TM	Transmembrane
71	LG:1098692.18:2001MAR30	58	124	forward 2	TM	Cytosolic
71	LG:1098692.18:2001MAR30	125	147	forward 2	TM	Transmembrane
71	LG:1098692.18:2001MAR30	148	176	forward 2	TM	Non-Cytosolic
71	LG:1098692.18:2001MAR30	177	199	forward 2	TM	Transmembrane
71	LG:1098692.18:2001MAR30	200	211	forward 2	TM	Cytosolic
71	LG:1098692.18:2001MAR30	212	231	forward 2	TM	Transmembrane
71	LG:1098692.18:2001MAR30	232	250	forward 2	TM	Non-Cytosolic
71	LG:1098692.18:2001MAR30	251	273	forward 2	TM	Transmembrane
71	LG:1098692.18:2001MAR30	274	588	forward 2	TM	Cytosolic
72	LG:1173104.22:2001MAR30	1	180	forward 1	TM	Non-Cytosolic
72	LG:1173104.22:2001MAR30	181	203	forward 1	TM	Transmembrane
72	LG:1173104.22:2001MAR30	204	265	forward 1	TM	Cytosolic
72	LG:1173104.22:2001MAR30	266	288	forward 1	TM	Transmembrane
72	LG:1173104.22:2001MAR30	289	297	forward 1	TM	Non-Cytosolic
72	LG:1173104.22:2001MAR30	298	320	forward 1	TM	Transmembrane
72	LG:1173104.22:2001MAR30	321	389	forward 1	TM	Cytosolic
72	LG:1173104.22:2001MAR30	1	265	forward 2	TM	Cytosolic
72	LG:1173104.22:2001MAR30	266	285	forward 2	TM	Transmembrane
72	LG:1173104.22:2001MAR30	286	299	forward 2	TM	Non-Cytosolic
72	LG:1173104.22:2001MAR30	300	322	forward 2	TM	Transmembrane
72	LG:1173104.22:2001MAR30	323	389	forward 2	TM	Cytosolic
72	LG:1173104.22:2001MAR30	1	267	forward 3	TM	Non-Cytosolic
72	LG:1173104.22:2001MAR30	268	290	forward 3	TM	Transmembrane
72	LG:1173104.22:2001MAR30	291	296	forward 3	TM	Cytosolic
72	LG:1173104.22:2001MAR30	297	319	forward 3	TM	Transmembrane
72	LG:1173104.22:2001MAR30	320	388	forward 3	TM	Non-Cytosolic
73	LG:1215335.7:2001MAR30	1	971	forward 1	TM	Non-Cytosolic
73	LG:1215335.7:2001MAR30	972	994	forward 1	TM	Transmembrane
73	LG:1215335.7:2001MAR30	995	1050	forward 1	TM	Cytosolic
73	LG:1215335.7:2001MAR30	1	160	forward 2	TM	Non-Cytosolic
73	LG:1215335.7:2001MAR30	161	183	forward 2	TM	Transmembrane
73	LG:1215335.7:2001MAR30	184	467	forward 2	TM	Cytosolic
73	LG:1215335.7:2001MAR30	468	490	forward 2	TM	Transmembrane
73	LG:1215335.7:2001MAR30	491	1050	forward 2	TM	Non-Cytosolic
74	LG:1256753.1:2001MAR30	1	10	forward 1	TM	Cytosolic
74	LG:1256753.1:2001MAR30	11	33	forward 1	TM	Transmembrane
74	LG:1256753.1:2001MAR30	34	614	forward 1	TM	Non-Cytosolic
74	LG:1256753.1:2001MAR30	615	637	forward 1	TM	Transmembrane
74	LG:1256753.1:2001MAR30	638	669	forward 1	TM	Cytosolic
74	LG:1256753.1:2001MAR30	1	573	forward 2	TM	Cytosolic
74	LG:1256753.1:2001MAR30	574	596	forward 2	TM	Transmembrane
74	LG:1256753.1:2001MAR30	597	615	forward 2	TM	Non-Cytosolic
74	LG:1256753.1:2001MAR30	616	638	forward 2	TM	Transmembrane
74	LG:1256753.1:2001MAR30	639	669	forward 2	TM	Cytosolic
74	LG:1256753.1:2001MAR30	1	45	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
74	LG:1256753.1:2001MAR30	46	68	forward 3	TM	Transmembrane
74	LG:1256753.1:2001MAR30	69	74	forward 3	TM	Cytosolic
74	LG:1256753.1:2001MAR30	75	97	forward 3	TM	Transmembrane
74	LG:1256753.1:2001MAR30	98	503	forward 3	TM	Non-Cytosolic
74	LG:1256753.1:2001MAR30	504	523	forward 3	TM	Transmembrane
74	LG:1256753.1:2001MAR30	524	669	forward 3	TM	Cytosolic
75	LG:1326702.10:2001MAR30	1	2173	forward 1	TM	Non-Cytosolic
75	LG:1326702.10:2001MAR30	2174	2196	forward 1	TM	Transmembrane
75	LG:1326702.10:2001MAR30	2197	2202	forward 1	TM	Cytosolic
75	LG:1326702.10:2001MAR30	2203	2225	forward 1	TM	Transmembrane
75	LG:1326702.10:2001MAR30	2226	2234	forward 1	TM	Non-Cytosolic
75	LG:1326702.10:2001MAR30	2235	2257	forward 1	TM	Transmembrane
75	LG:1326702.10:2001MAR30	2258	2258	forward 1	TM	Cytosolic
75	LG:1326702.10:2001MAR30	1	2174	forward 2	TM	Non-Cytosolic
75	LG:1326702.10:2001MAR30	2175	2197	forward 2	TM	Transmembrane
75	LG:1326702.10:2001MAR30	2198	2209	forward 2	TM	Cytosolic
75	LG:1326702.10:2001MAR30	2210	2232	forward 2	TM	Transmembrane
75	LG:1326702.10:2001MAR30	2233	2257	forward 2	TM	Non-Cytosolic
75	LG:1326702.10:2001MAR30	1	1425	forward 3	TM	Non-Cytosolic
75	LG:1326702.10:2001MAR30	1426	1448	forward 3	TM	Transmembrane
75	LG:1326702.10:2001MAR30	1449	1521	forward 3	TM	Cytosolic
75	LG:1326702.10:2001MAR30	1522	1541	forward 3	TM	Transmembrane
75	LG:1326702.10:2001MAR30	1542	1608	forward 3	TM	Non-Cytosolic
75	LG:1326702.10:2001MAR30	1609	1631	forward 3	TM	Transmembrane
75	LG:1326702.10:2001MAR30	1632	2174	forward 3	TM	Cytosolic
75	LG:1326702.10:2001MAR30	2175	2197	forward 3	TM	Transmembrane
75	LG:1326702.10:2001MAR30	2198	2211	forward 3	TM	Non-Cytosolic
75	LG:1326702.10:2001MAR30	2212	2234	forward 3	TM	Transmembrane
75	LG:1326702.10:2001MAR30	2235	2257	forward 3	TM	Cytosolic
76	LG:1327239.15:2001MAR30	1	59	forward 1	TM	Cytosolic
76	LG:1327239.15:2001MAR30	60	82	forward 1	TM	Transmembrane
76	LG:1327239.15:2001MAR30	83	253	forward 1	TM	Non-Cytosolic
76	LG:1327239.15:2001MAR30	254	276	forward 1	TM	Transmembrane
76	LG:1327239.15:2001MAR30	277	287	forward 1	TM	Cytosolic
76	LG:1327239.15:2001MAR30	288	310	forward 1	TM	Transmembrane
76	LG:1327239.15:2001MAR30	311	499	forward 1	TM	Non-Cytosolic
76	LG:1327239.15:2001MAR30	1	60	forward 2	TM	Cytosolic
76	LG:1327239.15:2001MAR30	61	83	forward 2	TM	Transmembrane
76	LG:1327239.15:2001MAR30	84	120	forward 2	TM	Non-Cytosolic
76	LG:1327239.15:2001MAR30	121	143	forward 2	TM	Transmembrane
76	LG:1327239.15:2001MAR30	144	155	forward 2	TM	Cytosolic
76	LG:1327239.15:2001MAR30	156	178	forward 2	TM	Transmembrane
76	LG:1327239.15:2001MAR30	179	499	forward 2	TM	Non-Cytosolic
76	LG:1327239.15:2001MAR30	1	33	forward 3	TM	Cytosolic
76	LG:1327239.15:2001MAR30	34	56	forward 3	TM	Transmembrane
76	LG:1327239.15:2001MAR30	57	60	forward 3	TM	Non-Cytosolic
76	LG:1327239.15:2001MAR30	61	83	forward 3	TM	Transmembrane
76	LG:1327239.15:2001MAR30	84	190	forward 3	TM	Cytosolic
76	LG:1327239.15:2001MAR30	191	213	forward 3	TM	Transmembrane
76	LG:1327239.15:2001MAR30	214	254	forward 3	TM	Non-Cytosolic
76	LG:1327239.15:2001MAR30	255	277	forward 3	TM	Transmembrane
76	LG:1327239.15:2001MAR30	278	468	forward 3	TM	Cytosolic
76	LG:1327239.15:2001MAR30	469	491	forward 3	TM	Transmembrane
76	LG:1327239.15:2001MAR30	492	499	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
77	LG:1327867.15:2001MAR30	1	508	forward 1	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	509	528	forward 1	TM	Transmembrane
77	LG:1327867.15:2001MAR30	529	548	forward 1	TM	Cytosolic
77	LG:1327867.15:2001MAR30	549	571	forward 1	TM	Transmembrane
77	LG:1327867.15:2001MAR30	572	575	forward 1	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	576	593	forward 1	TM	Transmembrane
77	LG:1327867.15:2001MAR30	594	706	forward 1	TM	Cytosolic
77	LG:1327867.15:2001MAR30	707	729	forward 1	TM	Transmembrane
77	LG:1327867.15:2001MAR30	730	774	forward 1	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	775	797	forward 1	TM	Transmembrane
77	LG:1327867.15:2001MAR30	798	803	forward 1	TM	Cytosolic
77	LG:1327867.15:2001MAR30	804	826	forward 1	TM	Transmembrane
77	LG:1327867.15:2001MAR30	827	851	forward 1	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	852	874	forward 1	TM	Transmembrane
77	LG:1327867.15:2001MAR30	875	893	forward 1	TM	Cytosolic
77	LG:1327867.15:2001MAR30	894	916	forward 1	TM	Transmembrane
77	LG:1327867.15:2001MAR30	917	930	forward 1	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	931	953	forward 1	TM	Transmembrane
77	LG:1327867.15:2001MAR30	954	1158	forward 1	TM	Cytosolic
77	LG:1327867.15:2001MAR30	1159	1181	forward 1	TM	Transmembrane
77	LG:1327867.15:2001MAR30	1182	1212	forward 1	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	1	450	forward 2	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	451	473	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	474	477	forward 2	TM	Cytosolic
77	LG:1327867.15:2001MAR30	478	496	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	497	505	forward 2	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	506	528	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	529	548	forward 2	TM	Cytosolic
77	LG:1327867.15:2001MAR30	549	571	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	572	574	forward 2	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	575	593	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	594	718	forward 2	TM	Cytosolic
77	LG:1327867.15:2001MAR30	719	741	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	742	760	forward 2	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	761	783	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	784	789	forward 2	TM	Cytosolic
77	LG:1327867.15:2001MAR30	790	812	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	813	854	forward 2	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	855	877	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	878	897	forward 2	TM	Cytosolic
77	LG:1327867.15:2001MAR30	898	920	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	921	934	forward 2	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	935	952	forward 2	TM	Transmembrane
77	LG:1327867.15:2001MAR30	953	1211	forward 2	TM	Cytosolic
77	LG:1327867.15:2001MAR30	1	447	forward 3	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	448	470	forward 3	TM	Transmembrane
77	LG:1327867.15:2001MAR30	471	548	forward 3	TM	Cytosolic
77	LG:1327867.15:2001MAR30	549	571	forward 3	TM	Transmembrane
77	LG:1327867.15:2001MAR30	572	574	forward 3	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	575	592	forward 3	TM	Transmembrane
77	LG:1327867.15:2001MAR30	593	771	forward 3	TM	Cytosolic
77	LG:1327867.15:2001MAR30	772	794	forward 3	TM	Transmembrane
77	LG:1327867.15:2001MAR30	795	798	forward 3	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	799	821	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
77	LG:1327867.15:2001MAR30	822	833	forward 3	TM	Cytosolic
77	LG:1327867.15:2001MAR30	834	856	forward 3	TM	Transmembrane
77	LG:1327867.15:2001MAR30	857	1174	forward 3	TM	Non-Cytosolic
77	LG:1327867.15:2001MAR30	1175	1197	forward 3	TM	Transmembrane
77	LG:1327867.15:2001MAR30	1198	1211	forward 3	TM	Cytosolic
78	LG:1383232.1:2001MAR30	1	20	forward 1	TM	Cytosolic
78	LG:1383232.1:2001MAR30	21	43	forward 1	TM	Transmembrane
78	LG:1383232.1:2001MAR30	44	754	forward 1	TM	Non-Cytosolic
78	LG:1383232.1:2001MAR30	755	777	forward 1	TM	Transmembrane
78	LG:1383232.1:2001MAR30	778	788	forward 1	TM	Cytosolic
78	LG:1383232.1:2001MAR30	1	14	forward 2	TM	Non-Cytosolic
78	LG:1383232.1:2001MAR30	15	34	forward 2	TM	Transmembrane
78	LG:1383232.1:2001MAR30	35	71	forward 2	TM	Cytosolic
78	LG:1383232.1:2001MAR30	72	94	forward 2	TM	Transmembrane
78	LG:1383232.1:2001MAR30	95	113	forward 2	TM	Non-Cytosolic
78	LG:1383232.1:2001MAR30	114	136	forward 2	TM	Transmembrane
78	LG:1383232.1:2001MAR30	137	190	forward 2	TM	Cytosolic
78	LG:1383232.1:2001MAR30	191	213	forward 2	TM	Transmembrane
78	LG:1383232.1:2001MAR30	214	401	forward 2	TM	Non-Cytosolic
78	LG:1383232.1:2001MAR30	402	424	forward 2	TM	Transmembrane
78	LG:1383232.1:2001MAR30	425	604	forward 2	TM	Cytosolic
78	LG:1383232.1:2001MAR30	605	627	forward 2	TM	Transmembrane
78	LG:1383232.1:2001MAR30	628	720	forward 2	TM	Non-Cytosolic
78	LG:1383232.1:2001MAR30	721	743	forward 2	TM	Transmembrane
78	LG:1383232.1:2001MAR30	744	749	forward 2	TM	Cytosolic
78	LG:1383232.1:2001MAR30	750	769	forward 2	TM	Transmembrane
78	LG:1383232.1:2001MAR30	770	787	forward 2	TM	Non-Cytosolic
78	LG:1383232.1:2001MAR30	1	405	forward 3	TM	Non-Cytosolic
78	LG:1383232.1:2001MAR30	406	428	forward 3	TM	Transmembrane
78	LG:1383232.1:2001MAR30	429	480	forward 3	TM	Cytosolic
78	LG:1383232.1:2001MAR30	481	503	forward 3	TM	Transmembrane
78	LG:1383232.1:2001MAR30	504	699	forward 3	TM	Non-Cytosolic
78	LG:1383232.1:2001MAR30	700	722	forward 3	TM	Transmembrane
78	LG:1383232.1:2001MAR30	723	728	forward 3	TM	Cytosolic
78	LG:1383232.1:2001MAR30	729	747	forward 3	TM	Transmembrane
78	LG:1383232.1:2001MAR30	748	756	forward 3	TM	Non-Cytosolic
78	LG:1383232.1:2001MAR30	757	776	forward 3	TM	Transmembrane
78	LG:1383232.1:2001MAR30	777	787	forward 3	TM	Cytosolic
79	LG:1383368.40:2001MAR30	1	393	forward 1	TM	Cytosolic
79	LG:1383368.40:2001MAR30	394	416	forward 1	TM	Transmembrane
79	LG:1383368.40:2001MAR30	417	482	forward 1	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	483	500	forward 1	TM	Transmembrane
79	LG:1383368.40:2001MAR30	501	574	forward 1	TM	Cytosolic
79	LG:1383368.40:2001MAR30	575	597	forward 1	TM	Transmembrane
79	LG:1383368.40:2001MAR30	598	695	forward 1	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	696	718	forward 1	TM	Transmembrane
79	LG:1383368.40:2001MAR30	719	753	forward 1	TM	Cytosolic
79	LG:1383368.40:2001MAR30	754	776	forward 1	TM	Transmembrane
79	LG:1383368.40:2001MAR30	777	795	forward 1	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	796	818	forward 1	TM	Transmembrane
79	LG:1383368.40:2001MAR30	819	838	forward 1	TM	Cytosolic
79	LG:1383368.40:2001MAR30	839	861	forward 1	TM	Transmembrane
79	LG:1383368.40:2001MAR30	862	922	forward 1	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	923	945	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
79	LG:1383368.40:2001MAR30	946	1030	forward 1	TM	Cytosolic
79	LG:1383368.40:2001MAR30	1031	1050	forward 1	TM	Transmembrane
79	LG:1383368.40:2001MAR30	1051	1077	forward 1	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	1078	1100	forward 1	TM	Transmembrane
79	LG:1383368.40:2001MAR30	1101	1112	forward 1	TM	Cytosolic
79	LG:1383368.40:2001MAR30	1	398	forward 2	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	399	421	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	422	578	forward 2	TM	Cytosolic
79	LG:1383368.40:2001MAR30	579	601	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	602	604	forward 2	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	605	627	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	628	704	forward 2	TM	Cytosolic
79	LG:1383368.40:2001MAR30	705	724	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	725	733	forward 2	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	734	756	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	757	767	forward 2	TM	Cytosolic
79	LG:1383368.40:2001MAR30	768	790	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	791	804	forward 2	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	805	823	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	824	829	forward 2	TM	Cytosolic
79	LG:1383368.40:2001MAR30	830	847	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	848	856	forward 2	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	857	879	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	880	1005	forward 2	TM	Cytosolic
79	LG:1383368.40:2001MAR30	1006	1028	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	1029	1032	forward 2	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	1033	1052	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	1053	1077	forward 2	TM	Cytosolic
79	LG:1383368.40:2001MAR30	1078	1100	forward 2	TM	Transmembrane
79	LG:1383368.40:2001MAR30	1101	1112	forward 2	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	1	129	forward 3	TM	Cytosolic
79	LG:1383368.40:2001MAR30	130	152	forward 3	TM	Transmembrane
79	LG:1383368.40:2001MAR30	153	396	forward 3	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	397	419	forward 3	TM	Transmembrane
79	LG:1383368.40:2001MAR30	420	443	forward 3	TM	Cytosolic
79	LG:1383368.40:2001MAR30	444	466	forward 3	TM	Transmembrane
79	LG:1383368.40:2001MAR30	467	485	forward 3	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	486	508	forward 3	TM	Transmembrane
79	LG:1383368.40:2001MAR30	509	574	forward 3	TM	Cytosolic
79	LG:1383368.40:2001MAR30	575	597	forward 3	TM	Transmembrane
79	LG:1383368.40:2001MAR30	598	611	forward 3	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	612	631	forward 3	TM	Transmembrane
79	LG:1383368.40:2001MAR30	632	855	forward 3	TM	Cytosolic
79	LG:1383368.40:2001MAR30	856	878	forward 3	TM	Transmembrane
79	LG:1383368.40:2001MAR30	879	913	forward 3	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	914	936	forward 3	TM	Transmembrane
79	LG:1383368.40:2001MAR30	937	1002	forward 3	TM	Cytosolic
79	LG:1383368.40:2001MAR30	1003	1025	forward 3	TM	Transmembrane
79	LG:1383368.40:2001MAR30	1026	1081	forward 3	TM	Non-Cytosolic
79	LG:1383368.40:2001MAR30	1082	1104	forward 3	TM	Transmembrane
79	LG:1383368.40:2001MAR30	1105	1111	forward 3	TM	Cytosolic
80	LG:1384477.1:2001MAR30	1	77	forward 1	TM	Non-Cytosolic
80	LG:1384477.1:2001MAR30	78	100	forward 1	TM	Transmembrane
80	LG:1384477.1:2001MAR30	101	112	forward 1	TM	Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
80	LG:1384477.1:2001MAR30	113	135	forward 1	TM	Transmembrane
80	LG:1384477.1:2001MAR30	136	601	forward 1	TM	Non-Cytosolic
80	LG:1384477.1:2001MAR30	602	624	forward 1	TM	Transmembrane
80	LG:1384477.1:2001MAR30	625	639	forward 1	TM	Cytosolic
80	LG:1384477.1:2001MAR30	1	127	forward 2	TM	Cytosolic
80	LG:1384477.1:2001MAR30	128	150	forward 2	TM	Transmembrane
80	LG:1384477.1:2001MAR30	151	639	forward 2	TM	Non-Cytosolic
80	LG:1384477.1:2001MAR30	1	62	forward 3	TM	Cytosolic
80	LG:1384477.1:2001MAR30	63	80	forward 3	TM	Transmembrane
80	LG:1384477.1:2001MAR30	81	639	forward 3	TM	Non-Cytosolic
81	LG:1390822.1:2001MAR30	1	550	forward 1	TM	Non-Cytosolic
81	LG:1390822.1:2001MAR30	551	573	forward 1	TM	Transmembrane
81	LG:1390822.1:2001MAR30	574	744	forward 1	TM	Cytosolic
81	LG:1390822.1:2001MAR30	745	767	forward 1	TM	Transmembrane
81	LG:1390822.1:2001MAR30	768	776	forward 1	TM	Non-Cytosolic
81	LG:1390822.1:2001MAR30	777	799	forward 1	TM	Transmembrane
81	LG:1390822.1:2001MAR30	800	811	forward 1	TM	Cytosolic
81	LG:1390822.1:2001MAR30	812	834	forward 1	TM	Transmembrane
81	LG:1390822.1:2001MAR30	835	921	forward 1	TM	Non-Cytosolic
81	LG:1390822.1:2001MAR30	922	944	forward 1	TM	Transmembrane
81	LG:1390822.1:2001MAR30	945	977	forward 1	TM	Cytosolic
81	LG:1390822.1:2001MAR30	978	1000	forward 1	TM	Transmembrane
81	LG:1390822.1:2001MAR30	1001	1049	forward 1	TM	Non-Cytosolic
81	LG:1390822.1:2001MAR30	1050	1067	forward 1	TM	Transmembrane
81	LG:1390822.1:2001MAR30	1068	1102	forward 1	TM	Cytosolic
81	LG:1390822.1:2001MAR30	1103	1125	forward 1	TM	Transmembrane
81	LG:1390822.1:2001MAR30	1126	1134	forward 1	TM	Non-Cytosolic
81	LG:1390822.1:2001MAR30	1135	1157	forward 1	TM	Transmembrane
81	LG:1390822.1:2001MAR30	1158	1236	forward 1	TM	Cytosolic
81	LG:1390822.1:2001MAR30	1	549	forward 3	TM	Non-Cytosolic
81	LG:1390822.1:2001MAR30	550	572	forward 3	TM	Transmembrane
81	LG:1390822.1:2001MAR30	573	765	forward 3	TM	Cytosolic
81	LG:1390822.1:2001MAR30	766	788	forward 3	TM	Transmembrane
81	LG:1390822.1:2001MAR30	789	816	forward 3	TM	Non-Cytosolic
81	LG:1390822.1:2001MAR30	817	839	forward 3	TM	Transmembrane
81	LG:1390822.1:2001MAR30	840	910	forward 3	TM	Cytosolic
81	LG:1390822.1:2001MAR30	911	933	forward 3	TM	Transmembrane
81	LG:1390822.1:2001MAR30	934	1049	forward 3	TM	Non-Cytosolic
81	LG:1390822.1:2001MAR30	1050	1067	forward 3	TM	Transmembrane
81	LG:1390822.1:2001MAR30	1068	1097	forward 3	TM	Cytosolic
81	LG:1390822.1:2001MAR30	1098	1120	forward 3	TM	Transmembrane
81	LG:1390822.1:2001MAR30	1121	1236	forward 3	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	1	9	forward 1	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	10	32	forward 1	TM	Transmembrane
82	LG:1398274.13:2001MAR30	33	36	forward 1	TM	Cytosolic
82	LG:1398274.13:2001MAR30	37	54	forward 1	TM	Transmembrane
82	LG:1398274.13:2001MAR30	55	901	forward 1	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	902	924	forward 1	TM	Transmembrane
82	LG:1398274.13:2001MAR30	925	973	forward 1	TM	Cytosolic
82	LG:1398274.13:2001MAR30	974	996	forward 1	TM	Transmembrane
82	LG:1398274.13:2001MAR30	997	1354	forward 1	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	1355	1377	forward 1	TM	Transmembrane
82	LG:1398274.13:2001MAR30	1378	1410	forward 1	TM	Cytosolic
82	LG:1398274.13:2001MAR30	1	4	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
82	LG:1398274.13:2001MAR30	5	27	forward 2	TM	Transmembrane
82	LG:1398274.13:2001MAR30	28	33	forward 2	TM	Cytosolic
82	LG:1398274.13:2001MAR30	34	56	forward 2	TM	Transmembrane
82	LG:1398274.13:2001MAR30	57	498	forward 2	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	499	516	forward 2	TM	Transmembrane
82	LG:1398274.13:2001MAR30	517	522	forward 2	TM	Cytosolic
82	LG:1398274.13:2001MAR30	523	545	forward 2	TM	Transmembrane
82	LG:1398274.13:2001MAR30	546	891	forward 2	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	892	914	forward 2	TM	Transmembrane
82	LG:1398274.13:2001MAR30	915	934	forward 2	TM	Cytosolic
82	LG:1398274.13:2001MAR30	935	952	forward 2	TM	Transmembrane
82	LG:1398274.13:2001MAR30	953	961	forward 2	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	962	984	forward 2	TM	Transmembrane
82	LG:1398274.13:2001MAR30	985	1349	forward 2	TM	Cytosolic
82	LG:1398274.13:2001MAR30	1350	1372	forward 2	TM	Transmembrane
82	LG:1398274.13:2001MAR30	1373	1410	forward 2	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	1	236	forward 3	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	237	259	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	260	353	forward 3	TM	Cytosolic
82	LG:1398274.13:2001MAR30	354	376	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	377	390	forward 3	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	391	413	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	414	448	forward 3	TM	Cytosolic
82	LG:1398274.13:2001MAR30	449	471	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	472	485	forward 3	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	486	508	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	509	520	forward 3	TM	Cytosolic
82	LG:1398274.13:2001MAR30	521	538	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	539	754	forward 3	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	755	774	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	775	802	forward 3	TM	Cytosolic
82	LG:1398274.13:2001MAR30	803	825	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	826	839	forward 3	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	840	862	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	863	894	forward 3	TM	Cytosolic
82	LG:1398274.13:2001MAR30	895	914	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	915	1286	forward 3	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	1287	1309	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	1310	1320	forward 3	TM	Cytosolic
82	LG:1398274.13:2001MAR30	1321	1343	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	1344	1352	forward 3	TM	Non-Cytosolic
82	LG:1398274.13:2001MAR30	1353	1375	forward 3	TM	Transmembrane
82	LG:1398274.13:2001MAR30	1376	1410	forward 3	TM	Cytosolic
83	LG:1398646.1:2001MAR30	1	6	forward 1	TM	Cytosolic
83	LG:1398646.1:2001MAR30	7	26	forward 1	TM	Transmembrane
83	LG:1398646.1:2001MAR30	27	431	forward 1	TM	Non-Cytosolic
83	LG:1398646.1:2001MAR30	432	454	forward 1	TM	Transmembrane
83	LG:1398646.1:2001MAR30	455	820	forward 1	TM	Cytosolic
83	LG:1398646.1:2001MAR30	821	843	forward 1	TM	Transmembrane
83	LG:1398646.1:2001MAR30	844	852	forward 1	TM	Non-Cytosolic
83	LG:1398646.1:2001MAR30	853	872	forward 1	TM	Transmembrane
83	LG:1398646.1:2001MAR30	873	873	forward 1	TM	Cytosolic
83	LG:1398646.1:2001MAR30	874	891	forward 1	TM	Transmembrane
83	LG:1398646.1:2001MAR30	892	905	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
83	LG:1398646.1:2001MAR30	906	928	forward 1	TM	Transmembrane
83	LG:1398646.1:2001MAR30	929	1081	forward 1	TM	Cytosolic
83	LG:1398646.1:2001MAR30	1	867	forward 2	TM	Non-Cytosolic
83	LG:1398646.1:2001MAR30	868	890	forward 2	TM	Transmembrane
83	LG:1398646.1:2001MAR30	891	1033	forward 2	TM	Cytosolic
83	LG:1398646.1:2001MAR30	1034	1053	forward 2	TM	Transmembrane
83	LG:1398646.1:2001MAR30	1054	1080	forward 2	TM	Non-Cytosolic
83	LG:1398646.1:2001MAR30	1	12	forward 3	TM	Cytosolic
83	LG:1398646.1:2001MAR30	13	35	forward 3	TM	Transmembrane
83	LG:1398646.1:2001MAR30	36	614	forward 3	TM	Non-Cytosolic
83	LG:1398646.1:2001MAR30	615	634	forward 3	TM	Transmembrane
83	LG:1398646.1:2001MAR30	635	866	forward 3	TM	Cytosolic
83	LG:1398646.1:2001MAR30	867	889	forward 3	TM	Transmembrane
83	LG:1398646.1:2001MAR30	890	903	forward 3	TM	Non-Cytosolic
83	LG:1398646.1:2001MAR30	904	926	forward 3	TM	Transmembrane
83	LG:1398646.1:2001MAR30	927	1032	forward 3	TM	Cytosolic
83	LG:1398646.1:2001MAR30	1033	1055	forward 3	TM	Transmembrane
83	LG:1398646.1:2001MAR30	1056	1080	forward 3	TM	Non-Cytosolic
84	LG:1398905.1:2001MAR30	1	278	forward 2	TM	Non-Cytosolic
84	LG:1398905.1:2001MAR30	279	296	forward 2	TM	Transmembrane
84	LG:1398905.1:2001MAR30	297	308	forward 2	TM	Cytosolic
84	LG:1398905.1:2001MAR30	309	331	forward 2	TM	Transmembrane
84	LG:1398905.1:2001MAR30	332	488	forward 2	TM	Non-Cytosolic
84	LG:1398905.1:2001MAR30	1	277	forward 3	TM	Non-Cytosolic
84	LG:1398905.1:2001MAR30	278	295	forward 3	TM	Transmembrane
84	LG:1398905.1:2001MAR30	296	487	forward 3	TM	Cytosolic
85	LG:1399785.1:2001MAR30	1	104	forward 1	TM	Non-Cytosolic
85	LG:1399785.1:2001MAR30	105	124	forward 1	TM	Transmembrane
85	LG:1399785.1:2001MAR30	125	145	forward 1	TM	Cytosolic
85	LG:1399785.1:2001MAR30	146	168	forward 1	TM	Transmembrane
85	LG:1399785.1:2001MAR30	169	1902	forward 1	TM	Non-Cytosolic
86	LG:1446193.10:2001MAR30	1	941	forward 1	TM	Non-Cytosolic
86	LG:1446193.10:2001MAR30	942	961	forward 1	TM	Transmembrane
86	LG:1446193.10:2001MAR30	962	1020	forward 1	TM	Cytosolic
87	LG:1446210.8:2001MAR30	1	50	forward 1	TM	Cytosolic
87	LG:1446210.8:2001MAR30	51	70	forward 1	TM	Transmembrane
87	LG:1446210.8:2001MAR30	71	74	forward 1	TM	Non-Cytosolic
87	LG:1446210.8:2001MAR30	75	97	forward 1	TM	Transmembrane
87	LG:1446210.8:2001MAR30	98	117	forward 1	TM	Cytosolic
87	LG:1446210.8:2001MAR30	118	140	forward 1	TM	Transmembrane
87	LG:1446210.8:2001MAR30	141	159	forward 1	TM	Non-Cytosolic
87	LG:1446210.8:2001MAR30	160	182	forward 1	TM	Transmembrane
87	LG:1446210.8:2001MAR30	183	333	forward 1	TM	Cytosolic
87	LG:1446210.8:2001MAR30	334	356	forward 1	TM	Transmembrane
87	LG:1446210.8:2001MAR30	357	375	forward 1	TM	Non-Cytosolic
87	LG:1446210.8:2001MAR30	376	398	forward 1	TM	Transmembrane
87	LG:1446210.8:2001MAR30	399	404	forward 1	TM	Cytosolic
87	LG:1446210.8:2001MAR30	405	427	forward 1	TM	Transmembrane
87	LG:1446210.8:2001MAR30	428	596	forward 1	TM	Non-Cytosolic
87	LG:1446210.8:2001MAR30	1	43	forward 2	TM	Cytosolic
87	LG:1446210.8:2001MAR30	44	66	forward 2	TM	Transmembrane
87	LG:1446210.8:2001MAR30	67	369	forward 2	TM	Non-Cytosolic
87	LG:1446210.8:2001MAR30	370	392	forward 2	TM	Transmembrane
87	LG:1446210.8:2001MAR30	393	563	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
87	LG:1446210.8:2001MAR30	564	586	forward 2	TM	Transmembrane
87	LG:1446210.8:2001MAR30	587	596	forward 2	TM	Non-Cytosolic
88	LG:1450054.6:2001MAR30	1	1807	forward 2	TM	Non-Cytosolic
88	LG:1450054.6:2001MAR30	1808	1827	forward 2	TM	Transmembrane
88	LG:1450054.6:2001MAR30	1828	1865	forward 2	TM	Cytosolic
89	LG:1452516.4:2001MAR30	1	567	forward 3	TM	Non-Cytosolic
89	LG:1452516.4:2001MAR30	568	590	forward 3	TM	Transmembrane
89	LG:1452516.4:2001MAR30	591	634	forward 3	TM	Cytosolic
90	LG:1455293.7:2001MAR30	1	27	forward 1	TM	Non-Cytosolic
90	LG:1455293.7:2001MAR30	28	46	forward 1	TM	Transmembrane
90	LG:1455293.7:2001MAR30	47	202	forward 1	TM	Cytosolic
90	LG:1455293.7:2001MAR30	203	225	forward 1	TM	Transmembrane
90	LG:1455293.7:2001MAR30	226	544	forward 1	TM	Non-Cytosolic
90	LG:1455293.7:2001MAR30	1	23	forward 2	TM	Non-Cytosolic
90	LG:1455293.7:2001MAR30	24	46	forward 2	TM	Transmembrane
90	LG:1455293.7:2001MAR30	47	200	forward 2	TM	Cytosolic
90	LG:1455293.7:2001MAR30	201	223	forward 2	TM	Transmembrane
90	LG:1455293.7:2001MAR30	224	242	forward 2	TM	Non-Cytosolic
90	LG:1455293.7:2001MAR30	243	260	forward 2	TM	Transmembrane
90	LG:1455293.7:2001MAR30	261	272	forward 2	TM	Cytosolic
90	LG:1455293.7:2001MAR30	273	290	forward 2	TM	Transmembrane
90	LG:1455293.7:2001MAR30	291	485	forward 2	TM	Non-Cytosolic
90	LG:1455293.7:2001MAR30	486	505	forward 2	TM	Transmembrane
90	LG:1455293.7:2001MAR30	506	511	forward 2	TM	Cytosolic
90	LG:1455293.7:2001MAR30	512	534	forward 2	TM	Transmembrane
90	LG:1455293.7:2001MAR30	535	543	forward 2	TM	Non-Cytosolic
90	LG:1455293.7:2001MAR30	1	202	forward 3	TM	Cytosolic
90	LG:1455293.7:2001MAR30	203	225	forward 3	TM	Transmembrane
90	LG:1455293.7:2001MAR30	226	262	forward 3	TM	Non-Cytosolic
90	LG:1455293.7:2001MAR30	263	285	forward 3	TM	Transmembrane
90	LG:1455293.7:2001MAR30	286	305	forward 3	TM	Cytosolic
90	LG:1455293.7:2001MAR30	306	328	forward 3	TM	Transmembrane
90	LG:1455293.7:2001MAR30	329	401	forward 3	TM	Non-Cytosolic
90	LG:1455293.7:2001MAR30	402	424	forward 3	TM	Transmembrane
90	LG:1455293.7:2001MAR30	425	461	forward 3	TM	Cytosolic
90	LG:1455293.7:2001MAR30	462	484	forward 3	TM	Transmembrane
90	LG:1455293.7:2001MAR30	485	489	forward 3	TM	Non-Cytosolic
90	LG:1455293.7:2001MAR30	490	512	forward 3	TM	Transmembrane
90	LG:1455293.7:2001MAR30	513	543	forward 3	TM	Cytosolic
91	LG:1498113.1:2001MAR30	1	216	forward 3	TM	Cytosolic
92	LG:1500042.1:2001MAR30	1	4	forward 1	TM	Non-Cytosolic
92	LG:1500042.1:2001MAR30	5	27	forward 1	TM	Transmembrane
92	LG:1500042.1:2001MAR30	28	31	forward 1	TM	Cytosolic
92	LG:1500042.1:2001MAR30	32	54	forward 1	TM	Transmembrane
92	LG:1500042.1:2001MAR30	55	68	forward 1	TM	Non-Cytosolic
92	LG:1500042.1:2001MAR30	69	91	forward 1	TM	Transmembrane
92	LG:1500042.1:2001MAR30	92	97	forward 1	TM	Cytosolic
92	LG:1500042.1:2001MAR30	98	117	forward 1	TM	Transmembrane
92	LG:1500042.1:2001MAR30	118	122	forward 1	TM	Non-Cytosolic
92	LG:1500042.1:2001MAR30	1	6	forward 2	TM	Cytosolic
92	LG:1500042.1:2001MAR30	7	29	forward 2	TM	Transmembrane
92	LG:1500042.1:2001MAR30	30	33	forward 2	TM	Non-Cytosolic
92	LG:1500042.1:2001MAR30	34	56	forward 2	TM	Transmembrane
92	LG:1500042.1:2001MAR30	57	62	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
92	LG:1500042.1:2001MAR30	63	85	forward 2	TM	Transmembrane
92	LG:1500042.1:2001MAR30	86	122	forward 2	TM	Non-Cytosolic
92	LG:1500042.1:2001MAR30	1	1	forward 3	TM	Cytosolic
92	LG:1500042.1:2001MAR30	2	24	forward 3	TM	Transmembrane
92	LG:1500042.1:2001MAR30	25	38	forward 3	TM	Non-Cytosolic
92	LG:1500042.1:2001MAR30	39	61	forward 3	TM	Transmembrane
92	LG:1500042.1:2001MAR30	62	87	forward 3	TM	Cytosolic
92	LG:1500042.1:2001MAR30	88	110	forward 3	TM	Transmembrane
92	LG:1500042.1:2001MAR30	111	122	forward 3	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	1	179	forward 1	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	180	202	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	203	405	forward 1	TM	Cytosolic
93	LG:1500434.4:2001MAR30	406	423	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	424	479	forward 1	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	480	502	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	503	543	forward 1	TM	Cytosolic
93	LG:1500434.4:2001MAR30	544	566	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	567	593	forward 1	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	594	616	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	617	660	forward 1	TM	Cytosolic
93	LG:1500434.4:2001MAR30	661	683	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	684	697	forward 1	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	698	720	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	721	726	forward 1	TM	Cytosolic
93	LG:1500434.4:2001MAR30	727	749	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	750	763	forward 1	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	764	786	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	787	951	forward 1	TM	Cytosolic
93	LG:1500434.4:2001MAR30	952	974	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	975	1002	forward 1	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	1003	1025	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1026	1098	forward 1	TM	Cytosolic
93	LG:1500434.4:2001MAR30	1099	1121	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1122	1135	forward 1	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	1136	1158	forward 1	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1159	1249	forward 1	TM	Cytosolic
93	LG:1500434.4:2001MAR30	1	428	forward 2	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	429	451	forward 2	TM	Transmembrane
93	LG:1500434.4:2001MAR30	452	551	forward 2	TM	Cytosolic
93	LG:1500434.4:2001MAR30	552	574	forward 2	TM	Transmembrane
93	LG:1500434.4:2001MAR30	575	588	forward 2	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	589	611	forward 2	TM	Transmembrane
93	LG:1500434.4:2001MAR30	612	696	forward 2	TM	Cytosolic
93	LG:1500434.4:2001MAR30	697	719	forward 2	TM	Transmembrane
93	LG:1500434.4:2001MAR30	720	733	forward 2	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	734	753	forward 2	TM	Transmembrane
93	LG:1500434.4:2001MAR30	754	834	forward 2	TM	Cytosolic
93	LG:1500434.4:2001MAR30	835	857	forward 2	TM	Transmembrane
93	LG:1500434.4:2001MAR30	858	871	forward 2	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	872	894	forward 2	TM	Transmembrane
93	LG:1500434.4:2001MAR30	895	984	forward 2	TM	Cytosolic
93	LG:1500434.4:2001MAR30	985	1007	forward 2	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1008	1096	forward 2	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	1097	1119	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
93	LG:1500434.4:2001MAR30	1120	1145	forward 2	TM	Cytosolic
93	LG:1500434.4:2001MAR30	1146	1168	forward 2	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1169	1172	forward 2	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	1173	1195	forward 2	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1196	1249	forward 2	TM	Cytosolic
93	LG:1500434.4:2001MAR30	1	511	forward 3	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	512	531	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	532	551	forward 3	TM	Cytosolic
93	LG:1500434.4:2001MAR30	552	574	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	575	610	forward 3	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	611	633	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	634	655	forward 3	TM	Cytosolic
93	LG:1500434.4:2001MAR30	656	678	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	679	697	forward 3	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	698	720	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	721	732	forward 3	TM	Cytosolic
93	LG:1500434.4:2001MAR30	733	755	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	756	963	forward 3	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	964	986	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	987	998	forward 3	TM	Cytosolic
93	LG:1500434.4:2001MAR30	999	1021	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1022	1060	forward 3	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	1061	1078	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1079	1145	forward 3	TM	Cytosolic
93	LG:1500434.4:2001MAR30	1146	1168	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1169	1171	forward 3	TM	Non-Cytosolic
93	LG:1500434.4:2001MAR30	1172	1189	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1190	1208	forward 3	TM	Cytosolic
93	LG:1500434.4:2001MAR30	1209	1231	forward 3	TM	Transmembrane
93	LG:1500434.4:2001MAR30	1232	1249	forward 3	TM	Non-Cytosolic
94	LG:1501102.4:2001MAR30	1	45	forward 1	TM	Non-Cytosolic
94	LG:1501102.4:2001MAR30	46	68	forward 1	TM	Transmembrane
94	LG:1501102.4:2001MAR30	69	98	forward 1	TM	Cytosolic
94	LG:1501102.4:2001MAR30	99	121	forward 1	TM	Transmembrane
94	LG:1501102.4:2001MAR30	122	426	forward 1	TM	Non-Cytosolic
94	LG:1501102.4:2001MAR30	1	91	forward 3	TM	Cytosolic
94	LG:1501102.4:2001MAR30	92	111	forward 3	TM	Transmembrane
94	LG:1501102.4:2001MAR30	112	114	forward 3	TM	Non-Cytosolic
94	LG:1501102.4:2001MAR30	115	134	forward 3	TM	Transmembrane
94	LG:1501102.4:2001MAR30	135	170	forward 3	TM	Cytosolic
94	LG:1501102.4:2001MAR30	171	193	forward 3	TM	Transmembrane
94	LG:1501102.4:2001MAR30	194	425	forward 3	TM	Non-Cytosolic
95	LG:1501768.2:2001MAR30	1	6	forward 1	TM	Cytosolic
95	LG:1501768.2:2001MAR30	7	29	forward 1	TM	Transmembrane
95	LG:1501768.2:2001MAR30	30	85	forward 1	TM	Non-Cytosolic
96	LG:1502155.6:2001MAR30	1	315	forward 2	TM	Non-Cytosolic
96	LG:1502155.6:2001MAR30	316	338	forward 2	TM	Transmembrane
96	LG:1502155.6:2001MAR30	339	401	forward 2	TM	Cytosolic
97	LG:1512304.2:2001MAR30	1	92	forward 1	TM	Cytosolic
97	LG:1512304.2:2001MAR30	93	115	forward 1	TM	Transmembrane
97	LG:1512304.2:2001MAR30	116	180	forward 1	TM	Non-Cytosolic
97	LG:1512304.2:2001MAR30	181	203	forward 1	TM	Transmembrane
97	LG:1512304.2:2001MAR30	204	245	forward 1	TM	Cytosolic
97	LG:1512304.2:2001MAR30	246	268	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
97	LG:1512304.2:2001MAR30	269	278	forward 1	TM	Non-Cytosolic
97	LG:1512304.2:2001MAR30	1	240	forward 2	TM	Non-Cytosolic
97	LG:1512304.2:2001MAR30	241	263	forward 2	TM	Transmembrane
97	LG:1512304.2:2001MAR30	264	278	forward 2	TM	Cytosolic
97	LG:1512304.2:2001MAR30	1	89	forward 3	TM	Cytosolic
97	LG:1512304.2:2001MAR30	90	112	forward 3	TM	Transmembrane
97	LG:1512304.2:2001MAR30	113	137	forward 3	TM	Non-Cytosolic
97	LG:1512304.2:2001MAR30	138	160	forward 3	TM	Transmembrane
97	LG:1512304.2:2001MAR30	161	176	forward 3	TM	Cytosolic
97	LG:1512304.2:2001MAR30	177	199	forward 3	TM	Transmembrane
97	LG:1512304.2:2001MAR30	200	231	forward 3	TM	Non-Cytosolic
97	LG:1512304.2:2001MAR30	232	254	forward 3	TM	Transmembrane
97	LG:1512304.2:2001MAR30	255	277	forward 3	TM	Cytosolic
98	LG:1512931.11:2001MAR30	1	260	forward 2	TM	Non-Cytosolic
98	LG:1512931.11:2001MAR30	261	280	forward 2	TM	Transmembrane
98	LG:1512931.11:2001MAR30	281	296	forward 2	TM	Cytosolic
98	LG:1512931.11:2001MAR30	1	260	forward 3	TM	Cytosolic
98	LG:1512931.11:2001MAR30	261	283	forward 3	TM	Transmembrane
98	LG:1512931.11:2001MAR30	284	296	forward 3	TM	Non-Cytosolic
99	LG:155076.18:2001MAR30	1	1165	forward 2	TM	Non-Cytosolic
99	LG:155076.18:2001MAR30	1166	1188	forward 2	TM	Transmembrane
99	LG:155076.18:2001MAR30	1189	1194	forward 2	TM	Cytosolic
99	LG:155076.18:2001MAR30	1195	1214	forward 2	TM	Transmembrane
99	LG:155076.18:2001MAR30	1215	1590	forward 2	TM	Non-Cytosolic
100	LG:159111.41:2001MAR30	1	193	forward 1	TM	Non-Cytosolic
100	LG:159111.41:2001MAR30	194	216	forward 1	TM	Transmembrane
100	LG:159111.41:2001MAR30	217	351	forward 1	TM	Cytosolic
100	LG:159111.41:2001MAR30	352	374	forward 1	TM	Transmembrane
100	LG:159111.41:2001MAR30	375	383	forward 1	TM	Non-Cytosolic
100	LG:159111.41:2001MAR30	384	406	forward 1	TM	Transmembrane
100	LG:159111.41:2001MAR30	407	412	forward 1	TM	Cytosolic
100	LG:159111.41:2001MAR30	413	430	forward 1	TM	Transmembrane
100	LG:159111.41:2001MAR30	431	2269	forward 1	TM	Non-Cytosolic
100	LG:159111.41:2001MAR30	1	191	forward 3	TM	Non-Cytosolic
100	LG:159111.41:2001MAR30	192	214	forward 3	TM	Transmembrane
100	LG:159111.41:2001MAR30	215	382	forward 3	TM	Cytosolic
100	LG:159111.41:2001MAR30	383	405	forward 3	TM	Transmembrane
100	LG:159111.41:2001MAR30	406	2269	forward 3	TM	Non-Cytosolic
101	LG:170604.1:2001MAR30	1	240	forward 3	TM	Cytosolic
101	LG:170604.1:2001MAR30	241	260	forward 3	TM	Transmembrane
101	LG:170604.1:2001MAR30	261	262	forward 3	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	1	4	forward 1	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	5	27	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	28	70	forward 1	TM	Cytosolic
102	LG:190477.4:2001MAR30	71	93	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	94	124	forward 1	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	125	147	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	148	153	forward 1	TM	Cytosolic
102	LG:190477.4:2001MAR30	154	176	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	177	207	forward 1	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	208	230	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	231	341	forward 1	TM	Cytosolic
102	LG:190477.4:2001MAR30	342	364	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	365	401	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
102	LG:190477.4:2001MAR30	402	421	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	422	427	forward 1	TM	Cytosolic
102	LG:190477.4:2001MAR30	428	445	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	446	449	forward 1	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	450	472	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	473	502	forward 1	TM	Cytosolic
102	LG:190477.4:2001MAR30	503	525	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	526	623	forward 1	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	624	646	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	647	652	forward 1	TM	Cytosolic
102	LG:190477.4:2001MAR30	653	672	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	673	691	forward 1	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	692	714	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	715	720	forward 1	TM	Cytosolic
102	LG:190477.4:2001MAR30	721	743	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	744	757	forward 1	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	758	780	forward 1	TM	Transmembrane
102	LG:190477.4:2001MAR30	781	827	forward 1	TM	Cytosolic
102	LG:190477.4:2001MAR30	1	51	forward 2	TM	Cytosolic
102	LG:190477.4:2001MAR30	52	74	forward 2	TM	Transmembrane
102	LG:190477.4:2001MAR30	75	83	forward 2	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	84	106	forward 2	TM	Transmembrane
102	LG:190477.4:2001MAR30	107	126	forward 2	TM	Cytosolic
102	LG:190477.4:2001MAR30	127	149	forward 2	TM	Transmembrane
102	LG:190477.4:2001MAR30	150	579	forward 2	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	580	602	forward 2	TM	Transmembrane
102	LG:190477.4:2001MAR30	603	622	forward 2	TM	Cytosolic
102	LG:190477.4:2001MAR30	623	645	forward 2	TM	Transmembrane
102	LG:190477.4:2001MAR30	646	664	forward 2	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	665	682	forward 2	TM	Transmembrane
102	LG:190477.4:2001MAR30	683	826	forward 2	TM	Cytosolic
102	LG:190477.4:2001MAR30	1	65	forward 3	TM	Cytosolic
102	LG:190477.4:2001MAR30	66	83	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	84	97	forward 3	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	98	117	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	118	123	forward 3	TM	Cytosolic
102	LG:190477.4:2001MAR30	124	146	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	147	206	forward 3	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	207	229	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	230	283	forward 3	TM	Cytosolic
102	LG:190477.4:2001MAR30	284	306	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	307	333	forward 3	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	334	356	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	357	399	forward 3	TM	Cytosolic
102	LG:190477.4:2001MAR30	400	417	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	418	436	forward 3	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	437	456	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	457	584	forward 3	TM	Cytosolic
102	LG:190477.4:2001MAR30	585	607	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	608	626	forward 3	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	627	649	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	650	661	forward 3	TM	Cytosolic
102	LG:190477.4:2001MAR30	662	684	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	685	693	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
102	LG:190477.4:2001MAR30	694	713	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	714	719	forward 3	TM	Cytosolic
102	LG:190477.4:2001MAR30	720	742	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	743	756	forward 3	TM	Non-Cytosolic
102	LG:190477.4:2001MAR30	757	779	forward 3	TM	Transmembrane
102	LG:190477.4:2001MAR30	780	826	forward 3	TM	Cytosolic
103	LG:198087.8:2001MAR30	1	312	forward 2	TM	Non-Cytosolic
103	LG:198087.8:2001MAR30	313	335	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	336	399	forward 2	TM	Cytosolic
103	LG:198087.8:2001MAR30	400	419	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	420	433	forward 2	TM	Non-Cytosolic
103	LG:198087.8:2001MAR30	434	456	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	457	468	forward 2	TM	Cytosolic
103	LG:198087.8:2001MAR30	469	491	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	492	584	forward 2	TM	Non-Cytosolic
103	LG:198087.8:2001MAR30	585	607	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	608	781	forward 2	TM	Cytosolic
103	LG:198087.8:2001MAR30	782	804	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	805	835	forward 2	TM	Non-Cytosolic
103	LG:198087.8:2001MAR30	836	858	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	859	864	forward 2	TM	Cytosolic
103	LG:198087.8:2001MAR30	865	887	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	888	997	forward 2	TM	Non-Cytosolic
103	LG:198087.8:2001MAR30	998	1017	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	1018	1023	forward 2	TM	Cytosolic
103	LG:198087.8:2001MAR30	1024	1046	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	1047	1055	forward 2	TM	Non-Cytosolic
103	LG:198087.8:2001MAR30	1056	1073	forward 2	TM	Transmembrane
103	LG:198087.8:2001MAR30	1074	1310	forward 2	TM	Cytosolic
103	LG:198087.8:2001MAR30	1	405	forward 3	TM	Non-Cytosolic
103	LG:198087.8:2001MAR30	406	428	forward 3	TM	Transmembrane
103	LG:198087.8:2001MAR30	429	434	forward 3	TM	Cytosolic
103	LG:198087.8:2001MAR30	435	457	forward 3	TM	Transmembrane
103	LG:198087.8:2001MAR30	458	987	forward 3	TM	Non-Cytosolic
103	LG:198087.8:2001MAR30	988	1010	forward 3	TM	Transmembrane
103	LG:198087.8:2001MAR30	1011	1022	forward 3	TM	Cytosolic
103	LG:198087.8:2001MAR30	1023	1040	forward 3	TM	Transmembrane
103	LG:198087.8:2001MAR30	1041	1054	forward 3	TM	Non-Cytosolic
103	LG:198087.8:2001MAR30	1055	1072	forward 3	TM	Transmembrane
103	LG:198087.8:2001MAR30	1073	1310	forward 3	TM	Cytosolic
104	LG:198743.2:2001MAR30	1	1132	forward 1	TM	Non-Cytosolic
104	LG:198743.2:2001MAR30	1133	1152	forward 1	TM	Transmembrane
104	LG:198743.2:2001MAR30	1153	1164	forward 1	TM	Cytosolic
104	LG:198743.2:2001MAR30	1165	1187	forward 1	TM	Transmembrane
104	LG:198743.2:2001MAR30	1188	1215	forward 1	TM	Non-Cytosolic
104	LG:198743.2:2001MAR30	1	1038	forward 2	TM	Non-Cytosolic
104	LG:198743.2:2001MAR30	1039	1058	forward 2	TM	Transmembrane
104	LG:198743.2:2001MAR30	1059	1105	forward 2	TM	Cytosolic
104	LG:198743.2:2001MAR30	1106	1128	forward 2	TM	Transmembrane
104	LG:198743.2:2001MAR30	1129	1215	forward 2	TM	Non-Cytosolic
104	LG:198743.2:2001MAR30	1	983	forward 3	TM	Non-Cytosolic
104	LG:198743.2:2001MAR30	984	1006	forward 3	TM	Transmembrane
104	LG:198743.2:2001MAR30	1007	1012	forward 3	TM	Cytosolic
104	LG:198743.2:2001MAR30	1013	1035	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
104	LG:198743.2:2001MAR30	1036	1044	forward 3	TM	Non-Cytosolic
104	LG:198743.2:2001MAR30	1045	1067	forward 3	TM	Transmembrane
104	LG:198743.2:2001MAR30	1068	1214	forward 3	TM	Cytosolic
105	LG:199194.1:2001MAR30	1	75	forward 1	TM	Cytosolic
105	LG:199194.1:2001MAR30	76	95	forward 1	TM	Transmembrane
105	LG:199194.1:2001MAR30	96	1183	forward 1	TM	Non-Cytosolic
105	LG:199194.1:2001MAR30	1	479	forward 3	TM	Non-Cytosolic
105	LG:199194.1:2001MAR30	480	502	forward 3	TM	Transmembrane
105	LG:199194.1:2001MAR30	503	597	forward 3	TM	Cytosolic
105	LG:199194.1:2001MAR30	598	617	forward 3	TM	Transmembrane
105	LG:199194.1:2001MAR30	618	631	forward 3	TM	Non-Cytosolic
105	LG:199194.1:2001MAR30	632	654	forward 3	TM	Transmembrane
105	LG:199194.1:2001MAR30	655	658	forward 3	TM	Cytosolic
105	LG:199194.1:2001MAR30	659	681	forward 3	TM	Transmembrane
105	LG:199194.1:2001MAR30	682	1182	forward 3	TM	Non-Cytosolic
106	LG:200727.6:2001MAR30	1	351	forward 2	TM	Non-Cytosolic
106	LG:200727.6:2001MAR30	352	374	forward 2	TM	Transmembrane
106	LG:200727.6:2001MAR30	375	474	forward 2	TM	Cytosolic
107	LG:201572.20:2001MAR30	1	12	forward 1	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	13	35	forward 1	TM	Transmembrane
107	LG:201572.20:2001MAR30	36	74	forward 1	TM	Cytosolic
107	LG:201572.20:2001MAR30	75	97	forward 1	TM	Transmembrane
107	LG:201572.20:2001MAR30	98	185	forward 1	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	186	203	forward 1	TM	Transmembrane
107	LG:201572.20:2001MAR30	204	485	forward 1	TM	Cytosolic
107	LG:201572.20:2001MAR30	486	508	forward 1	TM	Transmembrane
107	LG:201572.20:2001MAR30	509	546	forward 1	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	547	569	forward 1	TM	Transmembrane
107	LG:201572.20:2001MAR30	570	589	forward 1	TM	Cytosolic
107	LG:201572.20:2001MAR30	590	612	forward 1	TM	Transmembrane
107	LG:201572.20:2001MAR30	613	706	forward 1	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	707	729	forward 1	TM	Transmembrane
107	LG:201572.20:2001MAR30	730	861	forward 1	TM	Cytosolic
107	LG:201572.20:2001MAR30	862	884	forward 1	TM	Transmembrane
107	LG:201572.20:2001MAR30	885	898	forward 1	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	899	918	forward 1	TM	Transmembrane
107	LG:201572.20:2001MAR30	919	930	forward 1	TM	Cytosolic
107	LG:201572.20:2001MAR30	931	948	forward 1	TM	Transmembrane
107	LG:201572.20:2001MAR30	949	1215	forward 1	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	1	14	forward 2	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	15	37	forward 2	TM	Transmembrane
107	LG:201572.20:2001MAR30	38	234	forward 2	TM	Cytosolic
107	LG:201572.20:2001MAR30	235	257	forward 2	TM	Transmembrane
107	LG:201572.20:2001MAR30	258	486	forward 2	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	487	505	forward 2	TM	Transmembrane
107	LG:201572.20:2001MAR30	506	589	forward 2	TM	Cytosolic
107	LG:201572.20:2001MAR30	590	612	forward 2	TM	Transmembrane
107	LG:201572.20:2001MAR30	613	703	forward 2	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	704	726	forward 2	TM	Transmembrane
107	LG:201572.20:2001MAR30	727	790	forward 2	TM	Cytosolic
107	LG:201572.20:2001MAR30	791	813	forward 2	TM	Transmembrane
107	LG:201572.20:2001MAR30	814	897	forward 2	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	898	920	forward 2	TM	Transmembrane
107	LG:201572.20:2001MAR30	921	938	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
107	LG:201572.20:2001MAR30	939	961	forward 2	TM	Transmembrane
107	LG:201572.20:2001MAR30	962	964	forward 2	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	965	982	forward 2	TM	Transmembrane
107	LG:201572.20:2001MAR30	983	1215	forward 2	TM	Cytosolic
107	LG:201572.20:2001MAR30	1	14	forward 3	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	15	37	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	38	88	forward 3	TM	Cytosolic
107	LG:201572.20:2001MAR30	89	111	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	112	180	forward 3	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	181	203	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	204	348	forward 3	TM	Cytosolic
107	LG:201572.20:2001MAR30	349	368	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	369	494	forward 3	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	495	517	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	518	523	forward 3	TM	Cytosolic
107	LG:201572.20:2001MAR30	524	542	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	543	561	forward 3	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	562	584	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	585	590	forward 3	TM	Cytosolic
107	LG:201572.20:2001MAR30	591	613	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	614	808	forward 3	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	809	826	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	827	900	forward 3	TM	Cytosolic
107	LG:201572.20:2001MAR30	901	918	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	919	937	forward 3	TM	Non-Cytosolic
107	LG:201572.20:2001MAR30	938	960	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	961	1118	forward 3	TM	Cytosolic
107	LG:201572.20:2001MAR30	1119	1141	forward 3	TM	Transmembrane
107	LG:201572.20:2001MAR30	1142	1214	forward 3	TM	Non-Cytosolic
108	LG:201669.25:2001MAR30	1	20	forward 1	TM	Cytosolic
108	LG:201669.25:2001MAR30	21	43	forward 1	TM	Transmembrane
108	LG:201669.25:2001MAR30	44	1148	forward 1	TM	Non-Cytosolic
108	LG:201669.25:2001MAR30	1	195	forward 3	TM	Non-Cytosolic
108	LG:201669.25:2001MAR30	196	218	forward 3	TM	Transmembrane
108	LG:201669.25:2001MAR30	219	244	forward 3	TM	Cytosolic
108	LG:201669.25:2001MAR30	245	267	forward 3	TM	Transmembrane
108	LG:201669.25:2001MAR30	268	271	forward 3	TM	Non-Cytosolic
108	LG:201669.25:2001MAR30	272	294	forward 3	TM	Transmembrane
108	LG:201669.25:2001MAR30	295	320	forward 3	TM	Cytosolic
108	LG:201669.25:2001MAR30	321	338	forward 3	TM	Transmembrane
108	LG:201669.25:2001MAR30	339	342	forward 3	TM	Non-Cytosolic
108	LG:201669.25:2001MAR30	343	360	forward 3	TM	Transmembrane
108	LG:201669.25:2001MAR30	361	372	forward 3	TM	Cytosolic
108	LG:201669.25:2001MAR30	373	392	forward 3	TM	Transmembrane
108	LG:201669.25:2001MAR30	393	436	forward 3	TM	Non-Cytosolic
108	LG:201669.25:2001MAR30	437	454	forward 3	TM	Transmembrane
108	LG:201669.25:2001MAR30	455	466	forward 3	TM	Cytosolic
108	LG:201669.25:2001MAR30	467	489	forward 3	TM	Transmembrane
108	LG:201669.25:2001MAR30	490	1147	forward 3	TM	Non-Cytosolic
109	LG:208588.4:2001MAR30	1	35	forward 2	TM	Cytosolic
109	LG:208588.4:2001MAR30	36	55	forward 2	TM	Transmembrane
109	LG:208588.4:2001MAR30	56	93	forward 2	TM	Non-Cytosolic
110	LG:210412.29:2001MAR30	1	33	forward 1	TM	Cytosolic
110	LG:210412.29:2001MAR30	34	56	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
110	LG:210412.29:2001MAR30	57	373	forward 1	TM	Non-Cytosolic
110	LG:210412.29:2001MAR30	1	31	forward 2	TM	Non-Cytosolic
110	LG:210412.29:2001MAR30	32	54	forward 2	TM	Transmembrane
110	LG:210412.29:2001MAR30	55	134	forward 2	TM	Cytosolic
110	LG:210412.29:2001MAR30	135	157	forward 2	TM	Transmembrane
110	LG:210412.29:2001MAR30	158	373	forward 2	TM	Non-Cytosolic
110	LG:210412.29:2001MAR30	1	31	forward 3	TM	Cytosolic
110	LG:210412.29:2001MAR30	32	51	forward 3	TM	Transmembrane
110	LG:210412.29:2001MAR30	52	54	forward 3	TM	Non-Cytosolic
110	LG:210412.29:2001MAR30	55	77	forward 3	TM	Transmembrane
110	LG:210412.29:2001MAR30	78	372	forward 3	TM	Cytosolic
111	LG:215051.15:2001MAR30	1	67	forward 1	TM	Non-Cytosolic
111	LG:215051.15:2001MAR30	68	85	forward 1	TM	Transmembrane
111	LG:215051.15:2001MAR30	86	167	forward 1	TM	Cytosolic
111	LG:215051.15:2001MAR30	168	190	forward 1	TM	Transmembrane
111	LG:215051.15:2001MAR30	191	234	forward 1	TM	Non-Cytosolic
111	LG:215051.15:2001MAR30	235	254	forward 1	TM	Transmembrane
111	LG:215051.15:2001MAR30	255	292	forward 1	TM	Cytosolic
111	LG:215051.15:2001MAR30	293	315	forward 1	TM	Transmembrane
111	LG:215051.15:2001MAR30	316	329	forward 1	TM	Non-Cytosolic
111	LG:215051.15:2001MAR30	330	352	forward 1	TM	Transmembrane
111	LG:215051.15:2001MAR30	353	651	forward 1	TM	Cytosolic
111	LG:215051.15:2001MAR30	652	674	forward 1	TM	Transmembrane
111	LG:215051.15:2001MAR30	675	841	forward 1	TM	Non-Cytosolic
111	LG:215051.15:2001MAR30	842	864	forward 1	TM	Transmembrane
111	LG:215051.15:2001MAR30	865	931	forward 1	TM	Cytosolic
111	LG:215051.15:2001MAR30	1	167	forward 3	TM	Non-Cytosolic
111	LG:215051.15:2001MAR30	168	190	forward 3	TM	Transmembrane
111	LG:215051.15:2001MAR30	191	201	forward 3	TM	Cytosolic
111	LG:215051.15:2001MAR30	202	224	forward 3	TM	Transmembrane
111	LG:215051.15:2001MAR30	225	846	forward 3	TM	Non-Cytosolic
111	LG:215051.15:2001MAR30	847	869	forward 3	TM	Transmembrane
111	LG:215051.15:2001MAR30	870	930	forward 3	TM	Cytosolic
112	LG:215475.21:2001MAR30	1	153	forward 1	TM	Cytosolic
112	LG:215475.21:2001MAR30	154	176	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	177	185	forward 1	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	186	208	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	209	293	forward 1	TM	Cytosolic
112	LG:215475.21:2001MAR30	294	316	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	317	445	forward 1	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	446	468	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	469	474	forward 1	TM	Cytosolic
112	LG:215475.21:2001MAR30	475	497	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	498	506	forward 1	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	507	529	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	530	580	forward 1	TM	Cytosolic
112	LG:215475.21:2001MAR30	581	603	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	604	622	forward 1	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	623	641	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	642	647	forward 1	TM	Cytosolic
112	LG:215475.21:2001MAR30	648	670	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	671	684	forward 1	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	685	707	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	708	734	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
112	LG:215475.21:2001MAR30	735	757	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	758	795	forward 1	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	796	818	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	819	922	forward 1	TM	Cytosolic
112	LG:215475.21:2001MAR30	923	945	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	946	976	forward 1	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	977	999	forward 1	TM	Transmembrane
112	LG:215475.21:2001MAR30	1000	1128	forward 1	TM	Cytosolic
112	LG:215475.21:2001MAR30	1	142	forward 2	TM	Cytosolic
112	LG:215475.21:2001MAR30	143	165	forward 2	TM	Transmembrane
112	LG:215475.21:2001MAR30	166	231	forward 2	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	232	251	forward 2	TM	Transmembrane
112	LG:215475.21:2001MAR30	252	334	forward 2	TM	Cytosolic
112	LG:215475.21:2001MAR30	335	357	forward 2	TM	Transmembrane
112	LG:215475.21:2001MAR30	358	664	forward 2	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	665	687	forward 2	TM	Transmembrane
112	LG:215475.21:2001MAR30	688	693	forward 2	TM	Cytosolic
112	LG:215475.21:2001MAR30	694	716	forward 2	TM	Transmembrane
112	LG:215475.21:2001MAR30	717	730	forward 2	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	731	753	forward 2	TM	Transmembrane
112	LG:215475.21:2001MAR30	754	799	forward 2	TM	Cytosolic
112	LG:215475.21:2001MAR30	800	822	forward 2	TM	Transmembrane
112	LG:215475.21:2001MAR30	823	971	forward 2	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	972	994	forward 2	TM	Transmembrane
112	LG:215475.21:2001MAR30	995	1000	forward 2	TM	Cytosolic
112	LG:215475.21:2001MAR30	1001	1023	forward 2	TM	Transmembrane
112	LG:215475.21:2001MAR30	1024	1128	forward 2	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	1	589	forward 3	TM	Non-Cytosolic
112	LG:215475.21:2001MAR30	590	612	forward 3	TM	Transmembrane
112	LG:215475.21:2001MAR30	613	793	forward 3	TM	Cytosolic
112	LG:215475.21:2001MAR30	794	816	forward 3	TM	Transmembrane
112	LG:215475.21:2001MAR30	817	1127	forward 3	TM	Non-Cytosolic
113	LG:224523.1:2001MAR30	1	19	forward 1	TM	Non-Cytosolic
113	LG:224523.1:2001MAR30	20	42	forward 1	TM	Transmembrane
113	LG:224523.1:2001MAR30	43	116	forward 1	TM	Cytosolic
113	LG:224523.1:2001MAR30	117	134	forward 1	TM	Transmembrane
113	LG:224523.1:2001MAR30	135	148	forward 1	TM	Non-Cytosolic
113	LG:224523.1:2001MAR30	149	171	forward 1	TM	Transmembrane
113	LG:224523.1:2001MAR30	172	213	forward 1	TM	Cytosolic
113	LG:224523.1:2001MAR30	1	116	forward 2	TM	Cytosolic
113	LG:224523.1:2001MAR30	117	139	forward 2	TM	Transmembrane
113	LG:224523.1:2001MAR30	140	148	forward 2	TM	Non-Cytosolic
113	LG:224523.1:2001MAR30	149	171	forward 2	TM	Transmembrane
113	LG:224523.1:2001MAR30	172	212	forward 2	TM	Cytosolic
113	LG:224523.1:2001MAR30	1	115	forward 3	TM	Cytosolic
113	LG:224523.1:2001MAR30	116	135	forward 3	TM	Transmembrane
113	LG:224523.1:2001MAR30	136	139	forward 3	TM	Non-Cytosolic
113	LG:224523.1:2001MAR30	140	162	forward 3	TM	Transmembrane
113	LG:224523.1:2001MAR30	163	212	forward 3	TM	Cytosolic
114	LG:228186.1:2001MAR30	1	32	forward 1	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	33	55	forward 1	TM	Transmembrane
114	LG:228186.1:2001MAR30	56	105	forward 1	TM	Cytosolic
114	LG:228186.1:2001MAR30	106	125	forward 1	TM	Transmembrane
114	LG:228186.1:2001MAR30	126	139	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
114	LG:228186.1:2001MAR30	140	162	forward 1	TM	Transmembrane
114	LG:228186.1:2001MAR30	163	168	forward 1	TM	Cytosolic
114	LG:228186.1:2001MAR30	169	191	forward 1	TM	Transmembrane
114	LG:228186.1:2001MAR30	192	1292	forward 1	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	1293	1315	forward 1	TM	Transmembrane
114	LG:228186.1:2001MAR30	1316	1569	forward 1	TM	Cytosolic
114	LG:228186.1:2001MAR30	1570	1592	forward 1	TM	Transmembrane
114	LG:228186.1:2001MAR30	1593	1723	forward 1	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	1	6	forward 2	TM	Cytosolic
114	LG:228186.1:2001MAR30	7	25	forward 2	TM	Transmembrane
114	LG:228186.1:2001MAR30	26	39	forward 2	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	40	62	forward 2	TM	Transmembrane
114	LG:228186.1:2001MAR30	63	74	forward 2	TM	Cytosolic
114	LG:228186.1:2001MAR30	75	92	forward 2	TM	Transmembrane
114	LG:228186.1:2001MAR30	93	106	forward 2	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	107	126	forward 2	TM	Transmembrane
114	LG:228186.1:2001MAR30	127	167	forward 2	TM	Cytosolic
114	LG:228186.1:2001MAR30	168	190	forward 2	TM	Transmembrane
114	LG:228186.1:2001MAR30	191	1316	forward 2	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	1317	1339	forward 2	TM	Transmembrane
114	LG:228186.1:2001MAR30	1340	1449	forward 2	TM	Cytosolic
114	LG:228186.1:2001MAR30	1450	1472	forward 2	TM	Transmembrane
114	LG:228186.1:2001MAR30	1473	1723	forward 2	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	1	102	forward 3	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	103	122	forward 3	TM	Transmembrane
114	LG:228186.1:2001MAR30	123	134	forward 3	TM	Cytosolic
114	LG:228186.1:2001MAR30	135	157	forward 3	TM	Transmembrane
114	LG:228186.1:2001MAR30	158	467	forward 3	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	468	485	forward 3	TM	Transmembrane
114	LG:228186.1:2001MAR30	486	589	forward 3	TM	Cytosolic
114	LG:228186.1:2001MAR30	590	612	forward 3	TM	Transmembrane
114	LG:228186.1:2001MAR30	613	1448	forward 3	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	1449	1471	forward 3	TM	Transmembrane
114	LG:228186.1:2001MAR30	1472	1594	forward 3	TM	Cytosolic
114	LG:228186.1:2001MAR30	1595	1617	forward 3	TM	Transmembrane
114	LG:228186.1:2001MAR30	1618	1631	forward 3	TM	Non-Cytosolic
114	LG:228186.1:2001MAR30	1632	1651	forward 3	TM	Transmembrane
114	LG:228186.1:2001MAR30	1652	1671	forward 3	TM	Cytosolic
114	LG:228186.1:2001MAR30	1672	1694	forward 3	TM	Transmembrane
114	LG:228186.1:2001MAR30	1695	1722	forward 3	TM	Non-Cytosolic
115	LG:233138.2:2001MAR30	1	1464	forward 1	TM	Non-Cytosolic
115	LG:233138.2:2001MAR30	1465	1487	forward 1	TM	Transmembrane
115	LG:233138.2:2001MAR30	1488	1554	forward 1	TM	Cytosolic
115	LG:233138.2:2001MAR30	1	434	forward 2	TM	Non-Cytosolic
115	LG:233138.2:2001MAR30	435	457	forward 2	TM	Transmembrane
115	LG:233138.2:2001MAR30	458	463	forward 2	TM	Cytosolic
115	LG:233138.2:2001MAR30	464	486	forward 2	TM	Transmembrane
115	LG:233138.2:2001MAR30	487	1554	forward 2	TM	Non-Cytosolic
116	LG:234811.10:2001MAR30	1	312	forward 1	TM	Non-Cytosolic
116	LG:234811.10:2001MAR30	313	335	forward 1	TM	Transmembrane
116	LG:234811.10:2001MAR30	336	350	forward 1	TM	Cytosolic
116	LG:234811.10:2001MAR30	1	326	forward 2	TM	Non-Cytosolic
116	LG:234811.10:2001MAR30	327	346	forward 2	TM	Transmembrane
116	LG:234811.10:2001MAR30	347	349	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
117	LG:236092.1:2001MAR30	1	114	forward 1	TM	Cytosolic
117	LG:236092.1:2001MAR30	115	137	forward 1	TM	Transmembrane
117	LG:236092.1:2001MAR30	138	290	forward 1	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	291	313	forward 1	TM	Transmembrane
117	LG:236092.1:2001MAR30	314	399	forward 1	TM	Cytosolic
117	LG:236092.1:2001MAR30	400	422	forward 1	TM	Transmembrane
117	LG:236092.1:2001MAR30	423	441	forward 1	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	442	464	forward 1	TM	Transmembrane
117	LG:236092.1:2001MAR30	465	534	forward 1	TM	Cytosolic
117	LG:236092.1:2001MAR30	535	557	forward 1	TM	Transmembrane
117	LG:236092.1:2001MAR30	558	728	forward 1	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	1	54	forward 2	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	55	74	forward 2	TM	Transmembrane
117	LG:236092.1:2001MAR30	75	111	forward 2	TM	Cytosolic
117	LG:236092.1:2001MAR30	112	134	forward 2	TM	Transmembrane
117	LG:236092.1:2001MAR30	135	155	forward 2	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	156	178	forward 2	TM	Transmembrane
117	LG:236092.1:2001MAR30	179	416	forward 2	TM	Cytosolic
117	LG:236092.1:2001MAR30	417	439	forward 2	TM	Transmembrane
117	LG:236092.1:2001MAR30	440	448	forward 2	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	449	471	forward 2	TM	Transmembrane
117	LG:236092.1:2001MAR30	472	526	forward 2	TM	Cytosolic
117	LG:236092.1:2001MAR30	527	549	forward 2	TM	Transmembrane
117	LG:236092.1:2001MAR30	550	591	forward 2	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	592	609	forward 2	TM	Transmembrane
117	LG:236092.1:2001MAR30	610	728	forward 2	TM	Cytosolic
117	LG:236092.1:2001MAR30	1	14	forward 3	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	15	37	forward 3	TM	Transmembrane
117	LG:236092.1:2001MAR30	38	57	forward 3	TM	Cytosolic
117	LG:236092.1:2001MAR30	58	80	forward 3	TM	Transmembrane
117	LG:236092.1:2001MAR30	81	111	forward 3	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	112	131	forward 3	TM	Transmembrane
117	LG:236092.1:2001MAR30	132	143	forward 3	TM	Cytosolic
117	LG:236092.1:2001MAR30	144	166	forward 3	TM	Transmembrane
117	LG:236092.1:2001MAR30	167	453	forward 3	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	454	476	forward 3	TM	Transmembrane
117	LG:236092.1:2001MAR30	477	551	forward 3	TM	Cytosolic
117	LG:236092.1:2001MAR30	552	574	forward 3	TM	Transmembrane
117	LG:236092.1:2001MAR30	575	593	forward 3	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	594	616	forward 3	TM	Transmembrane
117	LG:236092.1:2001MAR30	617	622	forward 3	TM	Cytosolic
117	LG:236092.1:2001MAR30	623	642	forward 3	TM	Transmembrane
117	LG:236092.1:2001MAR30	643	673	forward 3	TM	Non-Cytosolic
117	LG:236092.1:2001MAR30	674	696	forward 3	TM	Transmembrane
117	LG:236092.1:2001MAR30	697	727	forward 3	TM	Cytosolic
118	LG:236098.12:2001MAR30	1	437	forward 1	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	438	460	forward 1	TM	Transmembrane
118	LG:236098.12:2001MAR30	461	504	forward 1	TM	Cytosolic
118	LG:236098.12:2001MAR30	505	526	forward 1	TM	Transmembrane
118	LG:236098.12:2001MAR30	527	1270	forward 1	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	1271	1293	forward 1	TM	Transmembrane
118	LG:236098.12:2001MAR30	1294	1346	forward 1	TM	Cytosolic
118	LG:236098.12:2001MAR30	1347	1369	forward 1	TM	Transmembrane
118	LG:236098.12:2001MAR30	1370	1378	forward 1	TM	Non-Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
118	LG:236098.12:2001MAR30	1379	1401	forward 1	TM	Transmembrane
118	LG:236098.12:2001MAR30	1402	1421	forward 1	TM	Cytosolic
118	LG:236098.12:2001MAR30	1422	1444	forward 1	TM	Transmembrane
118	LG:236098.12:2001MAR30	1445	1458	forward 1	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	1459	1481	forward 1	TM	Transmembrane
118	LG:236098.12:2001MAR30	1482	1494	forward 1	TM	Cytosolic
118	LG:236098.12:2001MAR30	1	400	forward 2	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	401	423	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	424	442	forward 2	TM	Cytosolic
118	LG:236098.12:2001MAR30	443	460	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	461	469	forward 2	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	470	487	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	488	499	forward 2	TM	Cytosolic
118	LG:236098.12:2001MAR30	500	522	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	523	541	forward 2	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	542	564	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	565	584	forward 2	TM	Cytosolic
118	LG:236098.12:2001MAR30	585	602	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	603	616	forward 2	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	617	639	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	640	888	forward 2	TM	Cytosolic
118	LG:236098.12:2001MAR30	889	911	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	912	920	forward 2	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	921	943	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	944	963	forward 2	TM	Cytosolic
118	LG:236098.12:2001MAR30	964	986	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	987	1005	forward 2	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	1006	1028	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	1029	1169	forward 2	TM	Cytosolic
118	LG:236098.12:2001MAR30	1170	1192	forward 2	TM	Transmembrane
118	LG:236098.12:2001MAR30	1193	1494	forward 2	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	1	433	forward 3	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	434	456	forward 3	TM	Transmembrane
118	LG:236098.12:2001MAR30	457	492	forward 3	TM	Cytosolic
118	LG:236098.12:2001MAR30	493	515	forward 3	TM	Transmembrane
118	LG:236098.12:2001MAR30	516	529	forward 3	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	530	552	forward 3	TM	Transmembrane
118	LG:236098.12:2001MAR30	553	615	forward 3	TM	Cytosolic
118	LG:236098.12:2001MAR30	616	638	forward 3	TM	Transmembrane
118	LG:236098.12:2001MAR30	639	759	forward 3	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	760	782	forward 3	TM	Transmembrane
118	LG:236098.12:2001MAR30	783	898	forward 3	TM	Cytosolic
118	LG:236098.12:2001MAR30	899	921	forward 3	TM	Transmembrane
118	LG:236098.12:2001MAR30	922	935	forward 3	TM	Non-Cytosolic
118	LG:236098.12:2001MAR30	936	953	forward 3	TM	Transmembrane
118	LG:236098.12:2001MAR30	954	957	forward 3	TM	Cytosolic
118	LG:236098.12:2001MAR30	958	980	forward 3	TM	Transmembrane
118	LG:236098.12:2001MAR30	981	1494	forward 3	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	1	90	forward 1	TM	Cytosolic
119	LG:236697.15:2001MAR30	91	113	forward 1	TM	Transmembrane
119	LG:236697.15:2001MAR30	114	127	forward 1	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	128	150	forward 1	TM	Transmembrane
119	LG:236697.15:2001MAR30	151	219	forward 1	TM	Cytosolic
119	LG:236697.15:2001MAR30	220	239	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
119	LG:236697.15:2001MAR30	240	258	forward 1	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	259	281	forward 1	TM	Transmembrane
119	LG:236697.15:2001MAR30	282	287	forward 1	TM	Cytosolic
119	LG:236697.15:2001MAR30	288	307	forward 1	TM	Transmembrane
119	LG:236697.15:2001MAR30	308	316	forward 1	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	317	336	forward 1	TM	Transmembrane
119	LG:236697.15:2001MAR30	337	524	forward 1	TM	Cytosolic
119	LG:236697.15:2001MAR30	525	547	forward 1	TM	Transmembrane
119	LG:236697.15:2001MAR30	548	566	forward 1	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	567	589	forward 1	TM	Transmembrane
119	LG:236697.15:2001MAR30	590	608	forward 1	TM	Cytosolic
119	LG:236697.15:2001MAR30	609	631	forward 1	TM	Transmembrane
119	LG:236697.15:2001MAR30	632	673	forward 1	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	1	80	forward 2	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	81	100	forward 2	TM	Transmembrane
119	LG:236697.15:2001MAR30	101	251	forward 2	TM	Cytosolic
119	LG:236697.15:2001MAR30	252	271	forward 2	TM	Transmembrane
119	LG:236697.15:2001MAR30	272	533	forward 2	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	534	556	forward 2	TM	Transmembrane
119	LG:236697.15:2001MAR30	557	568	forward 2	TM	Cytosolic
119	LG:236697.15:2001MAR30	569	586	forward 2	TM	Transmembrane
119	LG:236697.15:2001MAR30	587	600	forward 2	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	601	620	forward 2	TM	Transmembrane
119	LG:236697.15:2001MAR30	621	640	forward 2	TM	Cytosolic
119	LG:236697.15:2001MAR30	641	663	forward 2	TM	Transmembrane
119	LG:236697.15:2001MAR30	664	673	forward 2	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	1	454	forward 3	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	455	477	forward 3	TM	Transmembrane
119	LG:236697.15:2001MAR30	478	526	forward 3	TM	Cytosolic
119	LG:236697.15:2001MAR30	527	549	forward 3	TM	Transmembrane
119	LG:236697.15:2001MAR30	550	563	forward 3	TM	Non-Cytosolic
119	LG:236697.15:2001MAR30	564	583	forward 3	TM	Transmembrane
119	LG:236697.15:2001MAR30	584	605	forward 3	TM	Cytosolic
119	LG:236697.15:2001MAR30	606	628	forward 3	TM	Transmembrane
119	LG:236697.15:2001MAR30	629	672	forward 3	TM	Non-Cytosolic
120	LG:237503.21:2001MAR30	1	960	forward 1	TM	Non-Cytosolic
120	LG:237503.21:2001MAR30	961	983	forward 1	TM	Transmembrane
120	LG:237503.21:2001MAR30	984	989	forward 1	TM	Cytosolic
120	LG:237503.21:2001MAR30	990	1007	forward 1	TM	Transmembrane
120	LG:237503.21:2001MAR30	1008	1072	forward 1	TM	Non-Cytosolic
120	LG:237503.21:2001MAR30	1073	1095	forward 1	TM	Transmembrane
120	LG:237503.21:2001MAR30	1096	1218	forward 1	TM	Cytosolic
120	LG:237503.21:2001MAR30	1	9	forward 2	TM	Non-Cytosolic
120	LG:237503.21:2001MAR30	10	32	forward 2	TM	Transmembrane
120	LG:237503.21:2001MAR30	33	44	forward 2	TM	Cytosolic
120	LG:237503.21:2001MAR30	45	64	forward 2	TM	Transmembrane
120	LG:237503.21:2001MAR30	65	926	forward 2	TM	Non-Cytosolic
120	LG:237503.21:2001MAR30	927	949	forward 2	TM	Transmembrane
120	LG:237503.21:2001MAR30	950	961	forward 2	TM	Cytosolic
120	LG:237503.21:2001MAR30	962	984	forward 2	TM	Transmembrane
120	LG:237503.21:2001MAR30	985	1218	forward 2	TM	Non-Cytosolic
120	LG:237503.21:2001MAR30	1	115	forward 3	TM	Non-Cytosolic
120	LG:237503.21:2001MAR30	116	138	forward 3	TM	Transmembrane
120	LG:237503.21:2001MAR30	139	144	forward 3	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
120	LG:237503.21:2001MAR30	145	167	forward 3	TM	Transmembrane
120	LG:237503.21:2001MAR30	168	232	forward 3	TM	Non-Cytosolic
120	LG:237503.21:2001MAR30	233	255	forward 3	TM	Transmembrane
120	LG:237503.21:2001MAR30	256	465	forward 3	TM	Cytosolic
120	LG:237503.21:2001MAR30	466	488	forward 3	TM	Transmembrane
120	LG:237503.21:2001MAR30	489	960	forward 3	TM	Non-Cytosolic
120	LG:237503.21:2001MAR30	961	983	forward 3	TM	Transmembrane
120	LG:237503.21:2001MAR30	984	989	forward 3	TM	Cytosolic
120	LG:237503.21:2001MAR30	990	1009	forward 3	TM	Transmembrane
120	LG:237503.21:2001MAR30	1010	1217	forward 3	TM	Non-Cytosolic
121	LG:238023.7:2001MAR30	1	753	forward 1	TM	Non-Cytosolic
121	LG:238023.7:2001MAR30	754	776	forward 1	TM	Transmembrane
121	LG:238023.7:2001MAR30	777	843	forward 1	TM	Cytosolic
121	LG:238023.7:2001MAR30	844	866	forward 1	TM	Transmembrane
121	LG:238023.7:2001MAR30	867	893	forward 1	TM	Non-Cytosolic
121	LG:238023.7:2001MAR30	1	19	forward 2	TM	Non-Cytosolic
121	LG:238023.7:2001MAR30	20	42	forward 2	TM	Transmembrane
121	LG:238023.7:2001MAR30	43	53	forward 2	TM	Cytosolic
121	LG:238023.7:2001MAR30	54	76	forward 2	TM	Transmembrane
121	LG:238023.7:2001MAR30	77	85	forward 2	TM	Non-Cytosolic
121	LG:238023.7:2001MAR30	86	108	forward 2	TM	Transmembrane
121	LG:238023.7:2001MAR30	109	128	forward 2	TM	Cytosolic
121	LG:238023.7:2001MAR30	129	151	forward 2	TM	Transmembrane
121	LG:238023.7:2001MAR30	152	597	forward 2	TM	Non-Cytosolic
121	LG:238023.7:2001MAR30	598	620	forward 2	TM	Transmembrane
121	LG:238023.7:2001MAR30	621	639	forward 2	TM	Cytosolic
121	LG:238023.7:2001MAR30	640	659	forward 2	TM	Transmembrane
121	LG:238023.7:2001MAR30	660	859	forward 2	TM	Non-Cytosolic
121	LG:238023.7:2001MAR30	860	882	forward 2	TM	Transmembrane
121	LG:238023.7:2001MAR30	883	893	forward 2	TM	Cytosolic
122	LG:238209.1:2001MAR30	1	1179	forward 2	TM	Non-Cytosolic
122	LG:238209.1:2001MAR30	1180	1202	forward 2	TM	Transmembrane
122	LG:238209.1:2001MAR30	1203	1302	forward 2	TM	Cytosolic
122	LG:238209.1:2001MAR30	1	1111	forward 3	TM	Non-Cytosolic
122	LG:238209.1:2001MAR30	1112	1134	forward 3	TM	Transmembrane
122	LG:238209.1:2001MAR30	1135	1154	forward 3	TM	Cytosolic
122	LG:238209.1:2001MAR30	1155	1172	forward 3	TM	Transmembrane
122	LG:238209.1:2001MAR30	1173	1186	forward 3	TM	Non-Cytosolic
122	LG:238209.1:2001MAR30	1187	1209	forward 3	TM	Transmembrane
122	LG:238209.1:2001MAR30	1210	1215	forward 3	TM	Cytosolic
122	LG:238209.1:2001MAR30	1216	1235	forward 3	TM	Transmembrane
122	LG:238209.1:2001MAR30	1236	1268	forward 3	TM	Non-Cytosolic
122	LG:238209.1:2001MAR30	1269	1291	forward 3	TM	Transmembrane
122	LG:238209.1:2001MAR30	1292	1302	forward 3	TM	Cytosolic
123	LG:238456.10:2001MAR30	1	6	forward 3	TM	Cytosolic
123	LG:238456.10:2001MAR30	7	29	forward 3	TM	Transmembrane
123	LG:238456.10:2001MAR30	30	431	forward 3	TM	Non-Cytosolic
124	LG:239245.1:2001MAR30	1	158	forward 1	TM	Cytosolic
124	LG:239245.1:2001MAR30	159	181	forward 1	TM	Transmembrane
124	LG:239245.1:2001MAR30	182	782	forward 1	TM	Non-Cytosolic
124	LG:239245.1:2001MAR30	783	805	forward 1	TM	Transmembrane
124	LG:239245.1:2001MAR30	806	842	forward 1	TM	Cytosolic
124	LG:239245.1:2001MAR30	1	162	forward 2	TM	Non-Cytosolic
124	LG:239245.1:2001MAR30	163	185	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
124	LG:239245.1:2001MAR30	186	479	forward 2	TM	Cytosolic
124	LG:239245.1:2001MAR30	480	499	forward 2	TM	Transmembrane
124	LG:239245.1:2001MAR30	500	777	forward 2	TM	Non-Cytosolic
124	LG:239245.1:2001MAR30	778	800	forward 2	TM	Transmembrane
124	LG:239245.1:2001MAR30	801	842	forward 2	TM	Cytosolic
124	LG:239245.1:2001MAR30	1	159	forward 3	TM	Cytosolic
124	LG:239245.1:2001MAR30	160	182	forward 3	TM	Transmembrane
124	LG:239245.1:2001MAR30	183	475	forward 3	TM	Non-Cytosolic
124	LG:239245.1:2001MAR30	476	498	forward 3	TM	Transmembrane
124	LG:239245.1:2001MAR30	499	732	forward 3	TM	Cytosolic
124	LG:239245.1:2001MAR30	733	752	forward 3	TM	Transmembrane
124	LG:239245.1:2001MAR30	753	773	forward 3	TM	Non-Cytosolic
124	LG:239245.1:2001MAR30	774	796	forward 3	TM	Transmembrane
124	LG:239245.1:2001MAR30	797	842	forward 3	TM	Cytosolic
125	LG:239579.8:2001MAR30	1	45	forward 1	TM	Non-Cytosolic
125	LG:239579.8:2001MAR30	46	63	forward 1	TM	Transmembrane
125	LG:239579.8:2001MAR30	64	210	forward 1	TM	Cytosolic
125	LG:239579.8:2001MAR30	211	233	forward 1	TM	Transmembrane
125	LG:239579.8:2001MAR30	234	418	forward 1	TM	Non-Cytosolic
125	LG:239579.8:2001MAR30	419	441	forward 1	TM	Transmembrane
125	LG:239579.8:2001MAR30	442	469	forward 1	TM	Cytosolic
125	LG:239579.8:2001MAR30	1	224	forward 2	TM	Non-Cytosolic
125	LG:239579.8:2001MAR30	225	247	forward 2	TM	Transmembrane
125	LG:239579.8:2001MAR30	248	420	forward 2	TM	Cytosolic
125	LG:239579.8:2001MAR30	421	443	forward 2	TM	Transmembrane
125	LG:239579.8:2001MAR30	444	469	forward 2	TM	Non-Cytosolic
125	LG:239579.8:2001MAR30	1	222	forward 3	TM	Non-Cytosolic
125	LG:239579.8:2001MAR30	223	245	forward 3	TM	Transmembrane
125	LG:239579.8:2001MAR30	246	264	forward 3	TM	Cytosolic
125	LG:239579.8:2001MAR30	265	287	forward 3	TM	Transmembrane
125	LG:239579.8:2001MAR30	288	301	forward 3	TM	Non-Cytosolic
125	LG:239579.8:2001MAR30	302	324	forward 3	TM	Transmembrane
125	LG:239579.8:2001MAR30	325	418	forward 3	TM	Cytosolic
125	LG:239579.8:2001MAR30	419	441	forward 3	TM	Transmembrane
125	LG:239579.8:2001MAR30	442	468	forward 3	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	1	105	forward 1	TM	Cytosolic
126	LG:239601.22:2001MAR30	106	128	forward 1	TM	Transmembrane
126	LG:239601.22:2001MAR30	129	243	forward 1	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	244	266	forward 1	TM	Transmembrane
126	LG:239601.22:2001MAR30	267	314	forward 1	TM	Cytosolic
126	LG:239601.22:2001MAR30	315	337	forward 1	TM	Transmembrane
126	LG:239601.22:2001MAR30	338	346	forward 1	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	347	369	forward 1	TM	Transmembrane
126	LG:239601.22:2001MAR30	370	518	forward 1	TM	Cytosolic
126	LG:239601.22:2001MAR30	519	541	forward 1	TM	Transmembrane
126	LG:239601.22:2001MAR30	542	934	forward 1	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	1	114	forward 2	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	115	137	forward 2	TM	Transmembrane
126	LG:239601.22:2001MAR30	138	175	forward 2	TM	Cytosolic
126	LG:239601.22:2001MAR30	176	198	forward 2	TM	Transmembrane
126	LG:239601.22:2001MAR30	199	248	forward 2	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	249	271	forward 2	TM	Transmembrane
126	LG:239601.22:2001MAR30	272	291	forward 2	TM	Cytosolic
126	LG:239601.22:2001MAR30	292	314	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
126	LG:239601.22:2001MAR30	315	318	forward 2	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	319	341	forward 2	TM	Transmembrane
126	LG:239601.22:2001MAR30	342	352	forward 2	TM	Cytosolic
126	LG:239601.22:2001MAR30	353	375	forward 2	TM	Transmembrane
126	LG:239601.22:2001MAR30	376	933	forward 2	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	1	25	forward 3	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	26	45	forward 3	TM	Transmembrane
126	LG:239601.22:2001MAR30	46	109	forward 3	TM	Cytosolic
126	LG:239601.22:2001MAR30	110	129	forward 3	TM	Transmembrane
126	LG:239601.22:2001MAR30	130	182	forward 3	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	183	205	forward 3	TM	Transmembrane
126	LG:239601.22:2001MAR30	206	231	forward 3	TM	Cytosolic
126	LG:239601.22:2001MAR30	232	254	forward 3	TM	Transmembrane
126	LG:239601.22:2001MAR30	255	268	forward 3	TM	Non-Cytosolic
126	LG:239601.22:2001MAR30	269	291	forward 3	TM	Transmembrane
126	LG:239601.22:2001MAR30	292	303	forward 3	TM	Cytosolic
126	LG:239601.22:2001MAR30	304	326	forward 3	TM	Transmembrane
126	LG:239601.22:2001MAR30	327	933	forward 3	TM	Non-Cytosolic
127	LG:240121.1:2001MAR30	1	409	forward 1	TM	Non-Cytosolic
127	LG:240121.1:2001MAR30	410	432	forward 1	TM	Transmembrane
127	LG:240121.1:2001MAR30	433	723	forward 1	TM	Cytosolic
127	LG:240121.1:2001MAR30	724	742	forward 1	TM	Transmembrane
127	LG:240121.1:2001MAR30	743	756	forward 1	TM	Non-Cytosolic
127	LG:240121.1:2001MAR30	757	774	forward 1	TM	Transmembrane
127	LG:240121.1:2001MAR30	775	793	forward 1	TM	Cytosolic
127	LG:240121.1:2001MAR30	794	816	forward 1	TM	Transmembrane
127	LG:240121.1:2001MAR30	817	820	forward 1	TM	Non-Cytosolic
127	LG:240121.1:2001MAR30	821	843	forward 1	TM	Transmembrane
127	LG:240121.1:2001MAR30	844	898	forward 1	TM	Cytosolic
127	LG:240121.1:2001MAR30	1	409	forward 2	TM	Non-Cytosolic
127	LG:240121.1:2001MAR30	410	432	forward 2	TM	Transmembrane
127	LG:240121.1:2001MAR30	433	729	forward 2	TM	Cytosolic
127	LG:240121.1:2001MAR30	730	747	forward 2	TM	Transmembrane
127	LG:240121.1:2001MAR30	748	756	forward 2	TM	Non-Cytosolic
127	LG:240121.1:2001MAR30	757	774	forward 2	TM	Transmembrane
127	LG:240121.1:2001MAR30	775	785	forward 2	TM	Cytosolic
127	LG:240121.1:2001MAR30	786	808	forward 2	TM	Transmembrane
127	LG:240121.1:2001MAR30	809	827	forward 2	TM	Non-Cytosolic
127	LG:240121.1:2001MAR30	828	850	forward 2	TM	Transmembrane
127	LG:240121.1:2001MAR30	851	898	forward 2	TM	Cytosolic
127	LG:240121.1:2001MAR30	1	405	forward 3	TM	Non-Cytosolic
127	LG:240121.1:2001MAR30	406	428	forward 3	TM	Transmembrane
127	LG:240121.1:2001MAR30	429	785	forward 3	TM	Cytosolic
127	LG:240121.1:2001MAR30	786	808	forward 3	TM	Transmembrane
127	LG:240121.1:2001MAR30	809	827	forward 3	TM	Non-Cytosolic
127	LG:240121.1:2001MAR30	828	850	forward 3	TM	Transmembrane
127	LG:240121.1:2001MAR30	851	897	forward 3	TM	Cytosolic
128	LG:241110.2:2001MAR30	1	1348	forward 2	TM	Non-Cytosolic
128	LG:241110.2:2001MAR30	1349	1371	forward 2	TM	Transmembrane
128	LG:241110.2:2001MAR30	1372	1377	forward 2	TM	Cytosolic
128	LG:241110.2:2001MAR30	1378	1400	forward 2	TM	Transmembrane
128	LG:241110.2:2001MAR30	1401	2121	forward 2	TM	Non-Cytosolic
129	LG:244948.4:2001MAR30	1	309	forward 1	TM	Cytosolic
129	LG:244948.4:2001MAR30	310	332	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
129	LG:244948.4:2001MAR30	333	336	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1	294	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	295	312	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	313	321	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	322	344	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	345	390	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	391	413	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	414	464	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	465	487	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	488	574	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	575	597	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	598	606	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	607	629	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	630	805	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	806	828	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	829	842	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	843	862	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	863	886	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	887	909	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	910	955	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	956	978	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	979	989	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	990	1009	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1010	1013	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1014	1036	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1037	1070	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	1071	1090	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1091	1179	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1180	1202	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1203	1347	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	1348	1370	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1371	1412	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1413	1430	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1431	1509	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	1510	1532	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1533	1583	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1584	1606	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1607	1683	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	1684	1706	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1707	1725	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1726	1748	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1749	1760	forward 1	TM	Cytosolic
130	LG:245378.6:2001MAR30	1761	1783	forward 1	TM	Transmembrane
130	LG:245378.6:2001MAR30	1784	1796	forward 1	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1	389	forward 2	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	390	412	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	413	473	forward 2	TM	Cytosolic
130	LG:245378.6:2001MAR30	474	493	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	494	597	forward 2	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	598	620	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	621	690	forward 2	TM	Cytosolic
130	LG:245378.6:2001MAR30	691	713	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	714	839	forward 2	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	840	862	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
130	LG:245378.6:2001MAR30	863	874	forward 2	TM	Cytosolic
130	LG:245378.6:2001MAR30	875	897	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	898	916	forward 2	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	917	939	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	940	958	forward 2	TM	Cytosolic
130	LG:245378.6:2001MAR30	959	981	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	982	1086	forward 2	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1087	1109	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	1110	1257	forward 2	TM	Cytosolic
130	LG:245378.6:2001MAR30	1258	1280	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	1281	1440	forward 2	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1441	1463	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	1464	1483	forward 2	TM	Cytosolic
130	LG:245378.6:2001MAR30	1484	1506	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	1507	1580	forward 2	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1581	1598	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	1599	1641	forward 2	TM	Cytosolic
130	LG:245378.6:2001MAR30	1642	1664	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	1665	1683	forward 2	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1684	1706	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	1707	1722	forward 2	TM	Cytosolic
130	LG:245378.6:2001MAR30	1723	1745	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	1746	1754	forward 2	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1755	1777	forward 2	TM	Transmembrane
130	LG:245378.6:2001MAR30	1778	1796	forward 2	TM	Cytosolic
130	LG:245378.6:2001MAR30	1	78	forward 3	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	79	101	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	102	392	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	393	415	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	416	468	forward 3	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	469	486	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	487	569	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	570	592	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	593	615	forward 3	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	616	638	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	639	691	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	692	714	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	715	728	forward 3	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	729	748	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	749	772	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	773	795	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	796	914	forward 3	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	915	937	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	938	957	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	958	980	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	981	1021	forward 3	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1022	1044	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1045	1064	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	1065	1087	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1088	1096	forward 3	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1097	1114	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1115	1143	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	1144	1166	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1167	1185	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
130	LG:245378.6:2001MAR30	1186	1208	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1209	1368	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	1369	1391	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1392	1405	forward 3	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1406	1428	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1429	1440	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	1441	1463	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1464	1477	forward 3	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1478	1500	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1501	1512	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	1513	1532	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1533	1572	forward 3	TM	Non-Cytosolic
130	LG:245378.6:2001MAR30	1573	1590	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1591	1752	forward 3	TM	Cytosolic
130	LG:245378.6:2001MAR30	1753	1775	forward 3	TM	Transmembrane
130	LG:245378.6:2001MAR30	1776	1795	forward 3	TM	Non-Cytosolic
131	LG:248203.9:2001MAR30	1	197	forward 2	TM	Non-Cytosolic
131	LG:248203.9:2001MAR30	198	220	forward 2	TM	Transmembrane
131	LG:248203.9:2001MAR30	221	240	forward 2	TM	Cytosolic
131	LG:248203.9:2001MAR30	241	263	forward 2	TM	Transmembrane
131	LG:248203.9:2001MAR30	264	656	forward 2	TM	Non-Cytosolic
131	LG:248203.9:2001MAR30	1	242	forward 3	TM	Non-Cytosolic
131	LG:248203.9:2001MAR30	243	265	forward 3	TM	Transmembrane
131	LG:248203.9:2001MAR30	266	280	forward 3	TM	Cytosolic
131	LG:248203.9:2001MAR30	281	303	forward 3	TM	Transmembrane
131	LG:248203.9:2001MAR30	304	656	forward 3	TM	Non-Cytosolic
132	LG:249247.1:2001MAR30	1	489	forward 1	TM	Non-Cytosolic
132	LG:249247.1:2001MAR30	490	512	forward 1	TM	Transmembrane
132	LG:249247.1:2001MAR30	513	579	forward 1	TM	Cytosolic
132	LG:249247.1:2001MAR30	580	602	forward 1	TM	Transmembrane
132	LG:249247.1:2001MAR30	603	769	forward 1	TM	Non-Cytosolic
132	LG:249247.1:2001MAR30	1	480	forward 3	TM	Non-Cytosolic
132	LG:249247.1:2001MAR30	481	503	forward 3	TM	Transmembrane
132	LG:249247.1:2001MAR30	504	532	forward 3	TM	Cytosolic
132	LG:249247.1:2001MAR30	533	555	forward 3	TM	Transmembrane
132	LG:249247.1:2001MAR30	556	768	forward 3	TM	Non-Cytosolic
133	LG:267153.16:2001MAR30	1	1106	forward 3	TM	Non-Cytosolic
133	LG:267153.16:2001MAR30	1107	1129	forward 3	TM	Transmembrane
133	LG:267153.16:2001MAR30	1130	1135	forward 3	TM	Cytosolic
133	LG:267153.16:2001MAR30	1136	1158	forward 3	TM	Transmembrane
133	LG:267153.16:2001MAR30	1159	1190	forward 3	TM	Non-Cytosolic
134	LG:291759.5:2001MAR30	1	16	forward 2	TM	Cytosolic
134	LG:291759.5:2001MAR30	17	39	forward 2	TM	Transmembrane
134	LG:291759.5:2001MAR30	40	406	forward 2	TM	Non-Cytosolic
134	LG:291759.5:2001MAR30	1	4	forward 3	TM	Cytosolic
134	LG:291759.5:2001MAR30	5	34	forward 3	TM	Transmembrane
134	LG:291759.5:2001MAR30	35	405	forward 3	TM	Non-Cytosolic
135	LG:298102.1:2001MAR30	1	52	forward 2	TM	Cytosolic
135	LG:298102.1:2001MAR30	53	70	forward 2	TM	Transmembrane
135	LG:298102.1:2001MAR30	71	276	forward 2	TM	Non-Cytosolic
135	LG:298102.1:2001MAR30	1	9	forward 3	TM	Non-Cytosolic
135	LG:298102.1:2001MAR30	10	28	forward 3	TM	Transmembrane
135	LG:298102.1:2001MAR30	29	40	forward 3	TM	Cytosolic
135	LG:298102.1:2001MAR30	41	63	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
135	LG:298102.1:2001MAR30	64	276	forward 3	TM	Non-Cytosolic
136	LG:308891.1:2001MAR30	1	14	forward 2	TM	Non-Cytosolic
136	LG:308891.1:2001MAR30	15	37	forward 2	TM	Transmembrane
136	LG:308891.1:2001MAR30	38	191	forward 2	TM	Cytosolic
136	LG:308891.1:2001MAR30	192	214	forward 2	TM	Transmembrane
136	LG:308891.1:2001MAR30	215	219	forward 2	TM	Non-Cytosolic
137	LG:312668.4:2001MAR30	1	270	forward 3	TM	Non-Cytosolic
137	LG:312668.4:2001MAR30	271	293	forward 3	TM	Transmembrane
137	LG:312668.4:2001MAR30	294	408	forward 3	TM	Cytosolic
137	LG:312668.4:2001MAR30	409	431	forward 3	TM	Transmembrane
137	LG:312668.4:2001MAR30	432	625	forward 3	TM	Non-Cytosolic
138	LG:331642.6:2001MAR30	1	19	forward 1	TM	Cytosolic
138	LG:331642.6:2001MAR30	20	42	forward 1	TM	Transmembrane
138	LG:331642.6:2001MAR30	43	630	forward 1	TM	Non-Cytosolic
138	LG:331642.6:2001MAR30	1	12	forward 3	TM	Cytosolic
138	LG:331642.6:2001MAR30	13	35	forward 3	TM	Transmembrane
138	LG:331642.6:2001MAR30	36	65	forward 3	TM	Non-Cytosolic
138	LG:331642.6:2001MAR30	66	85	forward 3	TM	Transmembrane
138	LG:331642.6:2001MAR30	86	266	forward 3	TM	Cytosolic
138	LG:331642.6:2001MAR30	267	289	forward 3	TM	Transmembrane
138	LG:331642.6:2001MAR30	290	629	forward 3	TM	Non-Cytosolic
139	LG:331851.12:2001MAR30	1	904	forward 2	TM	Non-Cytosolic
139	LG:331851.12:2001MAR30	905	927	forward 2	TM	Transmembrane
139	LG:331851.12:2001MAR30	928	946	forward 2	TM	Cytosolic
139	LG:331851.12:2001MAR30	947	969	forward 2	TM	Transmembrane
139	LG:331851.12:2001MAR30	970	2183	forward 2	TM	Non-Cytosolic
139	LG:331851.12:2001MAR30	2184	2206	forward 2	TM	Transmembrane
139	LG:331851.12:2001MAR30	2207	2218	forward 2	TM	Cytosolic
139	LG:331851.12:2001MAR30	1	833	forward 3	TM	Non-Cytosolic
139	LG:331851.12:2001MAR30	834	856	forward 3	TM	Transmembrane
139	LG:331851.12:2001MAR30	857	875	forward 3	TM	Cytosolic
139	LG:331851.12:2001MAR30	876	898	forward 3	TM	Transmembrane
139	LG:331851.12:2001MAR30	899	902	forward 3	TM	Non-Cytosolic
139	LG:331851.12:2001MAR30	903	925	forward 3	TM	Transmembrane
139	LG:331851.12:2001MAR30	926	992	forward 3	TM	Cytosolic
139	LG:331851.12:2001MAR30	993	1015	forward 3	TM	Transmembrane
139	LG:331851.12:2001MAR30	1016	2217	forward 3	TM	Non-Cytosolic
140	LG:332414.5:2001MAR30	1	482	forward 2	TM	Non-Cytosolic
140	LG:332414.5:2001MAR30	483	505	forward 2	TM	Transmembrane
140	LG:332414.5:2001MAR30	506	521	forward 2	TM	Cytosolic
140	LG:332414.5:2001MAR30	1	111	forward 3	TM	Non-Cytosolic
140	LG:332414.5:2001MAR30	112	134	forward 3	TM	Transmembrane
140	LG:332414.5:2001MAR30	135	218	forward 3	TM	Cytosolic
140	LG:332414.5:2001MAR30	219	236	forward 3	TM	Transmembrane
140	LG:332414.5:2001MAR30	237	250	forward 3	TM	Non-Cytosolic
140	LG:332414.5:2001MAR30	251	273	forward 3	TM	Transmembrane
140	LG:332414.5:2001MAR30	274	480	forward 3	TM	Cytosolic
140	LG:332414.5:2001MAR30	481	503	forward 3	TM	Transmembrane
140	LG:332414.5:2001MAR30	504	521	forward 3	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	1	516	forward 1	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	517	539	forward 1	TM	Transmembrane
141	LG:332730.12:2001MAR30	540	684	forward 1	TM	Cytosolic
141	LG:332730.12:2001MAR30	685	707	forward 1	TM	Transmembrane
141	LG:332730.12:2001MAR30	708	710	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
141	LG:332730.12:2001MAR30	711	733	forward 1	TM	Transmembrane
141	LG:332730.12:2001MAR30	734	739	forward 1	TM	Cytosolic
141	LG:332730.12:2001MAR30	740	762	forward 1	TM	Transmembrane
141	LG:332730.12:2001MAR30	763	781	forward 1	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	782	804	forward 1	TM	Transmembrane
141	LG:332730.12:2001MAR30	805	1011	forward 1	TM	Cytosolic
141	LG:332730.12:2001MAR30	1012	1034	forward 1	TM	Transmembrane
141	LG:332730.12:2001MAR30	1035	1043	forward 1	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	1044	1063	forward 1	TM	Transmembrane
141	LG:332730.12:2001MAR30	1064	1083	forward 1	TM	Cytosolic
141	LG:332730.12:2001MAR30	1084	1106	forward 1	TM	Transmembrane
141	LG:332730.12:2001MAR30	1107	1302	forward 1	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	1	526	forward 2	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	527	549	forward 2	TM	Transmembrane
141	LG:332730.12:2001MAR30	550	739	forward 2	TM	Cytosolic
141	LG:332730.12:2001MAR30	740	762	forward 2	TM	Transmembrane
141	LG:332730.12:2001MAR30	763	781	forward 2	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	782	804	forward 2	TM	Transmembrane
141	LG:332730.12:2001MAR30	805	891	forward 2	TM	Cytosolic
141	LG:332730.12:2001MAR30	892	914	forward 2	TM	Transmembrane
141	LG:332730.12:2001MAR30	915	946	forward 2	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	947	969	forward 2	TM	Transmembrane
141	LG:332730.12:2001MAR30	970	1001	forward 2	TM	Cytosolic
141	LG:332730.12:2001MAR30	1002	1024	forward 2	TM	Transmembrane
141	LG:332730.12:2001MAR30	1025	1028	forward 2	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	1029	1048	forward 2	TM	Transmembrane
141	LG:332730.12:2001MAR30	1049	1079	forward 2	TM	Cytosolic
141	LG:332730.12:2001MAR30	1080	1102	forward 2	TM	Transmembrane
141	LG:332730.12:2001MAR30	1103	1301	forward 2	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	1	514	forward 3	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	515	537	forward 3	TM	Transmembrane
141	LG:332730.12:2001MAR30	538	738	forward 3	TM	Cytosolic
141	LG:332730.12:2001MAR30	739	761	forward 3	TM	Transmembrane
141	LG:332730.12:2001MAR30	762	780	forward 3	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	781	803	forward 3	TM	Transmembrane
141	LG:332730.12:2001MAR30	804	1094	forward 3	TM	Cytosolic
141	LG:332730.12:2001MAR30	1095	1117	forward 3	TM	Transmembrane
141	LG:332730.12:2001MAR30	1118	1181	forward 3	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	1182	1201	forward 3	TM	Transmembrane
141	LG:332730.12:2001MAR30	1202	1212	forward 3	TM	Cytosolic
141	LG:332730.12:2001MAR30	1213	1235	forward 3	TM	Transmembrane
141	LG:332730.12:2001MAR30	1236	1269	forward 3	TM	Non-Cytosolic
141	LG:332730.12:2001MAR30	1270	1287	forward 3	TM	Transmembrane
141	LG:332730.12:2001MAR30	1288	1301	forward 3	TM	Cytosolic
142	LG:333062.22:2001MAR30	1	14	forward 1	TM	Non-Cytosolic
142	LG:333062.22:2001MAR30	15	37	forward 1	TM	Transmembrane
142	LG:333062.22:2001MAR30	38	133	forward 1	TM	Cytosolic
142	LG:333062.22:2001MAR30	134	151	forward 1	TM	Transmembrane
142	LG:333062.22:2001MAR30	152	160	forward 1	TM	Non-Cytosolic
142	LG:333062.22:2001MAR30	161	180	forward 1	TM	Transmembrane
142	LG:333062.22:2001MAR30	181	229	forward 1	TM	Cytosolic
142	LG:333062.22:2001MAR30	1	100	forward 2	TM	Non-Cytosolic
142	LG:333062.22:2001MAR30	101	120	forward 2	TM	Transmembrane
142	LG:333062.22:2001MAR30	121	204	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
142	LG:333062.22:2001MAR30	205	227	forward 2	TM	Transmembrane
142	LG:333062.22:2001MAR30	228	229	forward 2	TM	Non-Cytosolic
143	LG:335705.2:2001MAR30	1	1114	forward 1	TM	Non-Cytosolic
143	LG:335705.2:2001MAR30	1115	1137	forward 1	TM	Transmembrane
143	LG:335705.2:2001MAR30	1138	1233	forward 1	TM	Cytosolic
143	LG:335705.2:2001MAR30	1234	1256	forward 1	TM	Transmembrane
143	LG:335705.2:2001MAR30	1257	1747	forward 1	TM	Non-Cytosolic
143	LG:335705.2:2001MAR30	1748	1770	forward 1	TM	Transmembrane
143	LG:335705.2:2001MAR30	1771	1790	forward 1	TM	Cytosolic
143	LG:335705.2:2001MAR30	1	1249	forward 2	TM	Non-Cytosolic
143	LG:335705.2:2001MAR30	1250	1272	forward 2	TM	Transmembrane
143	LG:335705.2:2001MAR30	1273	1283	forward 2	TM	Cytosolic
143	LG:335705.2:2001MAR30	1284	1306	forward 2	TM	Transmembrane
143	LG:335705.2:2001MAR30	1307	1315	forward 2	TM	Non-Cytosolic
143	LG:335705.2:2001MAR30	1316	1338	forward 2	TM	Transmembrane
143	LG:335705.2:2001MAR30	1339	1496	forward 2	TM	Cytosolic
143	LG:335705.2:2001MAR30	1497	1514	forward 2	TM	Transmembrane
143	LG:335705.2:2001MAR30	1515	1730	forward 2	TM	Non-Cytosolic
143	LG:335705.2:2001MAR30	1731	1753	forward 2	TM	Transmembrane
143	LG:335705.2:2001MAR30	1754	1790	forward 2	TM	Cytosolic
143	LG:335705.2:2001MAR30	1	1248	forward 3	TM	Non-Cytosolic
143	LG:335705.2:2001MAR30	1249	1271	forward 3	TM	Transmembrane
143	LG:335705.2:2001MAR30	1272	1283	forward 3	TM	Cytosolic
143	LG:335705.2:2001MAR30	1284	1306	forward 3	TM	Transmembrane
143	LG:335705.2:2001MAR30	1307	1315	forward 3	TM	Non-Cytosolic
143	LG:335705.2:2001MAR30	1316	1335	forward 3	TM	Transmembrane
143	LG:335705.2:2001MAR30	1336	1346	forward 3	TM	Cytosolic
143	LG:335705.2:2001MAR30	1347	1366	forward 3	TM	Transmembrane
143	LG:335705.2:2001MAR30	1367	1789	forward 3	TM	Non-Cytosolic
144	LG:337930.16:2001MAR30	1	12	forward 2	TM	Cytosolic
144	LG:337930.16:2001MAR30	13	35	forward 2	TM	Transmembrane
144	LG:337930.16:2001MAR30	36	645	forward 2	TM	Non-Cytosolic
145	LG:346481.15:2001MAR30	1	106	forward 2	TM	Non-Cytosolic
145	LG:346481.15:2001MAR30	107	129	forward 2	TM	Transmembrane
145	LG:346481.15:2001MAR30	130	161	forward 2	TM	Cytosolic
146	LG:349164.1:2001MAR30	1	48	forward 1	TM	Cytosolic
146	LG:349164.1:2001MAR30	49	67	forward 1	TM	Transmembrane
146	LG:349164.1:2001MAR30	68	76	forward 1	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	77	99	forward 1	TM	Transmembrane
146	LG:349164.1:2001MAR30	100	123	forward 1	TM	Cytosolic
146	LG:349164.1:2001MAR30	124	146	forward 1	TM	Transmembrane
146	LG:349164.1:2001MAR30	147	738	forward 1	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	739	761	forward 1	TM	Transmembrane
146	LG:349164.1:2001MAR30	762	807	forward 1	TM	Cytosolic
146	LG:349164.1:2001MAR30	808	830	forward 1	TM	Transmembrane
146	LG:349164.1:2001MAR30	831	844	forward 1	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	845	867	forward 1	TM	Transmembrane
146	LG:349164.1:2001MAR30	868	943	forward 1	TM	Cytosolic
146	LG:349164.1:2001MAR30	944	966	forward 1	TM	Transmembrane
146	LG:349164.1:2001MAR30	967	973	forward 1	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	1	45	forward 2	TM	Cytosolic
146	LG:349164.1:2001MAR30	46	68	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	69	124	forward 2	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	125	144	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
146	LG:349164.1:2001MAR30	145	150	forward 2	TM	Cytosolic
146	LG:349164.1:2001MAR30	151	173	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	174	187	forward 2	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	188	210	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	211	389	forward 2	TM	Cytosolic
146	LG:349164.1:2001MAR30	390	408	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	409	422	forward 2	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	423	442	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	443	478	forward 2	TM	Cytosolic
146	LG:349164.1:2001MAR30	479	496	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	497	660	forward 2	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	661	683	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	684	695	forward 2	TM	Cytosolic
146	LG:349164.1:2001MAR30	696	715	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	716	734	forward 2	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	735	757	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	758	776	forward 2	TM	Cytosolic
146	LG:349164.1:2001MAR30	777	799	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	800	824	forward 2	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	825	847	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	848	853	forward 2	TM	Cytosolic
146	LG:349164.1:2001MAR30	854	873	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	874	876	forward 2	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	877	899	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	900	932	forward 2	TM	Cytosolic
146	LG:349164.1:2001MAR30	933	955	forward 2	TM	Transmembrane
146	LG:349164.1:2001MAR30	956	973	forward 2	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	1	663	forward 3	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	664	681	forward 3	TM	Transmembrane
146	LG:349164.1:2001MAR30	682	692	forward 3	TM	Cytosolic
146	LG:349164.1:2001MAR30	693	715	forward 3	TM	Transmembrane
146	LG:349164.1:2001MAR30	716	741	forward 3	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	742	764	forward 3	TM	Transmembrane
146	LG:349164.1:2001MAR30	765	776	forward 3	TM	Cytosolic
146	LG:349164.1:2001MAR30	777	799	forward 3	TM	Transmembrane
146	LG:349164.1:2001MAR30	800	818	forward 3	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	819	841	forward 3	TM	Transmembrane
146	LG:349164.1:2001MAR30	842	852	forward 3	TM	Cytosolic
146	LG:349164.1:2001MAR30	853	875	forward 3	TM	Transmembrane
146	LG:349164.1:2001MAR30	876	878	forward 3	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	879	898	forward 3	TM	Transmembrane
146	LG:349164.1:2001MAR30	899	909	forward 3	TM	Cytosolic
146	LG:349164.1:2001MAR30	910	932	forward 3	TM	Transmembrane
146	LG:349164.1:2001MAR30	933	941	forward 3	TM	Non-Cytosolic
146	LG:349164.1:2001MAR30	942	964	forward 3	TM	Transmembrane
146	LG:349164.1:2001MAR30	965	973	forward 3	TM	Cytosolic
147	LG:350957.5:2001MAR30	1	71	forward 1	TM	Non-Cytosolic
147	LG:350957.5:2001MAR30	72	94	forward 1	TM	Transmembrane
147	LG:350957.5:2001MAR30	95	106	forward 1	TM	Cytosolic
147	LG:350957.5:2001MAR30	107	129	forward 1	TM	Transmembrane
147	LG:350957.5:2001MAR30	130	151	forward 1	TM	Non-Cytosolic
147	LG:350957.5:2001MAR30	152	174	forward 1	TM	Transmembrane
147	LG:350957.5:2001MAR30	175	238	forward 1	TM	Cytosolic
147	LG:350957.5:2001MAR30	239	261	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
147	LG:350957.5:2001MAR30	262	286	forward 1	TM	Non-Cytosolic
147	LG:350957.5:2001MAR30	287	309	forward 1	TM	Transmembrane
147	LG:350957.5:2001MAR30	310	379	forward 1	TM	Cytosolic
147	LG:350957.5:2001MAR30	1	18	forward 2	TM	Cytosolic
147	LG:350957.5:2001MAR30	19	41	forward 2	TM	Transmembrane
147	LG:350957.5:2001MAR30	42	71	forward 2	TM	Non-Cytosolic
147	LG:350957.5:2001MAR30	72	94	forward 2	TM	Transmembrane
147	LG:350957.5:2001MAR30	95	151	forward 2	TM	Cytosolic
147	LG:350957.5:2001MAR30	152	174	forward 2	TM	Transmembrane
147	LG:350957.5:2001MAR30	175	212	forward 2	TM	Non-Cytosolic
147	LG:350957.5:2001MAR30	213	232	forward 2	TM	Transmembrane
147	LG:350957.5:2001MAR30	233	244	forward 2	TM	Cytosolic
147	LG:350957.5:2001MAR30	245	262	forward 2	TM	Transmembrane
147	LG:350957.5:2001MAR30	263	271	forward 2	TM	Non-Cytosolic
147	LG:350957.5:2001MAR30	272	294	forward 2	TM	Transmembrane
147	LG:350957.5:2001MAR30	295	298	forward 2	TM	Cytosolic
147	LG:350957.5:2001MAR30	299	321	forward 2	TM	Transmembrane
147	LG:350957.5:2001MAR30	322	379	forward 2	TM	Non-Cytosolic
148	LG:383512.8:2001MAR30	1	833	forward 2	TM	Non-Cytosolic
148	LG:383512.8:2001MAR30	834	856	forward 2	TM	Transmembrane
148	LG:383512.8:2001MAR30	857	876	forward 2	TM	Cytosolic
148	LG:383512.8:2001MAR30	877	899	forward 2	TM	Transmembrane
148	LG:383512.8:2001MAR30	900	1052	forward 2	TM	Non-Cytosolic
149	LG:401163.10:2001MAR30	1	1167	forward 1	TM	Non-Cytosolic
149	LG:401163.10:2001MAR30	1168	1190	forward 1	TM	Transmembrane
149	LG:401163.10:2001MAR30	1191	1270	forward 1	TM	Cytosolic
149	LG:401163.10:2001MAR30	1271	1290	forward 1	TM	Transmembrane
149	LG:401163.10:2001MAR30	1291	1492	forward 1	TM	Non-Cytosolic
150	LG:402133.1:2001MAR30	1	6	forward 3	TM	Cytosolic
150	LG:402133.1:2001MAR30	7	26	forward 3	TM	Transmembrane
150	LG:402133.1:2001MAR30	27	68	forward 3	TM	Non-Cytosolic
150	LG:402133.1:2001MAR30	69	91	forward 3	TM	Transmembrane
150	LG:402133.1:2001MAR30	92	476	forward 3	TM	Cytosolic
150	LG:402133.1:2001MAR30	477	499	forward 3	TM	Transmembrane
150	LG:402133.1:2001MAR30	500	543	forward 3	TM	Non-Cytosolic
151	LG:405820.1:2001MAR30	1	242	forward 1	TM	Non-Cytosolic
151	LG:405820.1:2001MAR30	243	262	forward 1	TM	Transmembrane
151	LG:405820.1:2001MAR30	263	303	forward 1	TM	Cytosolic
152	LG:405846.1:2001MAR30	1	297	forward 1	TM	Non-Cytosolic
152	LG:405846.1:2001MAR30	298	320	forward 1	TM	Transmembrane
152	LG:405846.1:2001MAR30	321	356	forward 1	TM	Cytosolic
153	LG:407401.2:2001MAR30	1	542	forward 2	TM	Non-Cytosolic
153	LG:407401.2:2001MAR30	543	565	forward 2	TM	Transmembrane
153	LG:407401.2:2001MAR30	566	573	forward 2	TM	Cytosolic
153	LG:407401.2:2001MAR30	574	591	forward 2	TM	Transmembrane
153	LG:407401.2:2001MAR30	592	888	forward 2	TM	Non-Cytosolic
154	LG:408448.10:2001MAR30	1	636	forward 1	TM	Non-Cytosolic
154	LG:408448.10:2001MAR30	637	659	forward 1	TM	Transmembrane
154	LG:408448.10:2001MAR30	660	716	forward 1	TM	Cytosolic
154	LG:408448.10:2001MAR30	1	281	forward 2	TM	Non-Cytosolic
154	LG:408448.10:2001MAR30	282	304	forward 2	TM	Transmembrane
154	LG:408448.10:2001MAR30	305	324	forward 2	TM	Cytosolic
154	LG:408448.10:2001MAR30	325	347	forward 2	TM	Transmembrane
154	LG:408448.10:2001MAR30	348	715	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
154	LG:408448.10:2001MAR30	1	281	forward 3	TM	Non-Cytosolic
154	LG:408448.10:2001MAR30	282	304	forward 3	TM	Transmembrane
154	LG:408448.10:2001MAR30	305	324	forward 3	TM	Cytosolic
154	LG:408448.10:2001MAR30	325	347	forward 3	TM	Transmembrane
154	LG:408448.10:2001MAR30	348	715	forward 3	TM	Non-Cytosolic
155	LG:408854.13:2001MAR30	1	128	forward 1	TM	Non-Cytosolic
155	LG:408854.13:2001MAR30	129	148	forward 1	TM	Transmembrane
155	LG:408854.13:2001MAR30	149	191	forward 1	TM	Cytosolic
155	LG:408854.13:2001MAR30	192	214	forward 1	TM	Transmembrane
155	LG:408854.13:2001MAR30	215	218	forward 1	TM	Non-Cytosolic
155	LG:408854.13:2001MAR30	219	238	forward 1	TM	Transmembrane
155	LG:408854.13:2001MAR30	239	242	forward 1	TM	Cytosolic
155	LG:408854.13:2001MAR30	243	265	forward 1	TM	Transmembrane
155	LG:408854.13:2001MAR30	266	305	forward 1	TM	Non-Cytosolic
155	LG:408854.13:2001MAR30	306	328	forward 1	TM	Transmembrane
155	LG:408854.13:2001MAR30	329	544	forward 1	TM	Cytosolic
156	LG:411150.14:2001MAR30	1	676	forward 1	TM	Non-Cytosolic
156	LG:411150.14:2001MAR30	677	699	forward 1	TM	Transmembrane
156	LG:411150.14:2001MAR30	700	822	forward 1	TM	Cytosolic
156	LG:411150.14:2001MAR30	1	676	forward 2	TM	Non-Cytosolic
156	LG:411150.14:2001MAR30	677	699	forward 2	TM	Transmembrane
156	LG:411150.14:2001MAR30	700	822	forward 2	TM	Cytosolic
156	LG:411150.14:2001MAR30	1	99	forward 3	TM	Cytosolic
156	LG:411150.14:2001MAR30	100	117	forward 3	TM	Transmembrane
156	LG:411150.14:2001MAR30	118	699	forward 3	TM	Non-Cytosolic
156	LG:411150.14:2001MAR30	700	722	forward 3	TM	Transmembrane
156	LG:411150.14:2001MAR30	723	733	forward 3	TM	Cytosolic
156	LG:411150.14:2001MAR30	734	751	forward 3	TM	Transmembrane
156	LG:411150.14:2001MAR30	752	754	forward 3	TM	Non-Cytosolic
156	LG:411150.14:2001MAR30	755	777	forward 3	TM	Transmembrane
156	LG:411150.14:2001MAR30	778	821	forward 3	TM	Cytosolic
157	LG:411466.1:2001MAR30	1	111	forward 1	TM	Non-Cytosolic
157	LG:411466.1:2001MAR30	112	134	forward 1	TM	Transmembrane
157	LG:411466.1:2001MAR30	135	146	forward 1	TM	Cytosolic
157	LG:411466.1:2001MAR30	147	169	forward 1	TM	Transmembrane
157	LG:411466.1:2001MAR30	170	188	forward 1	TM	Non-Cytosolic
157	LG:411466.1:2001MAR30	189	211	forward 1	TM	Transmembrane
157	LG:411466.1:2001MAR30	212	217	forward 1	TM	Cytosolic
157	LG:411466.1:2001MAR30	218	240	forward 1	TM	Transmembrane
157	LG:411466.1:2001MAR30	241	254	forward 1	TM	Non-Cytosolic
157	LG:411466.1:2001MAR30	255	274	forward 1	TM	Transmembrane
157	LG:411466.1:2001MAR30	275	333	forward 1	TM	Cytosolic
157	LG:411466.1:2001MAR30	334	351	forward 1	TM	Transmembrane
157	LG:411466.1:2001MAR30	352	404	forward 1	TM	Non-Cytosolic
157	LG:411466.1:2001MAR30	405	427	forward 1	TM	Transmembrane
157	LG:411466.1:2001MAR30	428	525	forward 1	TM	Cytosolic
157	LG:411466.1:2001MAR30	526	548	forward 1	TM	Transmembrane
157	LG:411466.1:2001MAR30	549	918	forward 1	TM	Non-Cytosolic
157	LG:411466.1:2001MAR30	1	70	forward 3	TM	Cytosolic
157	LG:411466.1:2001MAR30	71	93	forward 3	TM	Transmembrane
157	LG:411466.1:2001MAR30	94	110	forward 3	TM	Non-Cytosolic
157	LG:411466.1:2001MAR30	111	133	forward 3	TM	Transmembrane
157	LG:411466.1:2001MAR30	134	145	forward 3	TM	Cytosolic
157	LG:411466.1:2001MAR30	146	168	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
157	LG:411466.1:2001MAR30	169	202	forward 3	TM	Non-Cytosolic
157	LG:411466.1:2001MAR30	203	225	forward 3	TM	Transmembrane
157	LG:411466.1:2001MAR30	226	231	forward 3	TM	Cytosolic
157	LG:411466.1:2001MAR30	232	254	forward 3	TM	Transmembrane
157	LG:411466.1:2001MAR30	255	918	forward 3	TM	Non-Cytosolic
158	LG:413969.68:2001MAR30	1	741	forward 2	TM	Non-Cytosolic
158	LG:413969.68:2001MAR30	742	764	forward 2	TM	Transmembrane
158	LG:413969.68:2001MAR30	765	770	forward 2	TM	Cytosolic
158	LG:413969.68:2001MAR30	771	793	forward 2	TM	Transmembrane
158	LG:413969.68:2001MAR30	794	807	forward 2	TM	Non-Cytosolic
158	LG:413969.68:2001MAR30	808	830	forward 2	TM	Transmembrane
158	LG:413969.68:2001MAR30	831	842	forward 2	TM	Cytosolic
158	LG:413969.68:2001MAR30	843	865	forward 2	TM	Transmembrane
158	LG:413969.68:2001MAR30	866	911	forward 2	TM	Non-Cytosolic
159	LG:419641.35:2001MAR30	1	347	forward 1	TM	Non-Cytosolic
159	LG:419641.35:2001MAR30	348	370	forward 1	TM	Transmembrane
159	LG:419641.35:2001MAR30	371	450	forward 1	TM	Cytosolic
159	LG:419641.35:2001MAR30	1	20	forward 2	TM	Cytosolic
159	LG:419641.35:2001MAR30	21	40	forward 2	TM	Transmembrane
159	LG:419641.35:2001MAR30	41	450	forward 2	TM	Non-Cytosolic
159	LG:419641.35:2001MAR30	1	352	forward 3	TM	Non-Cytosolic
159	LG:419641.35:2001MAR30	353	370	forward 3	TM	Transmembrane
159	LG:419641.35:2001MAR30	371	382	forward 3	TM	Cytosolic
159	LG:419641.35:2001MAR30	383	405	forward 3	TM	Transmembrane
159	LG:419641.35:2001MAR30	406	424	forward 3	TM	Non-Cytosolic
159	LG:419641.35:2001MAR30	425	447	forward 3	TM	Transmembrane
159	LG:419641.35:2001MAR30	448	450	forward 3	TM	Cytosolic
160	LG:428206.7:2001MAR30	1	367	forward 2	TM	Non-Cytosolic
160	LG:428206.7:2001MAR30	368	385	forward 2	TM	Transmembrane
160	LG:428206.7:2001MAR30	386	512	forward 2	TM	Cytosolic
161	LG:430059.1:2001MAR30	1	72	forward 1	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	73	95	forward 1	TM	Transmembrane
161	LG:430059.1:2001MAR30	96	106	forward 1	TM	Cytosolic
161	LG:430059.1:2001MAR30	107	129	forward 1	TM	Transmembrane
161	LG:430059.1:2001MAR30	130	143	forward 1	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	144	163	forward 1	TM	Transmembrane
161	LG:430059.1:2001MAR30	164	583	forward 1	TM	Cytosolic
161	LG:430059.1:2001MAR30	584	606	forward 1	TM	Transmembrane
161	LG:430059.1:2001MAR30	607	653	forward 1	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	654	676	forward 1	TM	Transmembrane
161	LG:430059.1:2001MAR30	677	783	forward 1	TM	Cytosolic
161	LG:430059.1:2001MAR30	784	806	forward 1	TM	Transmembrane
161	LG:430059.1:2001MAR30	807	869	forward 1	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	870	889	forward 1	TM	Transmembrane
161	LG:430059.1:2001MAR30	890	1017	forward 1	TM	Cytosolic
161	LG:430059.1:2001MAR30	1	20	forward 2	TM	Cytosolic
161	LG:430059.1:2001MAR30	21	43	forward 2	TM	Transmembrane
161	LG:430059.1:2001MAR30	44	76	forward 2	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	77	96	forward 2	TM	Transmembrane
161	LG:430059.1:2001MAR30	97	102	forward 2	TM	Cytosolic
161	LG:430059.1:2001MAR30	103	122	forward 2	TM	Transmembrane
161	LG:430059.1:2001MAR30	123	595	forward 2	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	596	618	forward 2	TM	Transmembrane
161	LG:430059.1:2001MAR30	619	645	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
161	LG:430059.1:2001MAR30	646	668	forward 2	TM	Transmembrane
161	LG:430059.1:2001MAR30	669	671	forward 2	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	672	694	forward 2	TM	Transmembrane
161	LG:430059.1:2001MAR30	695	787	forward 2	TM	Cytosolic
161	LG:430059.1:2001MAR30	788	810	forward 2	TM	Transmembrane
161	LG:430059.1:2001MAR30	811	835	forward 2	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	836	858	forward 2	TM	Transmembrane
161	LG:430059.1:2001MAR30	859	1017	forward 2	TM	Cytosolic
161	LG:430059.1:2001MAR30	1	75	forward 3	TM	Cytosolic
161	LG:430059.1:2001MAR30	76	95	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	96	104	forward 3	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	105	122	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	123	128	forward 3	TM	Cytosolic
161	LG:430059.1:2001MAR30	129	151	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	152	190	forward 3	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	191	213	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	214	456	forward 3	TM	Cytosolic
161	LG:430059.1:2001MAR30	457	479	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	480	513	forward 3	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	514	536	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	537	582	forward 3	TM	Cytosolic
161	LG:430059.1:2001MAR30	583	605	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	606	609	forward 3	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	610	632	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	633	651	forward 3	TM	Cytosolic
161	LG:430059.1:2001MAR30	652	674	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	675	710	forward 3	TM	Non-Cytosolic
161	LG:430059.1:2001MAR30	711	733	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	734	737	forward 3	TM	Cytosolic
161	LG:430059.1:2001MAR30	738	757	forward 3	TM	Transmembrane
161	LG:430059.1:2001MAR30	758	1017	forward 3	TM	Non-Cytosolic
162	LG:448040.3:2001MAR30	1	37	forward 1	TM	Cytosolic
162	LG:448040.3:2001MAR30	38	57	forward 1	TM	Transmembrane
162	LG:448040.3:2001MAR30	58	169	forward 1	TM	Non-Cytosolic
162	LG:448040.3:2001MAR30	1	39	forward 2	TM	Cytosolic
162	LG:448040.3:2001MAR30	40	62	forward 2	TM	Transmembrane
162	LG:448040.3:2001MAR30	63	66	forward 2	TM	Non-Cytosolic
162	LG:448040.3:2001MAR30	67	86	forward 2	TM	Transmembrane
162	LG:448040.3:2001MAR30	87	168	forward 2	TM	Cytosolic
162	LG:448040.3:2001MAR30	1	39	forward 3	TM	Cytosolic
162	LG:448040.3:2001MAR30	40	62	forward 3	TM	Transmembrane
162	LG:448040.3:2001MAR30	63	168	forward 3	TM	Non-Cytosolic
163	LG:451274.1:2001MAR30	1	25	forward 2	TM	Non-Cytosolic
163	LG:451274.1:2001MAR30	26	48	forward 2	TM	Transmembrane
163	LG:451274.1:2001MAR30	49	54	forward 2	TM	Cytosolic
163	LG:451274.1:2001MAR30	55	77	forward 2	TM	Transmembrane
163	LG:451274.1:2001MAR30	78	467	forward 2	TM	Non-Cytosolic
164	LG:456110.1:2001MAR30	1	103	forward 3	TM	Cytosolic
164	LG:456110.1:2001MAR30	104	126	forward 3	TM	Transmembrane
164	LG:456110.1:2001MAR30	127	140	forward 3	TM	Non-Cytosolic
164	LG:456110.1:2001MAR30	141	160	forward 3	TM	Transmembrane
164	LG:456110.1:2001MAR30	161	199	forward 3	TM	Cytosolic
165	LG:456954.1:2001MAR30	1	35	forward 1	TM	Cytosolic
165	LG:456954.1:2001MAR30	36	58	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
165	LG:456954.1:2001MAR30	59	102	forward 1	TM	Non-Cytosolic
165	LG:456954.1:2001MAR30	103	125	forward 1	TM	Transmembrane
165	LG:456954.1:2001MAR30	126	242	forward 1	TM	Cytosolic
165	LG:456954.1:2001MAR30	1	38	forward 3	TM	Cytosolic
165	LG:456954.1:2001MAR30	39	58	forward 3	TM	Transmembrane
165	LG:456954.1:2001MAR30	59	117	forward 3	TM	Non-Cytosolic
165	LG:456954.1:2001MAR30	118	140	forward 3	TM	Transmembrane
165	LG:456954.1:2001MAR30	141	242	forward 3	TM	Cytosolic
166	LG:474942.12:2001MAR30	1	6	forward 1	TM	Cytosolic
166	LG:474942.12:2001MAR30	7	29	forward 1	TM	Transmembrane
166	LG:474942.12:2001MAR30	30	872	forward 1	TM	Non-Cytosolic
166	LG:474942.12:2001MAR30	1	165	forward 3	TM	Cytosolic
166	LG:474942.12:2001MAR30	166	188	forward 3	TM	Transmembrane
166	LG:474942.12:2001MAR30	189	872	forward 3	TM	Non-Cytosolic
167	LG:475119.14:2001MAR30	1	122	forward 1	TM	Cytosolic
167	LG:475119.14:2001MAR30	123	145	forward 1	TM	Transmembrane
167	LG:475119.14:2001MAR30	146	149	forward 1	TM	Non-Cytosolic
167	LG:475119.14:2001MAR30	150	169	forward 1	TM	Transmembrane
167	LG:475119.14:2001MAR30	170	181	forward 1	TM	Cytosolic
167	LG:475119.14:2001MAR30	182	201	forward 1	TM	Transmembrane
167	LG:475119.14:2001MAR30	202	242	forward 1	TM	Non-Cytosolic
167	LG:475119.14:2001MAR30	243	265	forward 1	TM	Transmembrane
167	LG:475119.14:2001MAR30	266	459	forward 1	TM	Cytosolic
168	LG:479908.77:2001MAR30	1	41	forward 3	TM	Cytosolic
168	LG:479908.77:2001MAR30	42	64	forward 3	TM	Transmembrane
168	LG:479908.77:2001MAR30	65	150	forward 3	TM	Non-Cytosolic
169	LG:480127.47:2001MAR30	1	78	forward 3	TM	Non-Cytosolic
169	LG:480127.47:2001MAR30	79	101	forward 3	TM	Transmembrane
169	LG:480127.47:2001MAR30	102	190	forward 3	TM	Cytosolic
170	LG:481154.12:2001MAR30	1	91	forward 3	TM	Cytosolic
170	LG:481154.12:2001MAR30	92	111	forward 3	TM	Transmembrane
170	LG:481154.12:2001MAR30	112	1082	forward 3	TM	Non-Cytosolic
170	LG:481154.12:2001MAR30	1083	1105	forward 3	TM	Transmembrane
170	LG:481154.12:2001MAR30	1106	1152	forward 3	TM	Cytosolic
171	LG:481414.6:2001MAR30	1	376	forward 1	TM	Non-Cytosolic
171	LG:481414.6:2001MAR30	377	399	forward 1	TM	Transmembrane
171	LG:481414.6:2001MAR30	400	531	forward 1	TM	Cytosolic
171	LG:481414.6:2001MAR30	532	554	forward 1	TM	Transmembrane
171	LG:481414.6:2001MAR30	555	877	forward 1	TM	Non-Cytosolic
171	LG:481414.6:2001MAR30	1	752	forward 3	TM	Non-Cytosolic
171	LG:481414.6:2001MAR30	753	775	forward 3	TM	Transmembrane
171	LG:481414.6:2001MAR30	776	781	forward 3	TM	Cytosolic
171	LG:481414.6:2001MAR30	782	801	forward 3	TM	Transmembrane
171	LG:481414.6:2001MAR30	802	877	forward 3	TM	Non-Cytosolic
172	LG:481941.1:2001MAR30	1	19	forward 2	TM	Non-Cytosolic
172	LG:481941.1:2001MAR30	20	41	forward 2	TM	Transmembrane
172	LG:481941.1:2001MAR30	42	491	forward 2	TM	Cytosolic
172	LG:481941.1:2001MAR30	492	514	forward 2	TM	Transmembrane
172	LG:481941.1:2001MAR30	515	523	forward 2	TM	Non-Cytosolic
172	LG:481941.1:2001MAR30	524	546	forward 2	TM	Transmembrane
172	LG:481941.1:2001MAR30	547	759	forward 2	TM	Cytosolic
172	LG:481941.1:2001MAR30	760	782	forward 2	TM	Transmembrane
172	LG:481941.1:2001MAR30	783	801	forward 2	TM	Non-Cytosolic
172	LG:481941.1:2001MAR30	802	824	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
172	LG:481941.1:2001MAR30	825	836	forward 2	TM	Cytosolic
172	LG:481941.1:2001MAR30	837	859	forward 2	TM	Transmembrane
172	LG:481941.1:2001MAR30	860	1184	forward 2	TM	Non-Cytosolic
172	LG:481941.1:2001MAR30	1185	1204	forward 2	TM	Transmembrane
172	LG:481941.1:2001MAR30	1205	1263	forward 2	TM	Cytosolic
172	LG:481941.1:2001MAR30	1	11	forward 3	TM	Cytosolic
172	LG:481941.1:2001MAR30	12	34	forward 3	TM	Transmembrane
172	LG:481941.1:2001MAR30	35	1263	forward 3	TM	Non-Cytosolic
173	LG:887216.4:2001MAR30	1	248	forward 2	TM	Cytosolic
173	LG:887216.4:2001MAR30	249	266	forward 2	TM	Transmembrane
173	LG:887216.4:2001MAR30	267	283	forward 2	TM	Non-Cytosolic
174	LG:899402.3:2001MAR30	1	754	forward 2	TM	Non-Cytosolic
174	LG:899402.3:2001MAR30	755	774	forward 2	TM	Transmembrane
174	LG:899402.3:2001MAR30	775	914	forward 2	TM	Cytosolic
174	LG:899402.3:2001MAR30	915	937	forward 2	TM	Transmembrane
174	LG:899402.3:2001MAR30	938	1020	forward 2	TM	Non-Cytosolic
174	LG:899402.3:2001MAR30	1021	1043	forward 2	TM	Transmembrane
174	LG:899402.3:2001MAR30	1044	1098	forward 2	TM	Cytosolic
174	LG:899402.3:2001MAR30	1099	1121	forward 2	TM	Transmembrane
174	LG:899402.3:2001MAR30	1122	1784	forward 2	TM	Non-Cytosolic
174	LG:899402.3:2001MAR30	1	840	forward 3	TM	Non-Cytosolic
174	LG:899402.3:2001MAR30	841	863	forward 3	TM	Transmembrane
174	LG:899402.3:2001MAR30	864	875	forward 3	TM	Cytosolic
174	LG:899402.3:2001MAR30	876	898	forward 3	TM	Transmembrane
174	LG:899402.3:2001MAR30	899	926	forward 3	TM	Non-Cytosolic
174	LG:899402.3:2001MAR30	927	949	forward 3	TM	Transmembrane
174	LG:899402.3:2001MAR30	950	1136	forward 3	TM	Cytosolic
174	LG:899402.3:2001MAR30	1137	1159	forward 3	TM	Transmembrane
174	LG:899402.3:2001MAR30	1160	1649	forward 3	TM	Non-Cytosolic
174	LG:899402.3:2001MAR30	1650	1672	forward 3	TM	Transmembrane
174	LG:899402.3:2001MAR30	1673	1711	forward 3	TM	Cytosolic
174	LG:899402.3:2001MAR30	1712	1731	forward 3	TM	Transmembrane
174	LG:899402.3:2001MAR30	1732	1761	forward 3	TM	Non-Cytosolic
174	LG:899402.3:2001MAR30	1762	1779	forward 3	TM	Transmembrane
174	LG:899402.3:2001MAR30	1780	1783	forward 3	TM	Cytosolic
175	LG:899894.2:2001MAR30	1	8	forward 2	TM	Cytosolic
175	LG:899894.2:2001MAR30	9	26	forward 2	TM	Transmembrane
175	LG:899894.2:2001MAR30	27	35	forward 2	TM	Non-Cytosolic
175	LG:899894.2:2001MAR30	36	53	forward 2	TM	Transmembrane
175	LG:899894.2:2001MAR30	54	72	forward 2	TM	Cytosolic
175	LG:899894.2:2001MAR30	73	95	forward 2	TM	Transmembrane
175	LG:899894.2:2001MAR30	96	563	forward 2	TM	Non-Cytosolic
175	LG:899894.2:2001MAR30	1	495	forward 3	TM	Non-Cytosolic
175	LG:899894.2:2001MAR30	496	518	forward 3	TM	Transmembrane
175	LG:899894.2:2001MAR30	519	563	forward 3	TM	Cytosolic
176	LG:977908.1:2001MAR30	1	200	forward 1	TM	Cytosolic
176	LG:977908.1:2001MAR30	201	223	forward 1	TM	Transmembrane
176	LG:977908.1:2001MAR30	224	242	forward 1	TM	Non-Cytosolic
176	LG:977908.1:2001MAR30	243	262	forward 1	TM	Transmembrane
176	LG:977908.1:2001MAR30	263	563	forward 1	TM	Cytosolic
176	LG:977908.1:2001MAR30	564	586	forward 1	TM	Transmembrane
176	LG:977908.1:2001MAR30	587	595	forward 1	TM	Non-Cytosolic
176	LG:977908.1:2001MAR30	596	618	forward 1	TM	Transmembrane
176	LG:977908.1:2001MAR30	619	710	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
176	LG:977908.1:2001MAR30	711	733	forward 1	TM	Transmembrane
176	LG:977908.1:2001MAR30	734	1236	forward 1	TM	Non-Cytosolic
176	LG:977908.1:2001MAR30	1	561	forward 2	TM	Non-Cytosolic
176	LG:977908.1:2001MAR30	562	584	forward 2	TM	Transmembrane
176	LG:977908.1:2001MAR30	585	596	forward 2	TM	Cytosolic
176	LG:977908.1:2001MAR30	597	619	forward 2	TM	Transmembrane
176	LG:977908.1:2001MAR30	620	1236	forward 2	TM	Non-Cytosolic
177	LG:977929.1:2001MAR30	1	688	forward 1	TM	Non-Cytosolic
177	LG:977929.1:2001MAR30	689	708	forward 1	TM	Transmembrane
177	LG:977929.1:2001MAR30	709	810	forward 1	TM	Cytosolic
177	LG:977929.1:2001MAR30	811	828	forward 1	TM	Transmembrane
177	LG:977929.1:2001MAR30	829	837	forward 1	TM	Non-Cytosolic
177	LG:977929.1:2001MAR30	838	860	forward 1	TM	Transmembrane
177	LG:977929.1:2001MAR30	861	890	forward 1	TM	Cytosolic
177	LG:977929.1:2001MAR30	891	913	forward 1	TM	Transmembrane
177	LG:977929.1:2001MAR30	914	1006	forward 1	TM	Non-Cytosolic
177	LG:977929.1:2001MAR30	1	837	forward 2	TM	Non-Cytosolic
177	LG:977929.1:2001MAR30	838	860	forward 2	TM	Transmembrane
177	LG:977929.1:2001MAR30	861	1005	forward 2	TM	Cytosolic
177	LG:977929.1:2001MAR30	1	776	forward 3	TM	Non-Cytosolic
177	LG:977929.1:2001MAR30	777	799	forward 3	TM	Transmembrane
177	LG:977929.1:2001MAR30	800	834	forward 3	TM	Cytosolic
177	LG:977929.1:2001MAR30	835	857	forward 3	TM	Transmembrane
177	LG:977929.1:2001MAR30	858	889	forward 3	TM	Non-Cytosolic
177	LG:977929.1:2001MAR30	890	912	forward 3	TM	Transmembrane
177	LG:977929.1:2001MAR30	913	924	forward 3	TM	Cytosolic
177	LG:977929.1:2001MAR30	925	947	forward 3	TM	Transmembrane
177	LG:977929.1:2001MAR30	948	974	forward 3	TM	Non-Cytosolic
177	LG:977929.1:2001MAR30	975	997	forward 3	TM	Transmembrane
177	LG:977929.1:2001MAR30	998	1005	forward 3	TM	Cytosolic
178	LG:978008.14:2001MAR30	1	991	forward 2	TM	Non-Cytosolic
178	LG:978008.14:2001MAR30	992	1014	forward 2	TM	Transmembrane
178	LG:978008.14:2001MAR30	1015	1118	forward 2	TM	Cytosolic
178	LG:978008.14:2001MAR30	1119	1136	forward 2	TM	Transmembrane
178	LG:978008.14:2001MAR30	1137	1202	forward 2	TM	Non-Cytosolic
178	LG:978008.14:2001MAR30	1203	1222	forward 2	TM	Transmembrane
178	LG:978008.14:2001MAR30	1223	1431	forward 2	TM	Cytosolic
178	LG:978008.14:2001MAR30	1432	1449	forward 2	TM	Transmembrane
178	LG:978008.14:2001MAR30	1450	1463	forward 2	TM	Non-Cytosolic
178	LG:978008.14:2001MAR30	1464	1486	forward 2	TM	Transmembrane
178	LG:978008.14:2001MAR30	1487	1499	forward 2	TM	Cytosolic
179	LG:979054.18:2001MAR30	1	491	forward 1	TM	Non-Cytosolic
179	LG:979054.18:2001MAR30	492	514	forward 1	TM	Transmembrane
179	LG:979054.18:2001MAR30	515	520	forward 1	TM	Cytosolic
179	LG:979054.18:2001MAR30	521	543	forward 1	TM	Transmembrane
179	LG:979054.18:2001MAR30	544	1150	forward 1	TM	Non-Cytosolic
179	LG:979054.18:2001MAR30	1	490	forward 3	TM	Non-Cytosolic
179	LG:979054.18:2001MAR30	491	513	forward 3	TM	Transmembrane
179	LG:979054.18:2001MAR30	514	514	forward 3	TM	Cytosolic
179	LG:979054.18:2001MAR30	515	537	forward 3	TM	Transmembrane
179	LG:979054.18:2001MAR30	538	1149	forward 3	TM	Non-Cytosolic
180	LG:979185.10:2001MAR30	1	3	forward 1	TM	Non-Cytosolic
180	LG:979185.10:2001MAR30	4	26	forward 1	TM	Transmembrane
180	LG:979185.10:2001MAR30	27	277	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
180	LG:979185.10:2001MAR30	278	300	forward 1	TM	Transmembrane
180	LG:979185.10:2001MAR30	301	319	forward 1	TM	Non-Cytosolic
180	LG:979185.10:2001MAR30	320	339	forward 1	TM	Transmembrane
180	LG:979185.10:2001MAR30	340	533	forward 1	TM	Cytosolic
180	LG:979185.10:2001MAR30	1	241	forward 2	TM	Non-Cytosolic
180	LG:979185.10:2001MAR30	242	264	forward 2	TM	Transmembrane
180	LG:979185.10:2001MAR30	265	276	forward 2	TM	Cytosolic
180	LG:979185.10:2001MAR30	277	296	forward 2	TM	Transmembrane
180	LG:979185.10:2001MAR30	297	501	forward 2	TM	Non-Cytosolic
180	LG:979185.10:2001MAR30	502	524	forward 2	TM	Transmembrane
180	LG:979185.10:2001MAR30	525	533	forward 2	TM	Cytosolic
180	LG:979185.10:2001MAR30	1	6	forward 3	TM	Cytosolic
180	LG:979185.10:2001MAR30	7	24	forward 3	TM	Transmembrane
180	LG:979185.10:2001MAR30	25	38	forward 3	TM	Non-Cytosolic
180	LG:979185.10:2001MAR30	39	61	forward 3	TM	Transmembrane
180	LG:979185.10:2001MAR30	62	241	forward 3	TM	Cytosolic
180	LG:979185.10:2001MAR30	242	264	forward 3	TM	Transmembrane
180	LG:979185.10:2001MAR30	265	273	forward 3	TM	Non-Cytosolic
180	LG:979185.10:2001MAR30	274	296	forward 3	TM	Transmembrane
180	LG:979185.10:2001MAR30	297	315	forward 3	TM	Cytosolic
180	LG:979185.10:2001MAR30	316	338	forward 3	TM	Transmembrane
180	LG:979185.10:2001MAR30	339	362	forward 3	TM	Non-Cytosolic
180	LG:979185.10:2001MAR30	363	385	forward 3	TM	Transmembrane
180	LG:979185.10:2001MAR30	386	404	forward 3	TM	Cytosolic
180	LG:979185.10:2001MAR30	405	427	forward 3	TM	Transmembrane
180	LG:979185.10:2001MAR30	428	532	forward 3	TM	Non-Cytosolic
181	LG:983654.1:2001MAR30	1	319	forward 2	TM	Non-Cytosolic
181	LG:983654.1:2001MAR30	320	342	forward 2	TM	Transmembrane
181	LG:983654.1:2001MAR30	343	348	forward 2	TM	Cytosolic
181	LG:983654.1:2001MAR30	349	368	forward 2	TM	Transmembrane
181	LG:983654.1:2001MAR30	369	369	forward 2	TM	Non-Cytosolic
181	LG:983654.1:2001MAR30	1	237	forward 3	TM	Cytosolic
181	LG:983654.1:2001MAR30	238	255	forward 3	TM	Transmembrane
181	LG:983654.1:2001MAR30	256	319	forward 3	TM	Non-Cytosolic
181	LG:983654.1:2001MAR30	320	342	forward 3	TM	Transmembrane
181	LG:983654.1:2001MAR30	343	368	forward 3	TM	Cytosolic
182	LG:985092.12:2001MAR30	1	118	forward 3	TM	Cytosolic
182	LG:985092.12:2001MAR30	119	141	forward 3	TM	Transmembrane
182	LG:985092.12:2001MAR30	142	369	forward 3	TM	Non-Cytosolic
183	LG:987396.8:2001MAR30	1	132	forward 2	TM	Non-Cytosolic
183	LG:987396.8:2001MAR30	133	152	forward 2	TM	Transmembrane
183	LG:987396.8:2001MAR30	153	273	forward 2	TM	Cytosolic
183	LG:987396.8:2001MAR30	274	296	forward 2	TM	Transmembrane
183	LG:987396.8:2001MAR30	297	924	forward 2	TM	Non-Cytosolic
183	LG:987396.8:2001MAR30	1	270	forward 3	TM	Non-Cytosolic
183	LG:987396.8:2001MAR30	271	293	forward 3	TM	Transmembrane
183	LG:987396.8:2001MAR30	294	358	forward 3	TM	Cytosolic
183	LG:987396.8:2001MAR30	359	381	forward 3	TM	Transmembrane
183	LG:987396.8:2001MAR30	382	924	forward 3	TM	Non-Cytosolic
184	LG:987418.10:2001MAR30	1	454	forward 2	TM	Non-Cytosolic
184	LG:987418.10:2001MAR30	455	474	forward 2	TM	Transmembrane
184	LG:987418.10:2001MAR30	475	479	forward 2	TM	Cytosolic
185	LG:997203.25:2001MAR30	1	801	forward 1	TM	Non-Cytosolic
185	LG:997203.25:2001MAR30	802	824	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
185	LG:997203.25:2001MAR30	825	830	forward 1	TM	Cytosolic
185	LG:997203.25:2001MAR30	831	846	forward 1	TM	Transmembrane
185	LG:997203.25:2001MAR30	847	855	forward 1	TM	Non-Cytosolic
185	LG:997203.25:2001MAR30	856	875	forward 1	TM	Transmembrane
185	LG:997203.25:2001MAR30	876	924	forward 1	TM	Cytosolic
185	LG:997203.25:2001MAR30	925	947	forward 1	TM	Transmembrane
185	LG:997203.25:2001MAR30	948	980	forward 1	TM	Non-Cytosolic
185	LG:997203.25:2001MAR30	981	1003	forward 1	TM	Transmembrane
185	LG:997203.25:2001MAR30	1004	1292	forward 1	TM	Cytosolic
185	LG:997203.25:2001MAR30	1	974	forward 3	TM	Non-Cytosolic
185	LG:997203.25:2001MAR30	975	992	forward 3	TM	Transmembrane
185	LG:997203.25:2001MAR30	993	1048	forward 3	TM	Cytosolic
185	LG:997203.25:2001MAR30	1049	1071	forward 3	TM	Transmembrane
185	LG:997203.25:2001MAR30	1072	1291	forward 3	TM	Non-Cytosolic
186	LG:997477.8:2001MAR30	1	59	forward 2	TM	Non-Cytosolic
186	LG:997477.8:2001MAR30	60	82	forward 2	TM	Transmembrane
186	LG:997477.8:2001MAR30	83	275	forward 2	TM	Cytosolic
186	LG:997477.8:2001MAR30	276	298	forward 2	TM	Transmembrane
186	LG:997477.8:2001MAR30	299	301	forward 2	TM	Non-Cytosolic
186	LG:997477.8:2001MAR30	302	324	forward 2	TM	Transmembrane
186	LG:997477.8:2001MAR30	325	401	forward 2	TM	Cytosolic
187	LG:998855.4:2001MAR30	1	50	forward 1	TM	Cytosolic
187	LG:998855.4:2001MAR30	51	73	forward 1	TM	Transmembrane
187	LG:998855.4:2001MAR30	74	333	forward 1	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1	1115	forward 1	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1116	1138	forward 1	TM	Transmembrane
188	LG:999093.1:2001MAR30	1139	1316	forward 1	TM	Cytosolic
188	LG:999093.1:2001MAR30	1317	1339	forward 1	TM	Transmembrane
188	LG:999093.1:2001MAR30	1340	1554	forward 1	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1	1073	forward 2	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1074	1093	forward 2	TM	Transmembrane
188	LG:999093.1:2001MAR30	1094	1099	forward 2	TM	Cytosolic
188	LG:999093.1:2001MAR30	1100	1119	forward 2	TM	Transmembrane
188	LG:999093.1:2001MAR30	1120	1123	forward 2	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1124	1143	forward 2	TM	Transmembrane
188	LG:999093.1:2001MAR30	1144	1163	forward 2	TM	Cytosolic
188	LG:999093.1:2001MAR30	1164	1186	forward 2	TM	Transmembrane
188	LG:999093.1:2001MAR30	1187	1261	forward 2	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1262	1284	forward 2	TM	Transmembrane
188	LG:999093.1:2001MAR30	1285	1296	forward 2	TM	Cytosolic
188	LG:999093.1:2001MAR30	1297	1314	forward 2	TM	Transmembrane
188	LG:999093.1:2001MAR30	1315	1318	forward 2	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1319	1341	forward 2	TM	Transmembrane
188	LG:999093.1:2001MAR30	1342	1394	forward 2	TM	Cytosolic
188	LG:999093.1:2001MAR30	1395	1417	forward 2	TM	Transmembrane
188	LG:999093.1:2001MAR30	1418	1554	forward 2	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1	422	forward 3	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	423	445	forward 3	TM	Transmembrane
188	LG:999093.1:2001MAR30	446	536	forward 3	TM	Cytosolic
188	LG:999093.1:2001MAR30	537	559	forward 3	TM	Transmembrane
188	LG:999093.1:2001MAR30	560	760	forward 3	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	761	783	forward 3	TM	Transmembrane
188	LG:999093.1:2001MAR30	784	1077	forward 3	TM	Cytosolic
188	LG:999093.1:2001MAR30	1078	1100	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
188	LG:999093.1:2001MAR30	1101	1109	forward 3	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1110	1132	forward 3	TM	Transmembrane
188	LG:999093.1:2001MAR30	1133	1317	forward 3	TM	Cytosolic
188	LG:999093.1:2001MAR30	1318	1340	forward 3	TM	Transmembrane
188	LG:999093.1:2001MAR30	1341	1343	forward 3	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1344	1363	forward 3	TM	Transmembrane
188	LG:999093.1:2001MAR30	1364	1375	forward 3	TM	Cytosolic
188	LG:999093.1:2001MAR30	1376	1395	forward 3	TM	Transmembrane
188	LG:999093.1:2001MAR30	1396	1468	forward 3	TM	Non-Cytosolic
188	LG:999093.1:2001MAR30	1469	1488	forward 3	TM	Transmembrane
188	LG:999093.1:2001MAR30	1489	1499	forward 3	TM	Cytosolic
188	LG:999093.1:2001MAR30	1500	1522	forward 3	TM	Transmembrane
188	LG:999093.1:2001MAR30	1523	1553	forward 3	TM	Non-Cytosolic
189	LG:999183.1:2001MAR30	1	1406	forward 1	TM	Non-Cytosolic
189	LG:999183.1:2001MAR30	1407	1424	forward 1	TM	Transmembrane
189	LG:999183.1:2001MAR30	1425	1443	forward 1	TM	Cytosolic
189	LG:999183.1:2001MAR30	1444	1463	forward 1	TM	Transmembrane
189	LG:999183.1:2001MAR30	1464	1477	forward 1	TM	Non-Cytosolic
189	LG:999183.1:2001MAR30	1478	1500	forward 1	TM	Transmembrane
189	LG:999183.1:2001MAR30	1501	1615	forward 1	TM	Cytosolic
189	LG:999183.1:2001MAR30	1616	1638	forward 1	TM	Transmembrane
189	LG:999183.1:2001MAR30	1639	1642	forward 1	TM	Non-Cytosolic
190	LI:1032972.1:2001MAY17	1	55	forward 1	TM	Cytosolic
190	LI:1032972.1:2001MAY17	56	78	forward 1	TM	Transmembrane
190	LI:1032972.1:2001MAY17	79	336	forward 1	TM	Non-Cytosolic
190	LI:1032972.1:2001MAY17	1	58	forward 2	TM	Cytosolic
190	LI:1032972.1:2001MAY17	59	81	forward 2	TM	Transmembrane
190	LI:1032972.1:2001MAY17	82	295	forward 2	TM	Non-Cytosolic
190	LI:1032972.1:2001MAY17	296	318	forward 2	TM	Transmembrane
190	LI:1032972.1:2001MAY17	319	335	forward 2	TM	Cytosolic
190	LI:1032972.1:2001MAY17	1	12	forward 3	TM	Non-Cytosolic
190	LI:1032972.1:2001MAY17	13	35	forward 3	TM	Transmembrane
190	LI:1032972.1:2001MAY17	36	55	forward 3	TM	Cytosolic
190	LI:1032972.1:2001MAY17	56	78	forward 3	TM	Transmembrane
190	LI:1032972.1:2001MAY17	79	335	forward 3	TM	Non-Cytosolic
191	LI:170666.6:2001MAY17	1	155	forward 3	TM	Non-Cytosolic
191	LI:170666.6:2001MAY17	156	178	forward 3	TM	Transmembrane
191	LI:170666.6:2001MAY17	179	222	forward 3	TM	Cytosolic
192	LI:197048.10:2001MAY17	1	336	forward 1	TM	Non-Cytosolic
192	LI:197048.10:2001MAY17	337	359	forward 1	TM	Transmembrane
192	LI:197048.10:2001MAY17	360	598	forward 1	TM	Cytosolic
192	LI:197048.10:2001MAY17	599	621	forward 1	TM	Transmembrane
192	LI:197048.10:2001MAY17	622	640	forward 1	TM	Non-Cytosolic
192	LI:197048.10:2001MAY17	641	663	forward 1	TM	Transmembrane
192	LI:197048.10:2001MAY17	664	714	forward 1	TM	Cytosolic
192	LI:197048.10:2001MAY17	715	737	forward 1	TM	Transmembrane
192	LI:197048.10:2001MAY17	738	751	forward 1	TM	Non-Cytosolic
192	LI:197048.10:2001MAY17	752	771	forward 1	TM	Transmembrane
192	LI:197048.10:2001MAY17	772	829	forward 1	TM	Cytosolic
192	LI:197048.10:2001MAY17	1	324	forward 2	TM	Cytosolic
192	LI:197048.10:2001MAY17	325	347	forward 2	TM	Transmembrane
192	LI:197048.10:2001MAY17	348	361	forward 2	TM	Non-Cytosolic
192	LI:197048.10:2001MAY17	362	384	forward 2	TM	Transmembrane
192	LI:197048.10:2001MAY17	385	488	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
192	LI:197048.10:2001MAY17	489	506	forward 2	TM	Transmembrane
192	LI:197048.10:2001MAY17	507	509	forward 2	TM	Non-Cytosolic
192	LI:197048.10:2001MAY17	510	529	forward 2	TM	Transmembrane
192	LI:197048.10:2001MAY17	530	597	forward 2	TM	Cytosolic
192	LI:197048.10:2001MAY17	598	620	forward 2	TM	Transmembrane
192	LI:197048.10:2001MAY17	621	639	forward 2	TM	Non-Cytosolic
192	LI:197048.10:2001MAY17	640	662	forward 2	TM	Transmembrane
192	LI:197048.10:2001MAY17	663	797	forward 2	TM	Cytosolic
192	LI:197048.10:2001MAY17	798	820	forward 2	TM	Transmembrane
192	LI:197048.10:2001MAY17	821	828	forward 2	TM	Non-Cytosolic
192	LI:197048.10:2001MAY17	1	376	forward 3	TM	Non-Cytosolic
192	LI:197048.10:2001MAY17	377	399	forward 3	TM	Transmembrane
192	LI:197048.10:2001MAY17	400	436	forward 3	TM	Cytosolic
192	LI:197048.10:2001MAY17	437	459	forward 3	TM	Transmembrane
192	LI:197048.10:2001MAY17	460	488	forward 3	TM	Non-Cytosolic
192	LI:197048.10:2001MAY17	489	511	forward 3	TM	Transmembrane
192	LI:197048.10:2001MAY17	512	523	forward 3	TM	Cytosolic
192	LI:197048.10:2001MAY17	524	546	forward 3	TM	Transmembrane
192	LI:197048.10:2001MAY17	547	555	forward 3	TM	Non-Cytosolic
192	LI:197048.10:2001MAY17	556	578	forward 3	TM	Transmembrane
192	LI:197048.10:2001MAY17	579	597	forward 3	TM	Cytosolic
192	LI:197048.10:2001MAY17	598	617	forward 3	TM	Transmembrane
192	LI:197048.10:2001MAY17	618	828	forward 3	TM	Non-Cytosolic
193	LI:228655.5:2001MAY17	1	33	forward 1	TM	Non-Cytosolic
193	LI:228655.5:2001MAY17	34	56	forward 1	TM	Transmembrane
193	LI:228655.5:2001MAY17	57	76	forward 1	TM	Cytosolic
193	LI:228655.5:2001MAY17	77	94	forward 1	TM	Transmembrane
193	LI:228655.5:2001MAY17	95	108	forward 1	TM	Non-Cytosolic
193	LI:228655.5:2001MAY17	109	131	forward 1	TM	Transmembrane
193	LI:228655.5:2001MAY17	132	200	forward 1	TM	Cytosolic
193	LI:228655.5:2001MAY17	201	223	forward 1	TM	Transmembrane
193	LI:228655.5:2001MAY17	224	237	forward 1	TM	Non-Cytosolic
194	LI:229789.6:2001MAY17	1	367	forward 1	TM	Non-Cytosolic
194	LI:229789.6:2001MAY17	368	390	forward 1	TM	Transmembrane
194	LI:229789.6:2001MAY17	391	394	forward 1	TM	Cytosolic
195	LI:231500.8:2001MAY17	1	458	forward 1	TM	Non-Cytosolic
195	LI:231500.8:2001MAY17	459	477	forward 1	TM	Transmembrane
195	LI:231500.8:2001MAY17	478	481	forward 1	TM	Cytosolic
196	LI:253851.26:2001MAY17	1	6	forward 3	TM	Cytosolic
196	LI:253851.26:2001MAY17	7	25	forward 3	TM	Transmembrane
196	LI:253851.26:2001MAY17	26	34	forward 3	TM	Non-Cytosolic
196	LI:253851.26:2001MAY17	35	57	forward 3	TM	Transmembrane
196	LI:253851.26:2001MAY17	58	414	forward 3	TM	Cytosolic
196	LI:253851.26:2001MAY17	415	437	forward 3	TM	Transmembrane
196	LI:253851.26:2001MAY17	438	477	forward 3	TM	Non-Cytosolic
196	LI:253851.26:2001MAY17	478	497	forward 3	TM	Transmembrane
196	LI:253851.26:2001MAY17	498	517	forward 3	TM	Cytosolic
196	LI:253851.26:2001MAY17	518	537	forward 3	TM	Transmembrane
196	LI:253851.26:2001MAY17	538	556	forward 3	TM	Non-Cytosolic
196	LI:253851.26:2001MAY17	557	579	forward 3	TM	Transmembrane
196	LI:253851.26:2001MAY17	580	748	forward 3	TM	Cytosolic
197	LI:373302.1:2001MAY17	1	61	forward 1	TM	Non-Cytosolic
197	LI:373302.1:2001MAY17	62	84	forward 1	TM	Transmembrane
197	LI:373302.1:2001MAY17	85	104	forward 1	TM	Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
197	LI:373302.1:2001MAY17	105	124	forward 1	TM	Transmembrane
197	LI:373302.1:2001MAY17	125	457	forward 1	TM	Non-Cytosolic
197	LI:373302.1:2001MAY17	1	110	forward 2	TM	Non-Cytosolic
197	LI:373302.1:2001MAY17	111	133	forward 2	TM	Transmembrane
197	LI:373302.1:2001MAY17	134	161	forward 2	TM	Cytosolic
197	LI:373302.1:2001MAY17	162	184	forward 2	TM	Transmembrane
197	LI:373302.1:2001MAY17	185	214	forward 2	TM	Non-Cytosolic
197	LI:373302.1:2001MAY17	215	237	forward 2	TM	Transmembrane
197	LI:373302.1:2001MAY17	238	395	forward 2	TM	Cytosolic
197	LI:373302.1:2001MAY17	396	418	forward 2	TM	Transmembrane
197	LI:373302.1:2001MAY17	419	456	forward 2	TM	Non-Cytosolic
197	LI:373302.1:2001MAY17	1	98	forward 3	TM	Cytosolic
197	LI:373302.1:2001MAY17	99	121	forward 3	TM	Transmembrane
197	LI:373302.1:2001MAY17	122	368	forward 3	TM	Non-Cytosolic
197	LI:373302.1:2001MAY17	369	391	forward 3	TM	Transmembrane
197	LI:373302.1:2001MAY17	392	411	forward 3	TM	Cytosolic
197	LI:373302.1:2001MAY17	412	434	forward 3	TM	Transmembrane
197	LI:373302.1:2001MAY17	435	456	forward 3	TM	Non-Cytosolic
198	LI:405707.12:2001MAY17	1	14	forward 2	TM	Non-Cytosolic
198	LI:405707.12:2001MAY17	15	37	forward 2	TM	Transmembrane
198	LI:405707.12:2001MAY17	38	128	forward 2	TM	Cytosolic
198	LI:405707.12:2001MAY17	129	146	forward 2	TM	Transmembrane
198	LI:405707.12:2001MAY17	147	149	forward 2	TM	Non-Cytosolic
198	LI:405707.12:2001MAY17	150	172	forward 2	TM	Transmembrane
198	LI:405707.12:2001MAY17	173	438	forward 2	TM	Cytosolic
199	LI:411441.8:2001MAY17	1	92	forward 3	TM	Cytosolic
199	LI:411441.8:2001MAY17	93	115	forward 3	TM	Transmembrane
199	LI:411441.8:2001MAY17	116	497	forward 3	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	1	9	forward 1	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	10	32	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	33	52	forward 1	TM	Cytosolic
200	LI:758193.3:2001MAY17	53	75	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	76	99	forward 1	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	100	122	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	123	214	forward 1	TM	Cytosolic
200	LI:758193.3:2001MAY17	215	237	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	238	282	forward 1	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	283	305	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	306	311	forward 1	TM	Cytosolic
200	LI:758193.3:2001MAY17	312	334	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	335	343	forward 1	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	344	366	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	367	415	forward 1	TM	Cytosolic
200	LI:758193.3:2001MAY17	416	435	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	436	476	forward 1	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	477	499	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	500	552	forward 1	TM	Cytosolic
200	LI:758193.3:2001MAY17	553	575	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	576	584	forward 1	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	585	607	forward 1	TM	Transmembrane
200	LI:758193.3:2001MAY17	608	664	forward 1	TM	Cytosolic
200	LI:758193.3:2001MAY17	1	20	forward 2	TM	Cytosolic
200	LI:758193.3:2001MAY17	21	38	forward 2	TM	Transmembrane
200	LI:758193.3:2001MAY17	39	64	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
200	LI:758193.3:2001MAY17	65	87	forward 2	TM	Transmembrane
200	LI:758193.3:2001MAY17	88	211	forward 2	TM	Cytosolic
200	LI:758193.3:2001MAY17	212	234	forward 2	TM	Transmembrane
200	LI:758193.3:2001MAY17	235	243	forward 2	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	244	261	forward 2	TM	Transmembrane
200	LI:758193.3:2001MAY17	262	277	forward 2	TM	Cytosolic
200	LI:758193.3:2001MAY17	278	300	forward 2	TM	Transmembrane
200	LI:758193.3:2001MAY17	301	476	forward 2	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	477	499	forward 2	TM	Transmembrane
200	LI:758193.3:2001MAY17	500	552	forward 2	TM.	Cytosolic
200	LI:758193.3:2001MAY17	553	575	forward 2	TM	Transmembrane
200	LI:758193.3:2001MAY17	576	584	forward 2	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	585	607	forward 2	TM	Transmembrane
200	LI:758193.3:2001MAY17	608	664	forward 2	TM	Cytosolic
200	LI:758193.3:2001MAY17	1	19	forward 3	TM	Cytosolic
200	LI:758193.3:2001MAY17	20	42	forward 3	TM	Transmembrane
200	LI:758193.3:2001MAY17	43	56	forward 3	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	57	79	forward 3	TM	Transmembrane
200	LI:758193.3:2001MAY17	80	115	forward 3	TM	Cytosolic
200	LI:758193.3:2001MAY17	116	138	forward 3	TM	Transmembrane
200	LI:758193.3:2001MAY17	139	213	forward 3	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	214	236	forward 3	TM	Transmembrane
200	LI:758193.3:2001MAY17	237	278	forward 3	TM	Cytosolic
200	LI:758193.3:2001MAY17	279	301	forward 3	TM	Transmembrane
200	LI:758193.3:2001MAY17	302	360	forward 3	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	361	383	forward 3	TM	Transmembrane
200	LI:758193.3:2001MAY17	384	475	forward 3	TM	Cytosolic
200	LI:758193.3:2001MAY17	476	498	forward 3	TM	Transmembrane
200	LI:758193.3:2001MAY17	499	517	forward 3	TM	Non-Cytosolic
200	LI:758193.3:2001MAY17	518	540	forward 3	TM	Transmembrane
200	LI:758193.3:2001MAY17	541	664	forward 3	TM	Cytosolic
201	LI:1028562.3:2001MAY17	1	6	forward 2	TM	Cytosolic
201	LI:1028562.3:2001MAY17	7	24	forward 2	TM	Transmembrane
201	LI:1028562.3:2001MAY17	25	43	forward 2	TM	Non-Cytosolic
201	LI:1028562.3:2001MAY17	44	66	forward 2	TM	Transmembrane
201	LI:1028562.3:2001MAY17	67	69	forward 2	TM	Cytosolic
202	LI:104650.7:2001MAY17	1	6	forward 3	TM	Cytosolic
202	LI:104650.7:2001MAY17	7	29	forward 3	TM	Transmembrane
202	LI:104650.7:2001MAY17	30	38	forward 3	TM	Non-Cytosolic
202	LI:104650.7:2001MAY17	39	61	forward 3	TM	Transmembrane
202	LI:104650.7:2001MAY17	62	72	forward 3	TM	Cytosolic
202	LI:104650.7:2001MAY17	73	95	forward 3	TM	Transmembrane
202	LI:104650.7:2001MAY17	96	265	forward 3	TM	Non-Cytosolic
203	LI:1094557.4:2001MAY17	1	57	forward 1	TM	Non-Cytosolic
203	LI:1094557.4:2001MAY17	58	80	forward 1	TM	Transmembrane
203	LI:1094557.4:2001MAY17	81	311	forward 1	TM	Cytosolic
203	LI:1094557.4:2001MAY17	1	90	forward 3	TM	Cytosolic
203	LI:1094557.4:2001MAY17	91	113	forward 3	TM	Transmembrane
203	LI:1094557.4:2001MAY17	114	127	forward 3	TM	Non-Cytosolic
203	LI:1094557.4:2001MAY17	128	147	forward 3	TM	Transmembrane
203	LI:1094557.4:2001MAY17	148	310	forward 3	TM	Cytosolic
204	LI:1143528.4:2001MAY17	1	302	forward 1	TM	Non-Cytosolic
204	LI:1143528.4:2001MAY17	303	325	forward 1	TM	Transmembrane
204	LI:1143528.4:2001MAY17	326	331	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
204	LI:1143528.4:2001MAY17	1	298	forward 3	TM	Non-Cytosolic
204	LI:1143528.4:2001MAY17	299	321	forward 3	TM	Transmembrane
204	LI:1143528.4:2001MAY17	322	330	forward 3	TM	Cytosolic
205	LI:1172210.7:2001MAY17	1	582	forward 1	TM	Non-Cytosolic
205	LI:1172210.7:2001MAY17	583	600	forward 1	TM	Transmembrane
205	LI:1172210.7:2001MAY17	601	601	forward 1	TM	Cytosolic
206	LI:1178659.14:2001MAY17	1	694	forward 1	TM	Non-Cytosolic
206	LI:1178659.14:2001MAY17	695	717	forward 1	TM	Transmembrane
206	LI:1178659.14:2001MAY17	718	779	forward 1	TM	Cytosolic
206	LI:1178659.14:2001MAY17	780	802	forward 1	TM	Transmembrane
206	LI:1178659.14:2001MAY17	803	811	forward 1	TM	Non-Cytosolic
206	LI:1178659.14:2001MAY17	812	834	forward 1	TM	Transmembrane
206	LI:1178659.14:2001MAY17	835	835	forward 1	TM	Cytosolic
206	LI:1178659.14:2001MAY17	1	233	forward 2	TM	Cytosolic
206	LI:1178659.14:2001MAY17	234	256	forward 2	TM	Transmembrane
206	LI:1178659.14:2001MAY17	257	347	forward 2	TM	Non-Cytosolic
206	LI:1178659.14:2001MAY17	348	370	forward 2	TM	Transmembrane
206	LI:1178659.14:2001MAY17	371	689	forward 2	TM	Cytosolic
206	LI:1178659.14:2001MAY17	690	712	forward 2	TM	Transmembrane
206	LI:1178659.14:2001MAY17	713	808	forward 2	TM	Non-Cytosolic
206	LI:1178659.14:2001MAY17	809	831	forward 2	TM	Transmembrane
206	LI:1178659.14:2001MAY17	832	835	forward 2	TM	Cytosolic
206	LI:1178659.14:2001MAY17	1	57	forward 3	TM	Cytosolic
206	LI:1178659.14:2001MAY17	58	80	forward 3	TM	Transmembrane
206	LI:1178659.14:2001MAY17	81	235	forward 3	TM	Non-Cytosolic
206	LI:1178659.14:2001MAY17	236	258	forward 3	TM	Transmembrane
206	LI:1178659.14:2001MAY17	259	316	forward 3	TM	Cytosolic
206	LI:1178659.14:2001MAY17	317	339	forward 3	TM	Transmembrane
206	LI:1178659.14:2001MAY17	340	370	forward 3	TM	Non-Cytosolic
206	LI:1178659.14:2001MAY17	371	393	forward 3	TM	Transmembrane
206	LI:1178659.14:2001MAY17	394	457	forward 3	TM	Cytosolic
206	LI:1178659.14:2001MAY17	458	477	forward 3	TM	Transmembrane
206	LI:1178659.14:2001MAY17	478	779	forward 3	TM	Non-Cytosolic
206	LI:1178659.14:2001MAY17	780	802	forward 3	TM	Transmembrane
206	LI:1178659.14:2001MAY17	803	808	forward 3	TM	Cytosolic
206	LI:1178659.14:2001MAY17	809	831	forward 3	TM	Transmembrane
206	LI:1178659.14:2001MAY17	832	835	forward 3	TM	Non-Cytosolic
207	LI:1983726.3:2001MAY17	1	95	forward 3	TM	Cytosolic
207	LI:1983726.3:2001MAY17	96	118	forward 3	TM	Transmembrane
207	LI:1983726.3:2001MAY17	119	151	forward 3	TM	Non-Cytosolic
207	LI:1983726.3:2001MAY17	152	174	forward 3	TM	Transmembrane
207	LI:1983726.3:2001MAY17	175	186	forward 3	TM	Cytosolic
207	LI:1983726.3:2001MAY17	187	206	forward 3	TM	Transmembrane
207	LI:1983726.3:2001MAY17	207	211	forward 3	TM	Non-Cytosolic
207	LI:1983726.3:2001MAY17	212	231	forward 3	TM	Transmembrane
207	LI:1983726.3:2001MAY17	232	251	forward 3	TM	Cytosolic
207	LI:1983726.3:2001MAY17	252	274	forward 3	TM	Transmembrane
207	LI:1983726.3:2001MAY17	275	285	forward 3	TM	Non-Cytosolic
208	LI:2051495.3:2001MAY17	1	259	forward 1	TM	Non-Cytosolic
208	LI:2051495.3:2001MAY17	260	279	forward 1	TM	Transmembrane
208	LI:2051495.3:2001MAY17	280	291	forward 1	TM	Cytosolic
208	LI:2051495.3:2001MAY17	292	309	forward 1	TM	Transmembrane
208	LI:2051495.3:2001MAY17	310	337	forward 1	TM	Non-Cytosolic
208	LI:2051495.3:2001MAY17	338	360	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
208	LI:2051495.3:2001MAY17	361	527	forward 1	TM	Cytosolic
208	LI:2051495.3:2001MAY17	528	550	forward 1	TM	Transmembrane
208	LI:2051495.3:2001MAY17	551	706	forward 1	TM	Non-Cytosolic
208	LI:2051495.3:2001MAY17	1	320	forward 2	TM	Non-Cytosolic
208	LI:2051495.3:2001MAY17	321	343	forward 2	TM	Transmembrane
208	LI:2051495.3:2001MAY17	344	515	forward 2	TM	Cytosolic
208	LI:2051495.3:2001MAY17	516	538	forward 2	TM	Transmembrane
208	LI:2051495.3:2001MAY17	539	705	forward 2	TM	Non-Cytosolic
208	LI:2051495.3:2001MAY17	1	336	forward 3	TM	Non-Cytosolic
208	LI:2051495.3:2001MAY17	337	359	forward 3	TM	Transmembrane
208	LI:2051495.3:2001MAY17	360	705	forward 3	TM	Cytosolic
209	LI:2117629.1:2001MAY17	1	320	forward 1	TM	Non-Cytosolic
209	LI:2117629.1:2001MAY17	321	343	forward 1	TM	Transmembrane
209	LI:2117629.1:2001MAY17	344	355	forward 1	TM	Cytosolic
209	LI:2117629.1:2001MAY17	356	378	forward 1	TM	Transmembrane
209	LI:2117629.1:2001MAY17	379	397	forward 1	TM	Non-Cytosolic
209	LI:2117629.1:2001MAY17	398	416	forward 1	TM	Transmembrane
209	LI:2117629.1:2001MAY17	417	424	forward 1	TM	Cytosolic
210	LI:2118007.3:2001MAY17	1	37	forward 3	TM	Non-Cytosolic
210	LI:2118007.3:2001MAY17	38	60	forward 3	TM	Transmembrane
210	LI:2118007.3:2001MAY17	61	203	forward 3	TM	Cytosolic
210	LI:2118007.3:2001MAY17	204	226	forward 3	TM	Transmembrane
210	LI:2118007.3:2001MAY17	227	338	forward 3	TM	Non-Cytosolic
211	LI:2118292.9:2001MAY17	1	140	forward 1	TM	Non-Cytosolic
211	LI:2118292.9:2001MAY17	141	163	forward 1	TM	Transmembrane
211	LI:2118292.9:2001MAY17	164	286	forward 1	TM	Cytosolic
211	LI:2118292.9:2001MAY17	287	306	forward 1	TM	Transmembrane
211	LI:2118292.9:2001MAY17	307	344	forward 1	TM	Non-Cytosolic
211	LI:2118292.9:2001MAY17	345	367	forward 1	TM	Transmembrane
211	LI:2118292.9:2001MAY17	368	520	forward 1	TM	Cytosolic
211	LI:2118292.9:2001MAY17	1	299	forward 2	TM	Non-Cytosolic
211	LI:2118292.9:2001MAY17	300	319	forward 2	TM	Transmembrane
211	LI:2118292.9:2001MAY17	320	418	forward 2	TM	Cytosolic
211	LI:2118292.9:2001MAY17	419	441	forward 2	TM	Transmembrane
211	LI:2118292.9:2001MAY17	442	478	forward 2	TM	Non-Cytosolic
211	LI:2118292.9:2001MAY17	479	501	forward 2	TM	Transmembrane
211	LI:2118292.9:2001MAY17	502	520	forward 2	TM	Cytosolic
211	LI:2118292.9:2001MAY17	1	292	forward 3	TM	Cytosolic
211	LI:2118292.9:2001MAY17	293	312	forward 3	TM	Transmembrane
211	LI:2118292.9:2001MAY17	313	346	forward 3	TM	Non-Cytosolic
211	LI:2118292.9:2001MAY17	347	369	forward 3	TM	Transmembrane
211	LI:2118292.9:2001MAY17	370	452	forward 3	TM	Cytosolic
211	LI:2118292.9:2001MAY17	453	475	forward 3	TM	Transmembrane
211	LI:2118292.9:2001MAY17	476	489	forward 3	TM	Non-Cytosolic
211	LI:2118292.9:2001MAY17	490	512	forward 3	TM	Transmembrane
211	LI:2118292.9:2001MAY17	513	519	forward 3	TM	Cytosolic
212	LI:2118733.7:2001MAY17	1	48	forward 1	TM	Non-Cytosolic
212	LI:2118733.7:2001MAY17	49	71	forward 1	TM	Transmembrane
212	LI:2118733.7:2001MAY17	72	195	forward 1	TM	Cytosolic
212	LI:2118733.7:2001MAY17	196	218	forward 1	TM	Transmembrane
212	LI:2118733.7:2001MAY17	219	222	forward 1	TM	Non-Cytosolic
212	LI:2118733.7:2001MAY17	223	242	forward 1	TM	Transmembrane
212	LI:2118733.7:2001MAY17	243	292	forward 1	TM	Cytosolic
212	LI:2118733.7:2001MAY17	1	35	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
212	LI:2118733.7:2001MAY17	36	58	forward 2	TM	Transmembrane
212	LI:2118733.7:2001MAY17	59	110	forward 2	TM	Non-Cytosolic
212	LI:2118733.7:2001MAY17	111	133	forward 2	TM	Transmembrane
212	LI:2118733.7:2001MAY17	134	153	forward 2	TM	Cytosolic
212	LI:2118733.7:2001MAY17	154	176	forward 2	TM	Transmembrane
212	LI:2118733.7:2001MAY17	177	195	forward 2	TM	Non-Cytosolic
212	LI:2118733.7:2001MAY17	196	218	forward 2	TM	Transmembrane
212	LI:2118733.7:2001MAY17	219	291	forward 2	TM	Cytosolic
212	LI:2118733.7:2001MAY17	1	108	forward 3	TM	Cytosolic
212	LI:2118733.7:2001MAY17	109	131	forward 3	TM	Transmembrane
212	LI:2118733.7:2001MAY17	132	153	forward 3	TM	Non-Cytosolic
212	LI:2118733.7:2001MAY17	154	176	forward 3	TM	Transmembrane
212	LI:2118733.7:2001MAY17	177	199	forward 3	TM	Cytosolic
212	LI:2118733.7:2001MAY17	200	222	forward 3	TM	Transmembrane
212	LI:2118733.7:2001MAY17	223	249	forward 3	TM	Non-Cytosolic
212	LI:2118733.7:2001MAY17	250	272	forward 3	TM	Transmembrane
212	LI:2118733.7:2001MAY17	273	291	forward 3	TM	Cytosolic
213	LI:212702.3:2001MAY17	1	615	forward 1	TM	Non-Cytosolic
213	LI:212702.3:2001MAY17	616	638	forward 1	TM	Transmembrane
213	LI:212702.3:2001MAY17	639	854	forward 1	TM	Cytosolic
213	LI:212702.3:2001MAY17	855	874	forward 1	TM	Transmembrane
213	LI:212702.3:2001MAY17	875	902	forward 1	TM	Non-Cytosolic
213	LI:212702.3:2001MAY17	903	925	forward 1	TM	Transmembrane
213	LI:212702.3:2001MAY17	926	995	forward 1	TM	Cytosolic
213	LI:212702.3:2001MAY17	996	1018	forward 1	TM	Transmembrane
213	LI:212702.3:2001MAY17	1019	1410	forward 1	TM	Non-Cytosolic
213	LI:212702.3:2001MAY17	1	19	forward 2	TM	Non-Cytosolic
213	LI:212702.3:2001MAY17	20	42	forward 2	TM	Transmembrane
213	LI:212702.3:2001MAY17	43	369	forward 2	TM	Cytosolic
213	LI:212702.3:2001MAY17	370	392	forward 2	TM	Transmembrane
213	LI:212702.3:2001MAY17	393	547	forward 2	TM	Non-Cytosolic
213	LI:212702.3:2001MAY17	548	570	forward 2	TM	Transmembrane
213	LI:212702.3:2001MAY17	571	582	forward 2	TM	Cytosolic
213	LI:212702.3:2001MAY17	583	605	forward 2	TM	Transmembrane
213	LI:212702.3:2001MAY17	606	614	forward 2	TM	Non-Cytosolic
213	LI:212702.3:2001MAY17	615	637	forward 2	TM	Transmembrane
213	LI:212702.3:2001MAY17	638	835	forward 2	TM	Cytosolic
213	LI:212702.3:2001MAY17	836	855	forward 2	TM	Transmembrane
213	LI:212702.3:2001MAY17	856	1410	forward 2	TM	Non-Cytosolic
213	LI:212702.3:2001MAY17	1	19	forward 3	TM	Cytosolic
213	LI:212702.3:2001MAY17	20	42	forward 3	TM	Transmembrane
213	LI:212702.3:2001MAY17	43	1409	forward 3	TM	Non-Cytosolic
214	LI:2207871.10:2001MAY17	1	74	forward 2	TM	Cytosolic
214	LI:2207871.10:2001MAY17	75	97	forward 2	TM	Transmembrane
214	LI:2207871.10:2001MAY17	98	101	forward 2	TM	Non-Cytosolic
214	LI:2207871.10:2001MAY17	102	121	forward 2	TM	Transmembrane
214	LI:2207871.10:2001MAY17	122	132	forward 2	TM	Cytosolic
214	LI:2207871.10:2001MAY17	133	155	forward 2	TM	Transmembrane
214	LI:2207871.10:2001MAY17	156	169	forward 2	TM	Non-Cytosolic
214	LI:2207871.10:2001MAY17	170	187	forward 2	TM	Transmembrane
214	LI:2207871.10:2001MAY17	188	193	forward 2	TM	Cytosolic
214	LI:2207871.10:2001MAY17	194	216	forward 2	TM	Transmembrane
214	LI:2207871.10:2001MAY17	217	629	forward 2	TM	Non-Cytosolic
215	LI:2207876.5:2001MAY17	1	63	forward 2	TM	Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
216	LI:2208743.1:2001MAY17	1	115	forward 1	TM	Non-Cytosolic
216	LI:2208743.1:2001MAY17	116	138	forward 1	TM	Transmembrane
216	LI:2208743.1:2001MAY17	139	226	forward 1	TM	Cytosolic
216	LI:2208743.1:2001MAY17	227	249	forward 1	TM	Transmembrane
216	LI:2208743.1:2001MAY17	250	288	forward 1	TM	Non-Cytosolic
217	LI:2208744.1:2001MAY17	1	12	forward 1	TM	Cytosolic
217	LI:2208744.1:2001MAY17	13	35	forward 1	TM	Transmembrane
217	LI:2208744.1:2001MAY17	36	538	forward 1	TM	Non-Cytosolic
218	LI:230905.3:2001MAY17	1	252	forward 2	TM	Non-Cytosolic
218	LI:230905.3:2001MAY17	253	275	forward 2	TM	Transmembrane
218	LI:230905.3:2001MAY17	276	290	forward 2	TM	Cytosolic
218	LI:230905.3:2001MAY17	291	313	forward 2	TM	Transmembrane
218	LI:230905.3:2001MAY17	314	327	forward 2	TM	Non-Cytosolic
218	LI:230905.3:2001MAY17	328	350	forward 2	TM	Transmembrane
218	LI:230905.3:2001MAY17	351	373	forward 2	TM	Cytosolic
218	LI:230905.3:2001MAY17	1	4	forward 3	TM	Cytosolic
218	LI:230905.3:2001MAY17	5	27	forward 3	TM	Transmembrane
218	LI:230905.3:2001MAY17	28	31	forward 3	TM	Non-Cytosolic
218	LI:230905.3:2001MAY17	32	54	forward 3	TM	Transmembrane
218	LI:230905.3:2001MAY17	55	248	forward 3	TM	Cytosolic
218	LI:230905.3:2001MAY17	249	271	forward 3	TM	Transmembrane
218	LI:230905.3:2001MAY17	272	285	forward 3	TM	Non-Cytosolic
218	LI:230905.3:2001MAY17	286	308	forward 3	TM	Transmembrane
218	LI:230905.3:2001MAY17	309	372	forward 3	TM	Cytosolic
219	LI:235233.95:2001MAY17	1	19	forward 1	TM	Cytosolic
219	LI:235233.95:2001MAY17	20	42	forward 1	TM	Transmembrane
219	LI:235233.95:2001MAY17	43	307	forward 1	TM	Non-Cytosolic
220	LI:235359.24:2001MAY17	1	149	forward 3	TM	Cytosolic
220	LI:235359.24:2001MAY17	150	172	forward 3	TM	Transmembrane
220	LI:235359.24:2001MAY17	173	186	forward 3	TM	Non-Cytosolic
220	LI:235359.24:2001MAY17	187	206	forward 3	TM	Transmembrane
220	LI:235359.24:2001MAY17	207	335	forward 3	TM	Cytosolic
221	LI:238365.6:2001MAY17	1	437	forward 1	TM	Non-Cytosolic
221	LI:238365.6:2001MAY17	438	460	forward 1	TM	Transmembrane
221	LI:238365.6:2001MAY17	461	465	forward 1	TM	Cytosolic
222	LI:260259.23:2001MAY17	1	57	forward 1	TM	Cytosolic
222	LI:260259.23:2001MAY17	1	57	forward 2	TM	Cytosolic
222	LI:260259.23:2001MAY17	1	56	forward 3	TM	Cytosolic
223	LI:321069.2:2001MAY17	1	181	forward 1	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	182	204	forward 1	TM	Transmembrane
223	LI:321069.2:2001MAY17	205	449	forward 1	TM	Cytosolic
223	LI:321069.2:2001MAY17	450	469	forward 1	TM	Transmembrane
223	LI:321069.2:2001MAY17	470	478	forward 1	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	479	501	forward 1	TM	Transmembrane
223	LI:321069.2:2001MAY17	502	507	forward 1	TM	Cytosolic
223	LI:321069.2:2001MAY17	508	530	forward 1	TM	Transmembrane
223	LI:321069.2:2001MAY17	531	631	forward 1	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	632	654	forward 1	TM	Transmembrane
223	LI:321069.2:2001MAY17	655	666	forward 1	TM	Cytosolic
223	LI:321069.2:2001MAY17	667	689	forward 1	TM	Transmembrane
223	LI:321069.2:2001MAY17	690	693	forward 1	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	694	713	forward 1	TM	Transmembrane
223	LI:321069.2:2001MAY17	714	1071	forward 1	TM	Cytosolic
223	LI:321069.2:2001MAY17	1072	1094	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
223	LI:321069.2:2001MAY17	1095	1103	forward 1	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	1104	1123	forward 1	TM	Transmembrane
223	LI:321069.2:2001MAY17	1124	1129	forward 1	TM	Cytosolic
223	LI:321069.2:2001MAY17	1130	1152	forward 1	TM	Transmembrane
223	LI:321069.2:2001MAY17	1153	1344	forward 1	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	1	630	forward 2	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	631	653	forward 2	TM	Transmembrane
223	LI:321069.2:2001MAY17	654	665	forward 2	TM	Cytosolic
223	LI:321069.2:2001MAY17	666	688	forward 2	TM	Transmembrane
223	LI:321069.2:2001MAY17	689	702	forward 2	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	703	725	forward 2	TM	Transmembrane
223	LI:321069.2:2001MAY17	726	886	forward 2	TM	Cytosolic
223	LI:321069.2:2001MAY17	887	909	forward 2	TM	Transmembrane
223	LI:321069.2:2001MAY17	910	1343	forward 2	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	1	634	forward 3	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	635	653	forward 3	TM	Transmembrane
223	LI:321069.2:2001MAY17	654	664	forward 3	TM	Cytosolic
223	LI:321069.2:2001MAY17	665	687	forward 3	TM	Transmembrane
223	LI:321069.2:2001MAY17	688	806	forward 3	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	807	829	forward 3	TM	Transmembrane
223	LI:321069.2:2001MAY17	830	1078	forward 3	TM	Cytosolic
223	LI:321069.2:2001MAY17	1079	1101	forward 3	TM	Transmembrane
223	LI:321069.2:2001MAY17	1102	1127	forward 3	TM	Non-Cytosolic
223	LI:321069.2:2001MAY17	1128	1150	forward 3	TM	Transmembrane
223	LI:321069.2:2001MAY17	1151	1343	forward 3	TM	Cytosolic
224	LI:331499.8:2001MAY17	1	480	forward 1	TM	Non-Cytosolic
224	LI:331499.8:2001MAY17	481	503	forward 1	TM	Transmembrane
224	LI:331499.8:2001MAY17	504	564	forward 1	TM	Cytosolic
224	LI:331499.8:2001MAY17	565	584	forward 1	TM	Transmembrane
224	LI:331499.8:2001MAY17	585	593	forward 1	TM	Non-Cytosolic
224	LI:331499.8:2001MAY17	594	613	forward 1	TM	Transmembrane
224	LI:331499.8:2001MAY17	614	614	forward 1	TM	Cytosolic
224	LI:331499.8:2001MAY17	1	592	forward 3	TM	Non-Cytosolic
224	LI:331499.8:2001MAY17	593	612	forward 3	TM	Transmembrane
224	LI:331499.8:2001MAY17	613	613	forward 3	TM	Cytosolic
225	LI:332176.8:2001MAY17	1	124	forward 3	TM	Non-Cytosolic
225	LI:332176.8:2001MAY17	125	147	forward 3	TM	Transmembrane
225	LI:332176.8:2001MAY17	148	238	forward 3	TM	Cytosolic
225	LI:332176.8:2001MAY17	239	261	forward 3	TM	Transmembrane
225	LI:332176.8:2001MAY17	262	367	forward 3	TM	Non-Cytosolic
225	LI:332176.8:2001MAY17	368	390	forward 3	TM	Transmembrane
225	LI:332176.8:2001MAY17	391	457	forward 3	TM	Cytosolic
226	LI:333952.7:2001MAY17	1	68	forward 1	TM	Cytosolic
226	LI:333952.7:2001MAY17	69	91	forward 1	TM	Transmembrane
226	LI:333952.7:2001MAY17	92	105	forward 1	TM	Non-Cytosolic
226	LI:333952.7:2001MAY17	106	128	forward 1	TM	Transmembrane
226	LI:333952.7:2001MAY17	129	134	forward 1	TM	Cytosolic
226	LI:333952.7:2001MAY17	135	157	forward 1	TM	Transmembrane
226	LI:333952.7:2001MAY17	158	352	forward 1	TM	Non-Cytosolic
227	LI:338428.2:2001MAY17	1	71	forward 3	TM	Non-Cytosolic
227	LI:338428.2:2001MAY17	72	94	forward 3	TM	Transmembrane
227	LI:338428.2:2001MAY17	95	127	forward 3	TM	Cytosolic
228	LI:343869.2:2001MAY17	1	938	forward 1	TM	Non-Cytosolic
228	LI:343869.2:2001MAY17	939	961	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
228	LI:343869.2:2001MAY17	962	967	forward 1	TM	Cytosolic
228	LI:343869.2:2001MAY17	968	990	forward 1	TM	Transmembrane
228	LI:343869.2:2001MAY17	991	1154	forward 1	TM	Non-Cytosolic
228	LI:343869.2:2001MAY17	1155	1172	forward 1	TM	Transmembrane
228	LI:343869.2:2001MAY17	1173	1183	forward 1	TM	Cytosolic
228	LI:343869.2:2001MAY17	1184	1206	forward 1	TM	Transmembrane
228	LI:343869.2:2001MAY17	1207	1237	forward 1	TM	Non-Cytosolic
228	LI:343869.2:2001MAY17	1238	1260	forward 1	TM	Transmembrane
228	LI:343869.2:2001MAY17	1261	1334	forward 1	TM	Cytosolic
228	LI:343869.2:2001MAY17	1335	1354	forward 1	TM	Transmembrane
228	LI:343869.2:2001MAY17	1355	1363	forward 1	TM	Non-Cytosolic
228	LI:343869.2:2001MAY17	1364	1383	forward 1	TM	Transmembrane
228	LI:343869.2:2001MAY17	1384	1651	forward 1	TM	Cytosolic
228	LI:343869.2:2001MAY17	1	957	forward 3	TM	Non-Cytosolic
228	LI:343869.2:2001MAY17	958	980	forward 3	TM	Transmembrane
228	LI:343869.2:2001MAY17	981	1126	forward 3	TM	Cytosolic
228	LI:343869.2:2001MAY17	1127	1149	forward 3	TM	Transmembrane
228	LI:343869.2:2001MAY17	1150	1183	forward 3	TM	Non-Cytosolic
228	LI:343869.2:2001MAY17	1184	1206	forward 3	TM	Transmembrane
228	LI:343869.2:2001MAY17	1207	1236	forward 3	TM	Cytosolic
228	LI:343869.2:2001MAY17	1237	1259	forward 3	TM	Transmembrane
228	LI:343869.2:2001MAY17	1260	1650	forward 3	TM	Non-Cytosolic
229	LI:363532.1:2001MAY17	1	77	forward 3	TM	Non-Cytosolic
229	LI:363532.1:2001MAY17	78	95	forward 3	TM	Transmembrane
229	LI:363532.1:2001MAY17	96	189	forward 3	TM	Cytosolic
229	LI:363532.1:2001MAY17	190	209	forward 3	TM	Transmembrane
229	LI:363532.1:2001MAY17	210	234	forward 3	TM	Non-Cytosolic
229	LI:363532.1:2001MAY17	235	257	forward 3	TM	Transmembrane
229	LI:363532.1:2001MAY17	258	266	forward 3	TM	Cytosolic
230	LI:398153.37:2001MAY17	1	139	forward 2	TM	Cytosolic
230	LI:398153.37:2001MAY17	140	162	forward 2	TM	Transmembrane
230	LI:398153.37:2001MAY17	163	287	forward 2	TM	Non-Cytosolic
231	LI:416650.1:2001MAY17	1	26	forward 1	TM	Cytosolic
231	LI:416650.1:2001MAY17	27	49	forward 1	TM	Transmembrane
231	LI:416650.1:2001MAY17	50	231	forward 1	TM	Non-Cytosolic
231	LI:416650.1:2001MAY17	1	30	forward 3	TM	Cytosolic
231	LI:416650.1:2001MAY17	31	53	forward 3	TM	Transmembrane
231	LI:416650.1:2001MAY17	54	230	forward 3	TM	Non-Cytosolic
232	LI:444767.32:2001MAY17	1	24	forward 1	TM	Non-Cytosolic
232	LI:444767.32:2001MAY17	25	47	forward 1	TM	Transmembrane
232	LI:444767.32:2001MAY17	48	192	forward 1	TM	Cytosolic
232	LI:444767.32:2001MAY17	193	215	forward 1	TM	Transmembrane
232	LI:444767.32:2001MAY17	216	279	forward 1	TM	Non-Cytosolic
232	LI:444767.32:2001MAY17	280	302	forward 1	TM	Transmembrane
232	LI:444767.32:2001MAY17	303	440	forward 1	TM	Cytosolic
232	LI:444767.32:2001MAY17	441	463	forward 1	TM	Transmembrane
232	LI:444767.32:2001MAY17	464	596	forward 1	TM	Non-Cytosolic
232	LI:444767.32:2001MAY17	1	12	forward 2	TM	Cytosolic
232	LI:444767.32:2001MAY17	13	32	forward 2	TM	Transmembrane
232	LI:444767.32:2001MAY17	33	519	forward 2	TM	Non-Cytosolic
232	LI:444767.32:2001MAY17	520	542	forward 2	TM	Transmembrane
232	LI:444767.32:2001MAY17	543	595	forward 2	TM	Cytosolic
232	LI:444767.32:2001MAY17	1	12	forward 3	TM	Cytosolic
232	LI:444767.32:2001MAY17	13	35	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
232	LI:444767.32:2001MAY17	36	595	forward 3	TM	Non-Cytosolic
233	LI:759073.1:2001MAY17	1	9	forward 1	TM	Non-Cytosolic
233	LI:759073.1:2001MAY17	10	32	forward 1	TM	Transmembrane
233	LI:759073.1:2001MAY17	33	210	forward 1	TM	Cytosolic
233	LI:759073.1:2001MAY17	211	233	forward 1	TM	Transmembrane
233	LI:759073.1:2001MAY17	234	252	forward 1	TM	Non-Cytosolic
233	LI:759073.1:2001MAY17	253	270	forward 1	TM	Transmembrane
233	LI:759073.1:2001MAY17	271	441	forward 1	TM	Cytosolic
233	LI:759073.1:2001MAY17	442	464	forward 1	TM	Transmembrane
233	LI:759073.1:2001MAY17	465	574	forward 1	TM	Non-Cytosolic
233	LI:759073.1:2001MAY17	1	83	forward 2	TM	Cytosolic
233	LI:759073.1:2001MAY17	84	106	forward 2	TM	Transmembrane
233	LI:759073.1:2001MAY17	107	129	forward 2	TM	Non-Cytosolic
233	LI:759073.1:2001MAY17	130	152	forward 2	TM	Transmembrane
233	LI:759073.1:2001MAY17	153	156	forward 2	TM	Cytosolic
233	LI:759073.1:2001MAY17	157	179	forward 2	TM	Transmembrane
233	LI:759073.1:2001MAY17	180	393	forward 2	TM	Non-Cytosolic
233	LI:759073.1:2001MAY17	394	416	forward 2	TM	Transmembrane
233	LI:759073.1:2001MAY17	417	427	forward 2	TM	Cytosolic
233	LI:759073.1:2001MAY17	428	450	forward 2	TM	Transmembrane
233	LI:759073.1:2001MAY17	451	574	forward 2	TM	Non-Cytosolic
233	LI:759073.1:2001MAY17	1	79	forward 3	TM	Cytosolic
233	LI:759073.1:2001MAY17	80	102	forward 3	TM	Transmembrane
233	LI:759073.1:2001MAY17	103	116	forward 3	TM	Non-Cytosolic
233	LI:759073.1:2001MAY17	117	139	forward 3	TM	Transmembrane
233	LI:759073.1:2001MAY17	140	150	forward 3	TM	Cytosolic
233	LI:759073.1:2001MAY17	151	170	forward 3	TM	Transmembrane
233	LI:759073.1:2001MAY17	171	573	forward 3	TM	Non-Cytosolic
234	LI:759902.4:2001MAY17	1	3	forward 1	TM	Non-Cytosolic
234	LI:759902.4:2001MAY17	4	26	forward 1	TM	Transmembrane
234	LI:759902.4:2001MAY17	27	100	forward 1	TM	Cytosolic
235	LI:762268.1:2001MAY17	1	49	forward 1	TM	Cytosolic
235	LI:762268.1:2001MAY17	50	72	forward 1	TM	Transmembrane
235	LI:762268.1:2001MAY17	73	86	forward 1	TM	Non-Cytosolic
235	LI:762268.1:2001MAY17	87	109	forward 1	TM	Transmembrane
235	LI:762268.1:2001MAY17	110	136	forward 1	TM	Cytosolic
235	LI:762268.1:2001MAY17	137	159	forward 1	TM	Transmembrane
235	LI:762268.1:2001MAY17	160	594	forward 1	TM	Non-Cytosolic
235	LI:762268.1:2001MAY17	1	16	forward 2	TM	Cytosolic
235	LI:762268.1:2001MAY17	17	39	forward 2	TM	Transmembrane
235	LI:762268.1:2001MAY17	40	48	forward 2	TM	Non-Cytosolic
235	LI:762268.1:2001MAY17	49	71	forward 2	TM	Transmembrane
235	LI:762268.1:2001MAY17	72	91	forward 2	TM	Cytosolic
235	LI:762268.1:2001MAY17	92	111	forward 2	TM	Transmembrane
235	LI:762268.1:2001MAY17	112	125	forward 2	TM	Non-Cytosolic
235	LI:762268.1:2001MAY17	126	148	forward 2	TM	Transmembrane
235	LI:762268.1:2001MAY17	149	167	forward 2	TM	Cytosolic
235	LI:762268.1:2001MAY17	168	190	forward 2	TM	Transmembrane
235	LI:762268.1:2001MAY17	191	593	forward 2	TM	Non-Cytosolic
235	LI:762268.1:2001MAY17	1	45	forward 3	TM	Non-Cytosolic
235	LI:762268.1:2001MAY17	46	68	forward 3	TM	Transmembrane
235	LI:762268.1:2001MAY17	69	79	forward 3	TM	Cytosolic
235	LI:762268.1:2001MAY17	80	102	forward 3	TM	Transmembrane
235	LI:762268.1:2001MAY17	103	593	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
236	LI:813699.1:2001MAY17	1	394	forward 2	TM	Cytosolic
236	LI:813699.1:2001MAY17	395	417	forward 2	TM	Transmembrane
236	LI:813699.1:2001MAY17	418	457	forward 2	TM	Non-Cytosolic
237	LI:024142.16:2001MAY17	1	49	forward 1	TM	Non-Cytosolic
237	LI:024142.16:2001MAY17	50	72	forward 1	TM	Transmembrane
237	LI:024142.16:2001MAY17	73	311	forward 1	TM	Cytosolic
237	LI:024142.16:2001MAY17	312	334	forward 1	TM	Transmembrane
237	LI:024142.16:2001MAY17	335	348	forward 1	TM	Non-Cytosolic
237	LI:024142.16:2001MAY17	349	371	forward 1	TM	Transmembrane
237	LI:024142.16:2001MAY17	372	377	forward 1	TM	Cytosolic
237	LI:024142.16:2001MAY17	378	400	forward 1	TM	Transmembrane
237	LI:024142.16:2001MAY17	401	1142	forward 1	TM	Non-Cytosolic
237	LI:024142.16:2001MAY17	1	279	forward 2	TM	Cytosolic
237	LI:024142.16:2001MAY17	280	299	forward 2	TM	Transmembrane
237	LI:024142.16:2001MAY17	300	313	forward 2	TM	Non-Cytosolic
237	LI:024142.16:2001MAY17	314	348	forward 2	TM	Transmembrane
237	LI:024142.16:2001MAY17	349	360	forward 2	TM	Cytosolic
237	LI:024142.16:2001MAY17	361	383	forward 2	TM	Transmembrane
237	LI:024142.16:2001MAY17	384	397	forward 2	TM	Non-Cytosolic
237	LI:024142.16:2001MAY17	398	420	forward 2	TM	Transmembrane
237	LI:024142.16:2001MAY17	421	536	forward 2	TM	Cytosolic
237	LI:024142.16:2001MAY17	537	559	forward 2	TM	Transmembrane
237	LI:024142.16:2001MAY17	560	586	forward 2	TM	Non-Cytosolic
237	LI:024142.16:2001MAY17	587	609	forward 2	TM	Transmembrane
237	LI:024142.16:2001MAY17	610	636	forward 2	TM	Cytosolic
237	LI:024142.16:2001MAY17	637	659	forward 2	TM	Transmembrane
237	LI:024142.16:2001MAY17	660	1141	forward 2	TM	Non-Cytosolic
237	LI:024142.16:2001MAY17	1	323	forward 3	TM	Non-Cytosolic
237	LI:024142.16:2001MAY17	324	346	forward 3	TM	Transmembrane
237	LI:024142.16:2001MAY17	347	352	forward 3	TM	Cytosolic
237	LI:024142.16:2001MAY17	353	375	forward 3	TM	Transmembrane
237	LI:024142.16:2001MAY17	376	394	forward 3	TM	Non-Cytosolic
237	LI:024142.16:2001MAY17	395	414	forward 3	TM	Transmembrane
237	LI:024142.16:2001MAY17	415	570	forward 3	TM	Cytosolic
237	LI:024142.16:2001MAY17	571	593	forward 3	TM	Transmembrane
237	LI:024142.16:2001MAY17	594	1141	forward 3	TM	Non-Cytosolic
238	LI:1018424.4:2001MAY17	1	1194	forward 2	TM	Non-Cytosolic
238	LI:1018424.4:2001MAY17	1195	1217	forward 2	TM	Transmembrane
238	LI:1018424.4:2001MAY17	1218	1327	forward 2	TM	Cytosolic
239	LI:1085250.6:2001MAY17	1	840	forward 1	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	841	863	forward 1	TM	Transmembrane
239	LI:1085250.6:2001MAY17	864	929	forward 1	TM	Cytosolic
239	LI:1085250.6:2001MAY17	930	952	forward 1	TM	Transmembrane
239	LI:1085250.6:2001MAY17	953	955	forward 1	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	956	978	forward 1	TM	Transmembrane
239	LI:1085250.6:2001MAY17	979	990	forward 1	TM	Cytosolic
239	LI:1085250.6:2001MAY17	991	1013	forward 1	TM	Transmembrane
239	LI:1085250.6:2001MAY17	1014	1327	forward 1	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	1328	1350	forward 1	TM	Transmembrane
239	LI:1085250.6:2001MAY17	1351	1369	forward 1	TM	Cytosolic
239	LI:1085250.6:2001MAY17	1	59	forward 2	TM	Cytosolic
239	LI:1085250.6:2001MAY17	60	82	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	83	515	forward 2	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	516	538	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
239	LI:1085250.6:2001MAY17	539	558	forward 2	TM	Cytosolic
239	LI:1085250.6:2001MAY17	559	578	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	579	597	forward 2	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	598	620	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	621	803	forward 2	TM	Cytosolic
239	LI:1085250.6:2001MAY17	804	826	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	827	835	forward 2	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	836	858	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	859	878	forward 2	TM	Cytosolic
239	LI:1085250.6:2001MAY17	879	901	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	902	910	forward 2	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	911	933	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	934	986	forward 2	TM	Cytosolic
239	LI:1085250.6:2001MAY17	987	1009	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	1010	1211	forward 2	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	1212	1234	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	1235	1306	forward 2	TM	Cytosolic
239	LI:1085250.6:2001MAY17	1307	1329	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	1330	1338	forward 2	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	1339	1361	forward 2	TM	Transmembrane
239	LI:1085250.6:2001MAY17	1362	1368	forward 2	TM	Cytosolic
239	LI:1085250.6:2001MAY17	1	546	forward 3	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	547	569	forward 3	TM	Transmembrane
239	LI:1085250.6:2001MAY17	570	589	forward 3	TM	Cytosolic
239	LI:1085250.6:2001MAY17	590	612	forward 3	TM	Transmembrane
239	LI:1085250.6:2001MAY17	613	911	forward 3	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	912	931	forward 3	TM	Transmembrane
239	LI:1085250.6:2001MAY17	932	1203	forward 3	TM	Cytosolic
239	LI:1085250.6:2001MAY17	1204	1226	forward 3	TM	Transmembrane
239	LI:1085250.6:2001MAY17	1227	1240	forward 3	TM	Non-Cytosolic
239	LI:1085250.6:2001MAY17	1241	1260	forward 3	TM	Transmembrane
239	LI:1085250.6:2001MAY17	1261	1319	forward 3	TM	Cytosolic
239	LI:1085250.6:2001MAY17	1320	1342	forward 3	TM	Transmembrane
239	LI:1085250.6:2001MAY17	1343	1368	forward 3	TM	Non-Cytosolic
240	LI:179233.63:2001MAY17	1	173	forward 1	TM	Cytosolic
240	LI:179233.63:2001MAY17	174	196	forward 1	TM	Transmembrane
240	LI:179233.63:2001MAY17	197	210	forward 1	TM	Non-Cytosolic
240	LI:179233.63:2001MAY17	211	233	forward 1	TM	Transmembrane
240	LI:179233.63:2001MAY17	234	347	forward 1	TM	Cytosolic
241	LI:2207125.3:2001MAY17	1	12	forward 1	TM	Cytosolic
241	LI:2207125.3:2001MAY17	13	35	forward 1	TM	Transmembrane
241	LI:2207125.3:2001MAY17	36	204	forward 1	TM	Non-Cytosolic
242	LI:235153.44:2001MAY17	1	753	forward 2	TM	Non-Cytosolic
242	LI:235153.44:2001MAY17	754	776	forward 2	TM	Transmembrane
242	LI:235153.44:2001MAY17	777	1029	forward 2	TM	Cytosolic
243	LI:007101.10:2001MAY17	1	528	forward 3	TM	Non-Cytosolic
243	LI:007101.10:2001MAY17	529	551	forward 3	TM	Transmembrane
243	LI:007101.10:2001MAY17	552	694	forward 3	TM	Cytosolic
244	LI:008541.2:2001MAY17	1	79	forward 2	TM	Cytosolic
244	LI:008541.2:2001MAY17	80	102	forward 2	TM	Transmembrane
244	LI:008541.2:2001MAY17	103	568	forward 2	TM	Non-Cytosolic
245	LI:009658.13:2001MAY17	1	74	forward 1	TM	Cytosolic
245	LI:009658.13:2001MAY17	75	94	forward 1	TM	Transmembrane
245	LI:009658.13:2001MAY17	95	1317	forward 1	TM	Non-Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
245	LI:009658.13:2001MAY17	1318	1340	forward 1	TM	Transmembrane
245	LI:009658.13:2001MAY17	1341	1362	forward 1	TM	Cytosolic
245	LI:009658.13:2001MAY17	1363	1385	forward 1	TM	Transmembrane
245	LI:009658.13:2001MAY17	1386	1423	forward 1	TM	Non-Cytosolic
245	LI:009658.13:2001MAY17	1	927	forward 2	TM	Non-Cytosolic
245	LI:009658.13:2001MAY17	928	950	forward 2	TM	Transmembrane
245	LI:009658.13:2001MAY17	951	956	forward 2	TM	Cytosolic
245	LI:009658.13:2001MAY17	957	979	forward 2	TM	Transmembrane
245	LI:009658.13:2001MAY17	980	1321	forward 2	TM	Non-Cytosolic
245	LI:009658.13:2001MAY17	1322	1344	forward 2	TM	Transmembrane
245	LI:009658.13:2001MAY17	1345	1364	forward 2	TM	Cytosolic
245	LI:009658.13:2001MAY17	1365	1387	forward 2	TM	Transmembrane
245	LI:009658.13:2001MAY17	1388	1423	forward 2	TM	Non-Cytosolic
245	LI:009658.13:2001MAY17	1	706	forward 3	TM	Non-Cytosolic
245	LI:009658.13:2001MAY17	707	729	forward 3	TM	Transmembrane
245	LI:009658.13:2001MAY17	730	749	forward 3	TM	Cytosolic
245	LI:009658.13:2001MAY17	750	772	forward 3	TM	Transmembrane
245	LI:009658.13:2001MAY17	773	791	forward 3	TM	Non-Cytosolic
245	LI:009658.13:2001MAY17	792	811	forward 3	TM	Transmembrane
245	LI:009658.13:2001MAY17	812	934	forward 3	TM	Cytosolic
245	LI:009658.13:2001MAY17	935	957	forward 3	TM	Transmembrane
245	LI:009658.13:2001MAY17	958	971	forward 3	TM	Non-Cytosolic
245	LI:009658.13:2001MAY17	972	994	forward 3	TM	Transmembrane
245	LI:009658.13:2001MAY17	995	1319	forward 3	TM	Cytosolic
245	LI:009658.13:2001MAY17	1320	1342	forward 3	TM	Transmembrane
245	LI:009658.13:2001MAY17	1343	1356	forward 3	TM	Non-Cytosolic
245	LI:009658.13:2001MAY17	1357	1379	forward 3	TM	Transmembrane
245	LI:009658.13:2001MAY17	1380	1422	forward 3	TM	Cytosolic
246	LI:020012.14:2001MAY17	1	423	forward 1	TM	Cytosolic
246	LI:020012.14:2001MAY17	424	446	forward 1	TM	Transmembrane
246	LI:020012.14:2001MAY17	447	449	forward 1	TM	Non-Cytosolic
246	LI:020012.14:2001MAY17	450	469	forward 1	TM	Transmembrane
246	LI:020012.14:2001MAY17	470	884	forward 1	TM	Cytosolic
246	LI:020012.14:2001MAY17	885	907	forward 1	TM	Transmembrane
246	LI:020012.14:2001MAY17	908	955	forward 1	TM	Non-Cytosolic
246	LI:020012.14:2001MAY17	956	978	forward 1	TM	Transmembrane
246	LI:020012.14:2001MAY17	979	1013	forward 1	TM	Cytosolic
246	LI:020012.14:2001MAY17	1	582	forward 2	TM	Non-Cytosolic
246	LI:020012.14:2001MAY17	583	602	forward 2	TM	Transmembrane
246	LI:020012.14:2001MAY17	603	614	forward 2	TM	Cytosolic
246	LI:020012.14:2001MAY17	615	637	forward 2	TM	Transmembrane
246	LI:020012.14:2001MAY17	638	695	forward 2	TM	Non-Cytosolic
246	LI:020012.14:2001MAY17	696	718	forward 2	TM	Transmembrane
246	LI:020012.14:2001MAY17	719	724	forward 2	TM	Cytosolic
246	LI:020012.14:2001MAY17	725	747	forward 2	TM	Transmembrane
246	LI:020012.14:2001MAY17	748	761	forward 2	TM	Non-Cytosolic
246	LI:020012.14:2001MAY17	762	781	forward 2	TM	Transmembrane
246	LI:020012.14:2001MAY17	782	953	forward 2	TM	Cytosolic
246	LI:020012.14:2001MAY17	954	976	forward 2	TM	Transmembrane
246	LI:020012.14:2001MAY17	977	1012	forward 2	TM	Non-Cytosolic
246	LI:020012.14:2001MAY17	1	725	forward 3	TM	Non-Cytosolic
246	LI:020012.14:2001MAY17	726	748	forward 3	TM	Transmembrane
246	LI:020012.14:2001MAY17	749	760	forward 3	TM	Cytosolic
246	LI:020012.14:2001MAY17	761	780	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
246	LI:020012.14:2001MAY17	781	814	forward 3	TM	Non-Cytosolic
246	LI:020012.14:2001MAY17	815	837	forward 3	TM	Transmembrane
246	LI:020012.14:2001MAY17	838	849	forward 3	TM	Cytosolic
246	LI:020012.14:2001MAY17	850	869	forward 3	TM	Transmembrane
246	LI:020012.14:2001MAY17	870	883	forward 3	TM	Non-Cytosolic
246	LI:020012.14:2001MAY17	884	906	forward 3	TM	Transmembrane
246	LI:020012.14:2001MAY17	907	926	forward 3	TM	Cytosolic
246	LI:020012.14:2001MAY17	927	946	forward 3	TM	Transmembrane
246	LI:020012.14:2001MAY17	947	955	forward 3	TM	Non-Cytosolic
246	LI:020012.14:2001MAY17	956	978	forward 3	TM	Transmembrane
246	LI:020012.14:2001MAY17	979	1012	forward 3	TM	Cytosolic
247	LI:020691.1:2001MAY17	1	19	forward 1	TM	Cytosolic
247	LI:020691.1:2001MAY17	20	42	forward 1	TM	Transmembrane
247	LI:020691.1:2001MAY17	43	255	forward 1	TM	Non-Cytosolic
247	LI:020691.1:2001MAY17	1	12	forward 2	TM	Cytosolic
247	LI:020691.1:2001MAY17	13	35	forward 2	TM	Transmembrane
247	LI:020691.1:2001MAY17	36	255	forward 2	TM	Non-Cytosolic
248	LI:021188.12:2001MAY17	1	171	forward 3	TM	Non-Cytosolic
248	LI:021188.12:2001MAY17	172	194	forward 3	TM	Transmembrane
248	LI:021188.12:2001MAY17	195	377	forward 3	TM	Cytosolic
249	LI:021324.4:2001MAY17	1	53	forward 1	TM	Cytosolic
249	LI:021324.4:2001MAY17	54	76	forward 1	TM	Transmembrane
249	LI:021324.4:2001MAY17	77	90	forward 1	TM	Non-Cytosolic
249	LI:021324.4:2001MAY17	91	113	forward 1	TM	Transmembrane
249	LI:021324.4:2001MAY17	114	227	forward 1	TM	Cytosolic
249	LI:021324.4:2001MAY17	228	250	forward 1	TM	Transmembrane
249	LI:021324.4:2001MAY17	251	710	forward 1	TM	Non-Cytosolic
250	LI:021834.15:2001MAY17	1	552	forward 2	TM	Non-Cytosolic
250	LI:021834.15:2001MAY17	553	575	forward 2	TM	Transmembrane
250	LI:021834.15:2001MAY17	576	595	forward 2	TM	Cytosolic
250	LI:021834.15:2001MAY17	596	618	forward 2	TM	Transmembrane
250	LI:021834.15:2001MAY17	619	771	forward 2	TM	Non-Cytosolic
251	LI:024841.1:2001MAY17	1	752	forward 1	TM	Non-Cytosolic
251	LI:024841.1:2001MAY17	753	775	forward 1	TM	Transmembrane
251	LI:024841.1:2001MAY17	776	1017	forward 1	TM	Cytosolic
251	LI:024841.1:2001MAY17	1018	1040	forward 1	TM	Transmembrane
251	LI:024841.1:2001MAY17	1041	1054	forward 1	TM	Non-Cytosolic
251	LI:024841.1:2001MAY17	1055	1077	forward 1	TM	Transmembrane
251	LI:024841.1:2001MAY17	1078	1129	forward 1	TM	Cytosolic
251	LI:024841.1:2001MAY17	1	748	forward 2	TM	Non-Cytosolic
251	LI:024841.1:2001MAY17	749	771	forward 2	TM	Transmembrane
251	LI:024841.1:2001MAY17	772	1015	forward 2	TM	Cytosolic
251	LI:024841.1:2001MAY17	1016	1038	forward 2	TM	Transmembrane
251	LI:024841.1:2001MAY17	1039	1128	forward 2	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	1	446	forward 1	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	447	469	forward 1	TM	Transmembrane
252	LI:025724.12:2001MAY17	470	685	forward 1	TM	Cytosolic
252	LI:025724.12:2001MAY17	686	703	forward 1	TM	Transmembrane
252	LI:025724.12:2001MAY17	704	730	forward 1	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	731	753	forward 1	TM	Transmembrane
252	LI:025724.12:2001MAY17	754	895	forward 1	TM	Cytosolic
252	LI:025724.12:2001MAY17	896	918	forward 1	TM	Transmembrane
252	LI:025724.12:2001MAY17	919	984	forward 1	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	985	1007	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
252	LI:025724.12:2001MAY17	1008	1018	forward 1	TM	Cytosolic
252	LI:025724.12:2001MAY17	1019	1041	forward 1	TM	Transmembrane
252	LI:025724.12:2001MAY17	1042	1074	forward 1	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	1075	1097	forward 1	TM	Transmembrane
252	LI:025724.12:2001MAY17	1098	1201	forward 1	TM	Cytosolic
252	LI:025724.12:2001MAY17	1	457	forward 2	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	458	480	forward 2	TM	Transmembrane
252	LI:025724.12:2001MAY17	481	695	forward 2	TM	Cytosolic
252	LI:025724.12:2001MAY17	696	718	forward 2	TM	Transmembrane
252	LI:025724.12:2001MAY17	719	732	forward 2	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	733	755	forward 2	TM	Transmembrane
252	LI:025724.12:2001MAY17	756	777	forward 2	TM	Cytosolic
252	LI:025724.12:2001MAY17	778	797	forward 2	TM	Transmembrane
252	LI:025724.12:2001MAY17	798	806	forward 2	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	807	829	forward 2	TM	Transmembrane
252	LI:025724.12:2001MAY17	830	921	forward 2	TM	Cytosolic
252	LI:025724.12:2001MAY17	922	939	forward 2	TM	Transmembrane
252	LI:025724.12:2001MAY17	940	1018	forward 2	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	1019	1041	forward 2	TM	Transmembrane
252	LI:025724.12:2001MAY17	1042	1133	forward 2	TM	Cytosolic
252	LI:025724.12:2001MAY17	1134	1156	forward 2	TM	Transmembrane
252	LI:025724.12:2001MAY17	1157	1165	forward 2	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	1166	1185	forward 2	TM	Transmembrane
252	LI:025724.12:2001MAY17	1186	1201	forward 2	TM	Cytosolic
252	LI:025724.12:2001MAY17	1	729	forward 3	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	730	752	forward 3	TM	Transmembrane
252	LI:025724.12:2001MAY17	753	764	forward 3	TM	Cytosolic
252	LI:025724.12:2001MAY17	765	787	forward 3	TM	Transmembrane
252	LI:025724.12:2001MAY17	788	806	forward 3	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	807	829	forward 3	TM	Transmembrane
252	LI:025724.12:2001MAY17	830	873	forward 3	TM	Cytosolic
252	LI:025724.12:2001MAY17	874	896	forward 3	TM	Transmembrane
252	LI:025724.12:2001MAY17	897	910	forward 3	TM	Non-Cytosolic
252	LI:025724.12:2001MAY17	911	933	forward 3	TM	Transmembrane
252	LI:025724.12:2001MAY17	934	1042	forward 3	TM	Cytosolic
252	LI:025724.12:2001MAY17	1043	1065	forward 3	TM	Transmembrane
252	LI:025724.12:2001MAY17	1066	1200	forward 3	TM	Non-Cytosolic
253	LI:029328.2:2001MAY17	1	714	forward 1	TM	Non-Cytosolic
253	LI:029328.2:2001MAY17	715	737	forward 1	TM	Transmembrane
253	LI:029328.2:2001MAY17	738	1025	forward 1	TM	Cytosolic
253	LI:029328.2:2001MAY17	1026	1043	forward 1	TM	Transmembrane
253	LI:029328.2:2001MAY17	1044	1052	forward 1	TM	Non-Cytosolic
253	LI:029328.2:2001MAY17	1053	1075	forward 1	TM	Transmembrane
253	LI:029328.2:2001MAY17	1076	1179	forward 1	TM	Cytosolic
253	LI:029328.2:2001MAY17	1180	1202	forward 1	TM	Transmembrane
253	LI:029328.2:2001MAY17	1203	1283	forward 1	TM	Non-Cytosolic
253	LI:029328.2:2001MAY17	1284	1306	forward 1	TM	Transmembrane
253	LI:029328.2:2001MAY17	1307	1312	forward 1	TM	Cytosolic
253	LI:029328.2:2001MAY17	1313	1335	forward 1	TM	Transmembrane
253	LI:029328.2:2001MAY17	1336	2000	forward 1	TM	Non-Cytosolic
253	LI:029328.2:2001MAY17	1	301	forward 3	TM	Non-Cytosolic
253	LI:029328.2:2001MAY17	302	324	forward 3	TM	Transmembrane
253	LI:029328.2:2001MAY17	325	365	forward 3	TM	Cytosolic
253	LI:029328.2:2001MAY17	366	384	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
253	LI:029328.2:2001MAY17	385	1947	forward 3	TM	Non-Cytosolic
253	LI:029328.2:2001MAY17	1948	1970	forward 3	TM	Transmembrane
253	LI:029328.2:2001MAY17	1971	1999	forward 3	TM	Cytosolic
254	LI:032171.5:2001MAY17	1	459	forward 1	TM	Non-Cytosolic
254	LI:032171.5:2001MAY17	460	477	forward'I	TM	Transmembrane
254	LI:032171.5:2001MAY17	478	481	forward 1	TM	Cytosolic
254	LI:032171.5:2001MAY17	482	504	forward 1	TM	Transmembrane
254	LI:032171.5:2001MAY17	505	518	forward 1	TM	Non-Cytosolic
254	LI:032171.5:2001MAY17	519	541	forward 1	TM	Transmembrane
254	LI:032171.5:2001MAY17	542	553	forward 1	TM	Cytosolic
254	LI:032171.5:2001MAY17	554	576	forward 1	TM	Transmembrane
254	LI:032171.5:2001MAY17	577	626	forward 1	TM	Non-Cytosolic
254	LI:032171.5:2001MAY17	627	649	forward 1	TM	Transmembrane
254	LI:032171.5:2001MAY17	650	716	forward 1	TM	Cytosolic
254	LI:032171.5:2001MAY17	1	625	forward 2	TM	Non-Cytosolic
254	LI:032171.5:2001MAY17	626	648	forward 2	TM	Transmembrane
254	LI:032171.5:2001MAY17	649	660	forward 2	TM	Cytosolic
254	LI:032171.5:2001MAY17	661	683	forward 2	TM	Transmembrane
254	LI:032171.5:2001MAY17	684	686	forward 2	TM	Non-Cytosolic
254	LI:032171.5:2001MAY17	687	709	forward 2	TM	Transmembrane
254	LI:032171.5:2001MAY17	710	715	forward 2	TM	Cytosolic
255	LI:035055.1:2001MAY17	1	489	forward 2	TM	Non-Cytosolic
255	LI:035055.1:2001MAY17	490	512	forward 2	TM	Transmembrane
255	LI:035055.1:2001MAY17	513	584	forward 2	TM.	Cytosolic
255	LI:035055.1:2001MAY17	585	607	forward 2	TM	Transmembrane
255	LI:035055.1:2001MAY17	608	619	forward 2	TM	Non-Cytosolic
255	LI:035055.1:2001MAY17	620	642	forward 2	TM	Transmembrane
255	LI:035055.1:2001MAY17	643	673	forward 2	TM	Cytosolic
255	LI:035055.1:2001MAY17	1	619	forward 3	TM	Non-Cytosolic
255	LI:035055.1:2001MAY17	620	642	forward 3	TM	Transmembrane
255	LI:035055.1:2001MAY17	643	673	forward 3	TM	Cytosolic
256	LI:036747.17:2001MAY17	1	269	forward 1	TM	Cytosolic
256	LI:036747.17:2001MAY17	270	292	forward 1	TM	Transmembrane
256	LI:036747.17:2001MAY17	293	325	forward 1	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	326	348	forward 1	TM	Transmembrane
256	LI:036747.17:2001MAY17	349	427	forward 1	TM	Cytosolic
256	LI:036747.17:2001MAY17	428	450	forward 1	TM	Transmembrane
256	LI:036747.17:2001MAY17	451	464	forward 1	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	465	487	forward 1	TM	Transmembrane
256	LI:036747.17:2001MAY17	488	499	forward 1	TM	Cytosolic
256	LI:036747.17:2001MAY17	500	522	forward 1	TM	Transmembrane
256	LI:036747.17:2001MAY17	523	630	forward 1	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	631	653	forward 1	TM	Transmembrane
256	LI:036747.17:2001MAY17	654	665	forward 1	TM	Cytosolic
256	LI:036747.17:2001MAY17	666	687	forward 1	TM	Transmembrane
256	LI:036747.17:2001MAY17	688	762	forward 1	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	763	785	forward 1	TM	Transmembrane
256	LI:036747.17:2001MAY17	786	818	forward 1	TM	Cytosolic
256	LI:036747.17:2001MAY17	1	269	forward 2	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	270	292	forward 2	TM	Transmembrane
256	LI:036747.17:2001MAY17	293	478	forward 2	TM	Cytosolic
256	LI:036747.17:2001MAY17	479	501	forward 2	TM	Transmembrane
256	LI:036747.17:2001MAY17	502	515	forward 2	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	516	535	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
256	LI:036747.17:2001MAY17	536	624	forward 2	TM	Cytosolic
256	LI:036747.17:2001MAY17	625	647	forward 2	TM	Transmembrane
256	LI:036747.17:2001MAY17	648	666	forward 2	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	667	689	forward 2	TM	Transmembrane
256	LI:036747.17:2001MAY17	690	709	forward 2	TM	Cytosolic
256	LI:036747.17:2001MAY17	710	732	forward 2	TM	Transmembrane
256	LI:036747.17:2001MAY17	733	751	forward 2	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	752	774	forward 2	TM	Transmembrane
256	LI:036747.17:2001MAY17	775	785	forward 2	TM	Cytosolic
256	LI:036747.17:2001MAY17	786	808	forward 2	TM	Transmembrane
256	LI:036747.17:2001MAY17	809	817	forward 2	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	1	269	forward 3	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	270	292	forward 3	TM	Transmembrane
256	LI:036747.17:2001MAY17	293	399	forward 3	TM	Cytosolic
256	LI:036747.17:2001MAY17	400	422	forward 3	TM	Transmembrane
256	LI:036747.17:2001MAY17	423	499	forward 3	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	500	522	forward 3	TM	Transmembrane
256	LI:036747.17:2001MAY17	523	624	forward 3	TM	Cytosolic
256	LI:036747.17:2001MAY17	625	642	forward 3	TM	Transmembrane
256	LI:036747.17:2001MAY17	643	677	forward 3	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	678	697	forward 3	TM	Transmembrane
256	LI:036747.17:2001MAY17	698	709	forward 3	TM	Cytosolic
256	LI:036747.17:2001MAY17	710	732	forward 3	TM	Transmembrane
256	LI:036747.17:2001MAY17	733	751	forward 3	TM	Non-Cytosolic
256	LI:036747.17:2001MAY17	752	774	forward 3	TM	Transmembrane
256	LI:036747.17:2001MAY17	775	780	forward 3	TM	Cytosolic
256	LI:036747.17:2001MAY17	781	803	forward 3	TM	Transmembrane
256	LI:036747.17:2001MAY17	804	817	forward 3	TM	Non-Cytosolic
257	LI:044301.2:2001MAY17	1	965	forward 1	TM	Non-Cytosolic
257	LI:044301.2:2001MAY17	966	988	forward 1	TM	Transmembrane
257	LI:044301.2:2001MAY17	989	1000	forward 1	TM	Cytosolic
258	LI:061585.10:2001MAY17	1	672	forward 1	TM	Non-Cytosolic
258	LI:061585.10:2001MAY17	673	695	forward 1	TM	Transmembrane
258	LI:061585.10:2001MAY17	696	823	forward 1	TM	Cytosolic
258	LI:061585.10:2001MAY17	1	425	forward 2	TM	Non-Cytosolic
258	LI:061585.10:2001MAY17	426	445	forward 2	TM	Transmembrane
258	LI:061585.10:2001MAY17	446	451	forward 2	TM	Cytosolic
258	LI:061585.10:2001MAY17	452	471	forward 2	TM	Transmembrane
258	LI:061585.10:2001MAY17	472	680	forward 2	TM	Non-Cytosolic
258	LI:061585.10:2001MAY17	681	700	forward 2	TM	Transmembrane
258	LI:061585.10:2001MAY17	701	739	forward 2	TM	Cytosolic
258	LI:061585.10:2001MAY17	740	762	forward 2	TM	Transmembrane
258	LI:061585.10:2001MAY17	763	823	forward 2	TM	Non-Cytosolic
258	LI:061585.10:2001MAY17	1	202	forward 3	TM	Cytosolic
258	LI:061585.10:2001MAY17	203	225	forward 3	TM	Transmembrane
258	LI:061585.10:2001MAY17	226	250	forward 3	TM	Non-Cytosolic
258	LI:061585.10:2001MAY17	251	273	forward 3	TM	Transmembrane
258	LI:061585.10:2001MAY17	274	277	forward 3	TM	Cytosolic
258	LI:061585.10:2001MAY17	278	300	forward 3	TM	Transmembrane
258	LI:061585.10:2001MAY17	301	342	forward 3	TM	Non-Cytosolic
258	LI:061585.10:2001MAY17	343	365	forward 3	TM	Transmembrane
258	LI:061585.10:2001MAY17	366	371	forward 3	TM	Cytosolic
258	LI:061585.10:2001MAY17	372	394	forward 3	TM	Transmembrane
258	LI:061585.10:2001MAY17	395	822	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
259	LI:066742.21:2001MAY17	1	63	forward 1	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	64	86	forward 1	TM	Transmembrane
259	LI:066742.21:2001MAY17	87	318	forward 1	TM	Cytosolic
259	LI:066742.21:2001MAY17	319	341	forward 1	TM	Transmembrane
259	LI:066742.21:2001MAY17	342	355	forward 1	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	356	378	forward 1	TM	Transmembrane
259	LI:066742.21:2001MAY17	379	430	forward 1	TM	Cytosolic
259	LI:066742.21:2001MAY17	431	450	forward 1	TM	Transmembrane
259	LI:066742.21:2001MAY17	451	1022	forward 1	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	1023	1045	forward 1	TM	Transmembrane
259	LI:066742.21:2001MAY17	1046	1068	forward 1	TM	Cytosolic
259	LI:066742.21:2001MAY17	1069	1091	forward 1	TM	Transmembrane
259	LI:066742.21:2001MAY17	1092	1408	forward 1	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	1409	1431	forward 1	TM	Transmembrane
259	LI:066742.21:2001MAY17	1432	1437	forward 1	TM	Cytosolic
259	LI:066742.21:2001MAY17	1438	1460	forward 1	TM	Transmembrane
259	LI:066742.21:2001MAY17	1461	1508	forward 1	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	1509	1531	forward 1	TM	Transmembrane
259	LI:066742.21:2001MAY17	1532	1542	forward 1	TM	Cytosolic
259	LI:066742.21:2001MAY17	1543	1562	forward 1	TM	Transmembrane
259	LI:066742.21:2001MAY17	1563	1583	forward 1	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	1	119	forward 2	TM	Cytosolic
259	LI:066742.21:2001MAY17	120	142	forward 2	TM	Transmembrane
259	LI:066742.21:2001MAY17	143	146	forward 2	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	147	169	forward 2	TM	Transmembrane
259	LI:066742.21:2001MAY17	170	351	forward 2	TM	Cytosolic
259	LI:066742.21:2001MAY17	352	374	forward 2	TM	Transmembrane
259	LI:066742.21:2001MAY17	375	1202	forward 2	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	1203	1225	forward 2	TM	Transmembrane
259	LI:066742.21:2001MAY17	1226	1313	forward 2	TM	Cytosolic
259	LI:066742.21:2001MAY17	1314	1336	forward 2	TM	Transmembrane
259	LI:066742.21:2001MAY17	1337	1372	forward 2	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	1373	1395	forward 2	TM	Transmembrane
259	LI:066742.21:2001MAY17	1396	1582	forward 2	TM	Cytosolic
259	LI:066742.21:2001MAY17	1	16	forward 3	TM	Cytosolic
259	LI:066742.21:2001MAY17	17	39	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	40	53	forward 3	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	54	76	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	77	179	forward 3	TM	Cytosolic
259	LI:066742.21:2001MAY17	180	202	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	203	312	forward 3	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	313	332	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	333	351	forward 3	TM	Cytosolic
259	LI:066742.21:2001MAY17	352	374	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	375	378	forward 3	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	379	401	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	402	580	forward 3	TM	Cytosolic
259	LI:066742.21:2001MAY17	581	598	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	599	644	forward 3	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	645	664	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	665	717	forward 3	TM	Cytosolic
259	LI:066742.21:2001MAY17	718	740	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	741	759	forward 3	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	760	782	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
259	LI:066742.21:2001MAY17	783	1168	forward 3	TM	Cytosolic
259	LI:066742.21:2001MAY17	1169	1186	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	1187	1200	forward 3	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	1201	1223	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	1224	1409	forward 3	TM	Cytosolic
259	LI:066742.21:2001MAY17	1410	1432	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	1433	1507	forward 3	TM	Non-Cytosolic
259	LI:066742.21:2001MAY17	1508	1527	forward 3	TM	Transmembrane
259	LI:066742.21:2001MAY17	1528	1582	forward 3	TM	Cytosolic
260	LI:075492.206:2001MAY17	1	14	forward 1	TM	Non-Cytosolic
260	LI:075492.206:2001MAY17	15	37	forward 1	TM	Transmembrane
260	LI:075492.206:2001MAY17	38	206	forward 1	TM	Cytosolic
260	LI:075492.206:2001MAY17	207	229	forward 1	TM	Transmembrane
260	LI:075492.206:2001MAY17	230	476	forward 1	TM	Non-Cytosolic
260	LI:075492.206:2001MAY17	1	14	forward 2	TM	Non-Cytosolic
260	LI:075492.206:2001MAY17	15	34	forward 2	TM	Transmembrane
260	LI:075492.206:2001MAY17	35	46	forward 2	TM	Cytosolic
260	LI:075492.206:2001MAY17	47	69	forward 2	TM	Transmembrane
260	LI:075492.206:2001MAY17	70	476	forward 2	TM	Non-Cytosolic
260	LI:075492.206:2001MAY17	1	205	forward 3	TM	Cytosolic
260	LI:075492.206:2001MAY17	206	223	forward 3	TM	Transmembrane
260	LI:075492.206:2001MAY17	224	475	forward 3	TM	Non-Cytosolic
261	LI:090782.3:2001MAY17	1	131	forward 1	TM	Non-Cytosolic
261	LI:090782.3:2001MAY17	132	154	forward 1	TM	Transmembrane
261	LI:090782.3:2001MAY17	155	339	forward 1	TM	Cytosolic
261	LI:090782.3:2001MAY17	340	362	forward 1	TM	Transmembrane
261	LI:090782.3:2001MAY17	363	792	forward 1	TM	Non-Cytosolic
261	LI:090782.3:2001MAY17	1	417	forward 2	TM	Non-Cytosolic
261	LI:090782.3:2001MAY17	418	440	forward 2	TM	Transmembrane
261	LI:090782.3:2001MAY17	441	451	forward 2	TM	Cytosolic
261	LI:090782.3:2001MAY17	452	474	forward 2	TM	Transmembrane
261	LI:090782.3:2001MAY17	475	792	forward 2	TM	Non-Cytosolic
262	LI:1031308.1:2001MAY17	1	670	forward 1	TM	Non-Cytosolic
262	LI:1031308.1:2001MAY17	671	693	forward 1	TM	Transmembrane
262	LI:1031308.1:2001MAY17	694	785	forward 1	TM	Cytosolic
262	LI:1031308.1:2001MAY17	786	808	forward 1	TM	Transmembrane
262	LI:1031308.1:2001MAY17	809	848	forward 1	TM	Non-Cytosolic
262	LI:1031308.1:2001MAY17	849	866	forward 1	TM	Transmembrane
262	LI:1031308.1:2001MAY17	867	880	forward 1	TM	Cytosolic
262	LI:1031308.1:2001MAY17	1	675	forward 2	TM	Non-Cytosolic
262	LI:1031308.1:2001MAY17	676	698	forward 2	TM	Transmembrane
262	LI:1031308.1:2001MAY17	699	879	forward 2	TM	Cytosolic
262	LI:1031308.1:2001MAY17	1	560	forward 3	TM	Non-Cytosolic
262	LI:1031308.1:2001MAY17	561	583	forward 3	TM	Transmembrane
262	LI:1031308.1:2001MAY17	584	633	forward 3	TM	Cytosolic
262	LI:1031308.1:2001MAY17	634	656	forward 3	TM	Transmembrane
262	LI:1031308.1:2001MAY17	657	670	forward 3	TM	Non-Cytosolic
262	LI:1031308.1:2001MAY17	671	693	forward 3	TM	Transmembrane
262	LI:1031308.1:2001MAY17	694	879	forward 3	TM	Cytosolic
263	LI:1054377.1:2001MAY17	1	76	forward 2	TM	Cytosolic
263	LI:1054377.1:2001MAY17	77	99	forward 2	TM	Transmembrane
263	LI:1054377.1:2001MAY17	100	501	forward 2	TM	Non-Cytosolic
264	LI:1072074.10:2001MAY17	1	38	forward 3	TM	Cytosolic
264	LI:1072074.10:2001MAY17	39	58	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
264	LI:1072074.10:2001MAY17	59	1024	forward 3	TM	Non-Cytosolic
265	LI:1072889.15:2001MAY17	1	67	forward 1	TM	Cytosolic
265	LI:1072889.15:2001MAY17	68	87	forward 1	TM	Transmembrane
265	LI:1072889.15:2001MAY17	88	91	forward 1	TM	Non-Cytosolic
265	LI:1072889.15:2001MAY17	92	111	forward 1	TM	Transmembrane
265	LI:1072889.15:2001MAY17	112	310	forward 1	TM	Cytosolic
265	LI:1072889.15:2001MAY17	311	333	forward 1	TM	Transmembrane
265	LI:1072889.15:2001MAY17	334	627	forward 1	TM	Non-Cytosolic
265	LI:1072889.15:2001MAY17	628	650	forward 1	TM	Transmembrane
265	LI:1072889.15:2001MAY17	651	662	forward 1	TM	Cytosolic
265	LI:1072889.15:2001MAY17	663	685	forward 1	TM	Transmembrane
265	LI:1072889.15:2001MAY17	686	694	forward 1	TM	Non-Cytosolic
265	LI:1072889.15:2001MAY17	1	19	forward 2	TM	Cytosolic
265	LI:1072889.15:2001MAY17	20	42	forward 2	TM	Transmembrane
265	LI:1072889.15:2001MAY17	43	51	forward 2	TM	Non-Cytosolic
265	LI:1072889.15:2001MAY17	52	74	forward 2	TM	Transmembrane
265	LI:1072889.15:2001MAY17	75	94	forward 2	TM	Cytosolic
265	LI:1072889.15:2001MAY17	95	117	forward 2	TM	Transmembrane
265	LI:1072889.15:2001MAY17	118	139	forward 2	TM	Non-Cytosolic
265	LI:1072889.15:2001MAY17	140	162	forward 2	TM	Transmembrane
265	LI:1072889.15:2001MAY17	163	272	forward 2	TM	Cytosolic
265	LI:1072889.15:2001MAY17	273	295	forward 2	TM	Transmembrane
265	LI:1072889.15:2001MAY17	296	520	forward 2	TM	Non-Cytosolic
265	LI:1072889.15:2001MAY17	521	543	forward 2	TM	Transmembrane
265	LI:1072889.15:2001MAY17	544	612	forward 2	TM	Cytosolic
265	LI:1072889.15:2001MAY17	613	635	forward 2	TM	Transmembrane
265	LI:1072889.15:2001MAY17	636	657	forward 2	TM	Non-Cytosolic
265	LI:1072889.15:2001MAY17	658	680	forward 2	TM	Transmembrane
265	LI:1072889.15:2001MAY17	681	694	forward 2	TM	Cytosolic
265	LI:1072889.15:2001MAY17	1	38	forward 3	TM	Cytosolic
265	LI:1072889.15:2001MAY17	39	61	forward 3	TM	Transmembrane
265	LI:1072889.15:2001MAY17	62	92	forward 3	TM	Non-Cytosolic
265	LI:1072889.15:2001MAY17	93	115	forward 3	TM	Transmembrane
265	LI:1072889.15:2001MAY17	116	266	forward 3	TM	Cytosolic
265	LI:1072889.15:2001MAY17	267	289	forward 3	TM	Transmembrane
265	LI:1072889.15:2001MAY17	290	611	forward 3	TM	Non-Cytosolic
265	LI:1072889.15:2001MAY17	612	634	forward 3	TM	Transmembrane
265	LI:1072889.15:2001MAY17	635	654	forward 3	TM	Cytosolic
265	LI:1072889.15:2001MAY17	655	677	forward 3	TM	Transmembrane
265	LI:1072889.15:2001MAY17	678	694	forward 3	TM	Non-Cytosolic
266	LI:1077480.1:2001MAY17	1	11	forward 1	TM	Cytosolic
266	LI:1077480.1:2001MAY17	12	34	forward 1	TM	Transmembrane
266	LI:1077480.1:2001MAY17	35	53	forward 1	TM	Non-Cytosolic
266	LI:1077480.1:2001MAY17	54	76	forward 1	TM	Transmembrane
266	LI:1077480.1:2001MAY17	77	109	forward 1	TM	Cytosolic
266	LI:1077480.1:2001MAY17	110	132	forward 1	TM	Transmembrane
266	LI:1077480.1:2001MAY17	133	176	forward 1	TM	Non-Cytosolic
266	LI:1077480.1:2001MAY17	177	199	forward 1	TM	Transmembrane
266	LI:1077480.1:2001MAY17	200	240	forward 1	TM	Cytosolic
266	LI:1077480.1:2001MAY17	241	263	forward 1	TM	Transmembrane
266	LI:1077480.1:2001MAY17	264	484	forward 1	TM	Non-Cytosolic
266	LI:1077480.1:2001MAY17	1	147	forward 2	TM	Cytosolic
266	LI:1077480.1:2001MAY17	148	170	forward 2	TM	Transmembrane
266	LI:1077480.1:2001MAY17	171	189	forward 2	TM	Non-Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
266	LI:1077480.1:2001MAY17	190	207	forward 2	TM	Transmembrane
266	LI:1077480.1:2001MAY17	208	251	forward 2	TM	Cytosolic
266	LI:1077480.1:2001MAY17	252	274	forward 2	TM	Transmembrane
266	LI:1077480.1:2001MAY17	275	331	forward 2	TM	Non-Cytosolic
266	LI:1077480.1:2001MAY17	332	354	forward 2	TM	Transmembrane
266	LI:1077480.1:2001MAY17	355	365	forward 2	TM	Cytosolic
266	LI:1077480.1:2001MAY17	366	388	forward 2	TM	Transmembrane
266	LI:1077480.1:2001MAY17	389	484	forward 2	TM	Non-Cytosolic
266	LI:1077480.1:2001MAY17	1	59	forward 3	TM	Cytosolic
266	LI:1077480.1:2001MAY17	60	82	forward 3	TM	Transmembrane
266	LI:1077480.1:2001MAY17	83	101	forward 3	TM	Non-Cytosolic
266	LI:1077480.1:2001MAY17	102	121	forward 3	TM	Transmembrane
266	LI:1077480.1:2001MAY17	122	132	forward 3	TM	Cytosolic
266	LI:1077480.1:2001MAY17	133	155	forward 3	TM	Transmembrane
266	LI:1077480.1:2001MAY17	156	241	forward 3	TM	Non-Cytosolic
266	LI:1077480.1:2001MAY17	242	264	forward 3	TM	Transmembrane
266	LI:1077480.1:2001MAY17	265	484	forward 3	TM	Cytosolic
267	LI:1079555.1:2001MAY17	1	38	forward 2	TM	Cytosolic
267	LI:1079555.1:2001MAY17	39	61	forward 2	TM	Transmembrane
267	LI:1079555.1:2001MAY17	62	444	forward 2	TM	Non-Cytosolic
268	LI:1084992.28:2001MAY17	1	68	forward 3	TM	Cytosolic
268	LI:1084992.28:2001MAY17	69	91	forward 3	TM	Transmembrane
268	LI:1084992.28:2001MAY17	92	263	forward 3	TM	Non-Cytosolic
269	LI:1085472.5:2001MAY17	1	52	forward 1	TM	Cytosolic
269	LI:1085472.5:2001MAY17	53	75	forward 1	TM	Transmembrane
269	LI:1085472.5:2001MAY17	76	1590	forward 1	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	1	84	forward 1	TM	Cytosolic
270	LI:1086800.7:2001MAY17	85	107	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	108	140	forward 1	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	141	163	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	164	431	forward 1	TM	Cytosolic
270	LI:1086800.7:2001MAY17	432	451	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	452	479	forward 1	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	480	502	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	503	521	forward 1	TM	Cytosolic
270	LI:1086800.7:2001MAY17	522	541	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	542	593	forward 1	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	594	616	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	617	622	forward 1	TM	Cytosolic
270	LI:1086800.7:2001MAY17	623	645	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	646	686	forward 1	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	687	709	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	710	981	forward 1	TM	Cytosolic
270	LI:1086800.7:2001MAY17	982	1004	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	1005	1471	forward 1	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	1472	1489	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	1490	1578	forward 1	TM	Cytosolic
270	LI:1086800.7:2001MAY17	1579	1601	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	1602	1641	forward 1	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	1642	1664	forward 1	TM	Transmembrane
270	LI:1086800.7:2001MAY17	1665	1671	forward 1	TM	Cytosolic
270	LI:1086800.7:2001MAY17	1	49	forward 2	TM	Cytosolic
270	LI:1086800.7:2001MAY17	50	72	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	73	86	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
270	LI:1086800.7:2001MAY17	87	109	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	110	115	forward 2	TM	Cytosolic
270	LI:1086800.7:2001MAY17	116	138	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	139	180	forward 2	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	181	203	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	204	238	forward 2	TM	Cytosolic
270	LI:1086800.7:2001MAY17	239	261	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	262	275	forward 2	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	276	298	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	299	309	forward 2	TM	Cytosolic
270	LI:1086800.7:2001MAY17	310	332	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	333	592	forward 2	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	593	615	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	616	868	forward 2	TM	Cytosolic
270	LI:1086800.7:2001MAY17	869	891	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	892	905	forward 2	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	906	928	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	929	1036	forward 2	TM	Cytosolic
270	LI:1086800.7:2001MAY17	1037	1059	forward 2	TM	Transmembrane
270	LI:1086800.7:2001MAY17	1060	1670	forward 2	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	1	46	forward 3	TM	Cytosolic
270	LI:1086800.7:2001MAY17	47	66	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	67	80	forward 3	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	81	103	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	104	233	forward 3	TM	Cytosolic
270	LI:1086800.7:2001MAY17	234	256	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	257	275	forward 3	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	276	298	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	299	388	forward 3	TM	Cytosolic
270	LI:1086800.7:2001MAY17	389	411	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	412	584	forward 3	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	585	607	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	608	775	forward 3	TM	Cytosolic
270	LI:1086800.7:2001MAY17	776	795	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	796	1206	forward 3	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	1207	1229	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	1230	1262	forward 3	TM	Cytosolic
270	LI:1086800.7:2001MAY17	1263	1285	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	1286	1294	forward 3	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	1295	1314	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	1315	1446	forward 3	TM	Cytosolic
270	LI:1086800.7:2001MAY17	1447	1469	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	1470	1630	forward 3	TM	Non-Cytosolic
270	LI:1086800.7:2001MAY17	1631	1653	forward 3	TM	Transmembrane
270	LI:1086800.7:2001MAY17	1654	1670	forward 3	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1	343	forward 1	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	344	363	forward 1	TM	Transmembrane
271	LI:1089871.9:2001MAY17	364	369	forward 1	TM	Cytosolic
271	LI:1089871.9:2001MAY17	370	392	forward 1	TM	Transmembrane
271	LI:1089871.9:2001MAY17	393	1441	forward 1	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1442	1464	forward 1	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1465	1483	forward 1	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1484	1503	forward 1	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1504	1546	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
271	LI:1089871.9:2001MAY17	1547	1569	forward 1	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1570	1575	forward 1	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1576	1598	forward 1	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1599	1617	forward 1	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1618	1639	forward 1	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1640	1753	forward 1	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1754	1773	forward 1	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1774	1928	forward 1	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1	1219	forward 2	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1220	1242	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1243	1408	forward 2	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1409	1426	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1427	1430	forward 2	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1431	1448	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1449	1454	forward 2	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1455	1477	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1478	1481	forward 2	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1482	1504	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1505	1579	forward 2	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1580	1602	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1603	1673	forward 2	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1674	1693	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1694	1713	forward 2	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1714	1736	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1737	1759	forward 2	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1760	1782	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1783	1836	forward 2	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1837	1859	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1860	1862	forward 2	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1863	1885	forward 2	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1886	1928	forward 2	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1	1382	forward 3	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1383	1405	forward 3	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1406	1425	forward 3	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1426	1448	forward 3	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1449	1471	forward 3	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1472	1494	forward 3	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1495	1571	forward 3	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1572	1594	forward 3	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1595	1669	forward 3	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1670	1687	forward 3	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1688	1706	forward 3	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1707	1729	forward 3	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1730	1748	forward 3	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1749	1771	forward 3	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1772	1849	forward 3	TM	Cytosolic
271	LI:1089871.9:2001MAY17	1850	1872	forward 3	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1873	1881	forward 3	TM	Non-Cytosolic
271	LI:1089871.9:2001MAY17	1882	1904	forward 3	TM	Transmembrane
271	LI:1089871.9:2001MAY17	1905	1927	forward 3	TM	Cytosolic
272	LI:110297.6:2001MAY17	1	63	forward 1	TM	Cytosolic
272	LI:110297.6:2001MAY17	64	86	forward 1	TM	Transmembrane
272	LI:110297.6:2001MAY17	87	127	forward 1	TM	Non-Cytosolic
272	LI:110297.6:2001MAY17	128	145	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
272	LI:110297.6:2001MAY17	146	156	forward 1	TM	Cytosolic
272	LI:110297.6:2001MAY17	157	179	forward 1	TM	Transmembrane
272	LI:110297.6:2001MAY17	180	293	forward 1	TM	Non-Cytosolic
272	LI:110297.6:2001MAY17	294	311	forward 1	TM	Transmembrane
272	LI:110297.6:2001MAY17	312	587	forward 1	TM	Cytosolic
272	LI:110297.6:2001MAY17	588	610	forward 1	TM	Transmembrane
272	LI:110297.6:2001MAY17	611	684	forward 1	TM	Non-Cytosolic
272	LI:110297.6:2001MAY17	685	702	forward 1	TM	Transmembrane
272	LI:110297.6:2001MAY17	703	737	forward 1	TM	Cytosolic
272	LI:110297.6:2001MAY17	738	760	forward 1	TM	Transmembrane
272	LI:110297.6:2001MAY17	761	769	forward 1	TM	Non-Cytosolic
272	LI:110297.6:2001MAY17	770	792	forward 1	TM	Transmembrane
272	LI:110297.6:2001MAY17	793	801	forward 1	TM	Cytosolic
272	LI:110297.6:2001MAY17	1	735	forward 2	TM	Non-Cytosolic
272	LI:110297.6:2001MAY17	736	758	forward 2	TM	Transmembrane
272	LI:110297.6:2001MAY17	759	769	forward 2	TM	Cytosolic
272	LI:110297.6:2001MAY17	770	792	forward 2	TM	Transmembrane
272	LI:110297.6:2001MAY17	793	801	forward 2	TM	Non-Cytosolic
272	LI:110297.6:2001MAY17	1	11	forward 3	TM	Cytosolic
272	LI:110297.6:2001MAY17	12	29	forward 3	TM	Transmembrane
272	LI:110297.6:2001MAY17	30	604	forward 3	TM	Non-Cytosolic
272	LI:110297.6:2001MAY17	605	627	forward 3	TM	Transmembrane
272	LI:110297.6:2001MAY17	628	738	forward 3	TM	Cytosolic
272	LI:110297.6:2001MAY17	739	761	forward 3	TM	Transmembrane
272	LI:110297.6:2001MAY17	762	775	forward 3	TM	Non-Cytosolic
272	LI:110297.6:2001MAY17	776	798	forward 3	TM	Transmembrane
272	LI:110297.6:2001MAY17	799	800	forward 3	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1	1373	forward 1	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1374	1396	forward 1	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1397	1555	forward 1	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1556	1578	forward 1	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1579	1648	forward 1	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1649	1668	forward 1	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1669	1712	forward 1	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1713	1735	forward 1	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1736	1744	forward 1	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1745	1764	forward 1	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1765	1835	forward 1	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1836	1858	forward 1	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1859	1872	forward 1	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1873	1892	forward 1	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1893	1912	forward 1	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1913	1935	forward 1	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1936	1946	forward 1	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1	12	forward 2	TM	Cytosolic
273	LI:1143463.8:2001MAY17	13	35	forward 2	TM	Transmembrane
273	LI:1143463.8:2001MAY17	36	721	forward 2	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	722	739	forward 2	TM	Transmembrane
273	LI:1143463.8:2001MAY17	740	751	forward 2	TM	Cytosolic
273	LI:1143463.8:2001MAY17	752	774	forward 2	TM	Transmembrane
273	LI:1143463.8:2001MAY17	775	777	forward 2	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	778	797	forward 2	TM	Transmembrane
273	LI:1143463.8:2001MAY17	798	837	forward 2	TM	Cytosolic
273	LI:1143463.8:2001MAY17	838	860	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
273	LI:1143463.8:2001MAY17	861	1641	forward 2	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1642	1664	forward 2	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1665	1690	forward 2	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1691	1710	forward 2	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1711	1738	forward 2	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1739	1761	forward 2	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1762	1835	forward 2	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1836	1858	forward 2	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1859	1877	forward 2	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1878	1900	forward 2	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1901	1946	forward 2	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1	1257	forward 3	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1258	1280	forward 3	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1281	1381	forward 3	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1382	1404	forward 3	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1405	1744	forward 3	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1745	1767	forward 3	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1768	1816	forward 3	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1817	1839	forward 3	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1840	1848	forward 3	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1849	1871	forward 3	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1872	1877	forward 3	TM	Cytosolic
273	LI:1143463.8:2001MAY17	1878	1897	forward 3	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1898	1911	forward 3	TM	Non-Cytosolic
273	LI:1143463.8:2001MAY17	1912	1931	forward 3	TM	Transmembrane
273	LI:1143463.8:2001MAY17	1932	1946	forward 3	TM	Cytosolic
274	LI:1144466.1:2001MAY17	1	708	forward 1	TM	Non-Cytosolic
274	LI:1144466.1:2001MAY17	709	728	forward 1	TM	Transmembrane
274	LI:1144466.1:2001MAY17	729	741	forward 1	TM	Cytosolic
274	LI:1144466.1:2001MAY17	1	707	forward 3	TM	Non-Cytosolic
274	LI:1144466.1:2001MAY17	708	727	forward 3	TM	Transmembrane
274	LI:1144466.1:2001MAY17	728	740	forward 3	TM	Cytosolic
275	LI:1170624.2:2001MAY17	1	354	forward 1	TM	Cytosolic
275	LI:1170624.2:2001MAY17	355	377	forward 1	TM	Transmembrane
275	LI:1170624.2:2001MAY17	378	378	forward 1	TM	Non-Cytosolic
275	LI:1170624.2:2001MAY17	1	356	forward 3	TM	Non-Cytosolic
275	LI:1170624.2:2001MAY17	357	374	forward 3	TM	Transmembrane
275	LI:1170624.2:2001MAY17	375	378	forward 3	TM	Cytosolic
276	LI:1171602.39:2001MAY17	1	133	forward 1	TM	Non-Cytosolic
276	LI:1171602.39:2001MAY17	134	156	forward 1	TM	Transmembrane
276	LI:1171602.39:2001MAY17	157	234	forward 1	TM	Cytosolic
276	LI:1171602.39:2001MAY17	1	4	forward 2	TM	Cytosolic
276	LI:1171602.39:2001MAY17	5	22	forward 2	TM	Transmembrane
276	LI:1171602.39:2001MAY17	23	36	forward 2	TM	Non-Cytosolic
276	LI:1171602.39:2001MAY17	37	59	forward 2	TM	Transmembrane
276	LI:1171602.39:2001MAY17	60	234	forward 2	TM	Cytosolic
277	LI:1182361.3:2001MAY17	1	33	forward 1	TM	Cytosolic
277	LI:1182361.3:2001MAY17	34	56	forward 1	TM	Transmembrane
277	LI:1182361.3:2001MAY17	57	245	forward 1	TM	Non-Cytosolic
278	LI:1188194.15:2001MAY17	1	542	forward 2	TM	Non-Cytosolic
278	LI:1188194.15:2001MAY17	543	565	forward 2	TM	Transmembrane
278	LI:1188194.15:2001MAY17	566	585	forward 2	TM	Cytosolic
278	LI:1188194.15:2001MAY17	586	608	forward 2	TM	Transmembrane
278	LI:1188194.15:2001MAY17	609	640	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
278	LI:1188194.15:2001MAY17	641	659	forward 2	TM	Transmembrane
278	LI:1188194.15:2001MAY17	660	662	forward 2	TM	Cytosolic
278	LI:1188194.15:2001MAY17	1	538	forward 3	TM	Non-Cytosolic
278	LI:1188194.15:2001MAY17	539	561	forward 3	TM	Transmembrane
278	LI:1188194.15:2001MAY17	562	634	forward 3	TM	Cytosolic
278	LI:1188194.15:2001MAY17	635	657	forward 3	TM	Transmembrane
278	LI:1188194.15:2001MAY17	658	662	forward 3	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	1	426	forward 1	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	427	445	forward 1	TM	Transmembrane
279	LI:1189195.7:2001MAY17	446	457	forward 1	TM	Cytosolic
279	LI:1189195.7:2001MAY17	458	480	forward 1	TM	Transmembrane
279	LI:1189195.7:2001MAY17	481	521	forward 1	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	522	539	forward 1	TM	Transmembrane
279	LI:1189195.7:2001MAY17	540	567	forward 1	TM	Cytosolic
279	LI:1189195.7:2001MAY17	568	590	forward 1	TM	Transmembrane
279	LI:1189195.7:2001MAY17	591	661	forward 1	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	1	283	forward 2	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	284	306	forward 2	TM	Transmembrane
279	LI:1189195.7:2001MAY17	307	380	forward 2	TM	Cytosolic
279	LI:1189195.7:2001MAY17	381	403	forward 2	TM	Transmembrane
279	LI:1189195.7:2001MAY17	404	422	forward 2	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	423	445	forward 2	TM	Transmembrane
279	LI:1189195.7:2001MAY17	446	457	forward 2	TM	Cytosolic
279	LI:1189195.7:2001MAY17	458	480	forward 2	TM	Transmembrane
279	LI:1189195.7:2001MAY17	481	489	forward 2	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	490	509	forward 2	TM	Transmembrane
279	LI:1189195.7:2001MAY17	510	521	forward 2	TM	Cytosolic
279	LI:1189195.7:2001MAY17	522	539	forward 2	TM	Transmembrane
279	LI:1189195.7:2001MAY17	540	573	forward 2	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	574	596	forward 2	TM	Transmembrane
279	LI:1189195.7:2001MAY17	597	602	forward 2	TM	Cytosolic
279	LI:1189195.7:2001MAY17	603	625	forward 2	TM	Transmembrane
279	LI:1189195.7:2001MAY17	626	661	forward 2	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	1	67	forward 3	TM	Cytosolic
279	LI:1189195.7:2001MAY17	68	90	forward 3	TM	Transmembrane
279	LI:1189195.7:2001MAY17	91	109	forward 3	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	110	132	forward 3	TM	Transmembrane
279	LI:1189195.7:2001MAY17	133	270	forward 3	TM	Cytosolic
279	LI:1189195.7:2001MAY17	271	293	forward 3	TM	Transmembrane
279	LI:1189195.7:2001MAY17	294	359	forward 3	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	360	382	forward 3	TM	Transmembrane
279	LI:1189195.7:2001MAY17	383	388	forward 3	TM	Cytosolic
279	LI:1189195.7:2001MAY17	389	411	forward 3	TM	Transmembrane
279	LI:1189195.7:2001MAY17	412	458	forward 3	TM	Non-Cytosolic
279	LI:1189195.7:2001MAY17	459	481	forward 3	TM	Transmembrane
279	LI:1189195.7:2001MAY17	482	517	forward 3	TM	Cytosolic
279	LI:1189195.7:2001MAY17	518	537	forward 3	TM	Transmembrane
279	LI:1189195.7:2001MAY17	538	660	forward 3	TM	Non-Cytosolic
280	LI:1190092.13:2001MAY17	1	127	forward 1	TM	Non-Cytosolic
280	LI:1190092.13:2001MAY17	128	150	forward 1	TM	Transmembrane
280	LI:1190092.13:2001MAY17	151	162	forward 1	TM	Cytosolic
280	LI:1190092.13:2001MAY17	1	162	forward 2	TM	Cytosolic
281	LI:1190318.4:2001MAY17	1	328	forward 1	TM	Non-Cytosolic
281	LI:1190318.4:2001MAY17	329	351	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
281	LI:1190318.4:2001MAY17	352	375	forward 1	TM	Cytosolic
282	LI:144233.1:2001MAY17	1	20	forward 1	TM	Cytosolic
282	LI:144233.1:2001MAY17	21	43	forward 1	TM	Transmembrane
282	LI:144233.1:2001MAY17	44	241	forward 1	TM	Non-Cytosolic
283	LI:154608.1:2001MAY17	1	246	forward 1	TM	Non-Cytosolic
283	LI:154608.1:2001MAY17	247	269	forward 1	TM	Transmembrane
283	LI:154608.1:2001MAY17	270	307	forward 1	TM	Cytosolic
283	LI:154608.1:2001MAY17	1	40	forward 2	TM	Cytosolic
283	LI:154608.1:2001MAY17	41	63	forward 2	TM	Transmembrane
283	LI:154608.1:2001MAY17	64	196	forward 2	TM	Non-Cytosolic
283	LI:154608.1:2001MAY17	197	219	forward 2	TM	Transmembrane
283	LI:154608.1:2001MAY17	220	307	forward 2	TM	Cytosolic
283	LI:154608.1:2001MAY17	1	203	forward 3	TM	Non-Cytosolic
283	LI:154608.1:2001MAY17	204	226	forward 3	TM	Transmembrane
283	LI:154608.1:2001MAY17	227	245	forward 3	TM	Cytosolic
283	LI:154608.1:2001MAY17	246	268	forward 3	TM	Transmembrane
283	LI:154608.1:2001MAY17	269	306	forward 3	TM	Non-Cytosolic
284	LI:170101.1:2001MAY17	1	99	forward 1	TM	Cytosolic
284	LI:170101.1:2001MAY17	100	122	forward 1	TM	Transmembrane
284	LI:170101.1:2001MAY17	123	386	forward 1	TM	Non-Cytosolic
284	LI:170101.1:2001MAY17	1	35	forward 2	TM	Non-Cytosolic
284	LI:170101.1:2001MAY17	36	58	forward 2	TM	Transmembrane
284	LI:170101.1:2001MAY17	59	99	forward 2	TM	Cytosolic
284	LI:170101.1:2001MAY17	100	122	forward 2	TM	Transmembrane
284	LI:170101.1:2001MAY17	123	136	forward 2	TM	Non-Cytosolic
284	LI:170101.1:2001MAY17	137	156	forward 2	TM	Transmembrane
284	LI:170101.1:2001MAY17	157	386	forward 2	TM	Cytosolic
284	LI:170101.1:2001MAY17	1	81	forward 3	TM	Cytosolic
284	LI:170101.1:2001MAY17	82	101	forward 3	TM	Transmembrane
284	LI:170101.1:2001MAY17	102	110	forward 3	TM	Non-Cytosolic
284	LI:170101.1:2001MAY17	111	133	forward 3	TM	Transmembrane
284	LI:170101.1:2001MAY17	134	139	forward 3	TM	Cytosolic
284	LI:170101.1:2001MAY17	140	157	forward 3	TM	Transmembrane
284	LI:170101.1:2001MAY17	158	386	forward 3	TM	Non-Cytosolic
285	LI:180043.1:2001MAY17	1	4	forward 1	TM	Cytosolic
285	LI:180043.1:2001MAY17	5	27	forward 1	TM	Transmembrane
285	LI:180043.1:2001MAY17	28	46	forward 1	TM	Non-Cytosolic
285	LI:180043.1:2001MAY17	47	69	forward 1	TM	Transmembrane
285	LI:180043.1:2001MAY17	70	238	forward 1	TM	Cytosolic
285	LI:180043.1:2001MAY17	239	261	forward 1	TM	Transmembrane
285	LI:180043.1:2001MAY17	262	373	forward 1	TM	Non-Cytosolic
285	LI:180043.1:2001MAY17	1	208	forward 3	TM	Non-Cytosolic
285	LI:180043.1:2001MAY17	209	228	forward 3	TM	Transmembrane
285	LI:180043.1:2001MAY17	229	373	forward 3	TM	Cytosolic
286	LI:193050.1:2001MAY17	1	142	forward 1	TM	Non-Cytosolic
286	LI:193050.1:2001MAY17	143	162	forward 1	TM	Transmembrane
286	LI:193050.1:2001MAY17	163	339	forward 1	TM	Cytosolic
286	LI:193050.1:2001MAY17	340	358	forward 1	TM	Transmembrane
286	LI:193050.1:2001MAY17	359	777	forward 1	TM	Non-Cytosolic
286	LI:193050.1:2001MAY17	1	182	forward 2	TM	Non-Cytosolic
286	LI:193050.1:2001MAY17	183	205	forward 2	TM	Transmembrane
286	LI:193050.1:2001MAY17	206	247	forward 2	TM	Cytosolic
286	LI:193050.1:2001MAY17	248	270	forward 2	TM	Transmembrane
286	LI:193050.1:2001MAY17	271	329	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
286	LI:193050.1:2001MAY17	330	352	forward 2	TM	Transmembrane
286	LI:193050.1:2001MAY17	353	482	forward 2	TM	Cytosolic
286	LI:193050.1:2001MAY17	483	505	forward 2	TM	Transmembrane
286	LI:193050.1:2001MAY17	506	536	forward 2	TM	Non-Cytosolic
286	LI:193050.1:2001MAY17	537	559	forward 2	TM	Transmembrane
286	LI:193050.1:2001MAY17	560	684	forward 2	TM	Cytosolic
286	LI:193050.1:2001MAY17	685	704	forward 2	TM	Transmembrane
286	LI:193050.1:2001MAY17	705	734	forward 2	TM	Non-Cytosolic
286	LI:193050.1:2001MAY17	735	757	forward 2	TM	Transmembrane
286	LI:193050.1:2001MAY17	758	777	forward 2	TM	Cytosolic
286	LI:193050.1:2001MAY17	1	144	forward 3	TM	Cytosolic
286	LI:193050.1:2001MAY17	145	167	forward 3	TM	Transmembrane
286	LI:193050.1:2001MAY17	168	181	forward 3	TM	Non-Cytosolic
286	LI:193050.1:2001MAY17	182	204	forward 3	TM	Transmembrane
286	LI:193050.1:2001MAY17	205	255	forward 3	TM	Cytosolic
286	LI:193050.1:2001MAY17	256	278	forward 3	TM	Transmembrane
286	LI:193050.1:2001MAY17	279	327	forward 3	TM	Non-Cytosolic
286	LI:193050.1:2001MAY17	328	350	forward 3	TM	Transmembrane
286	LI:193050.1:2001MAY17	351	419	forward 3	TM	Cytosolic
286	LI:193050.1:2001MAY17	420	439	forward 3	TM	Transmembrane
286	LI:193050.1:2001MAY17	440	776	forward 3	TM	Non-Cytosolic
287	LI:197477.31:2001MAY17	1	447	forward 1	TM	Non-Cytosolic
287	LI:197477.31:2001MAY17	448	470	forward 1	TM	Transmembrane
287	LI:197477.31:2001MAY17	471	500	forward 1	TM	Cytosolic
287	LI:197477.31:2001MAY17	501	523	forward 1	TM	Transmembrane
287	LI:197477.31:2001MAY17	524	532	forward 1	TM	Non-Cytosolic
287	LI:197477.31:2001MAY17	533	550	forward 1	TM	Transmembrane
287	LI:197477.31:2001MAY17	551	655	forward 1	TM	Cytosolic
288	LI:199639.12:2001MAY17	1	266	forward 1	TM	Non-Cytosolic
288	LI:199639.12:2001MAY17	267	289	forward 1	TM	Transmembrane
288	LI:199639.12:2001MAY17	290	334	forward 1	TM	Cytosolic
288	LI:199639.12:2001MAY17	335	357	forward 1	TM	Transmembrane
288	LI:199639.12:2001MAY17	358	360	forward 1	TM	Non-Cytosolic
288	LI:199639.12:2001MAY17	361	383	forward 1	TM	Transmembrane
288	LI:199639.12:2001MAY17	384	509	forward 1	TM	Cytosolic
288	LI:199639.12:2001MAY17	510	532	forward 1	TM	Transmembrane
288	LI:199639.12:2001MAY17	533	556	forward 1	TM	Non-Cytosolic
288	LI:199639.12:2001MAY17	557	579	forward 1	TM	Transmembrane
288	LI:199639.12:2001MAY17	580	585	forward 1	TM	Cytosolic
288	LI:199639.12:2001MAY17	586	608	forward 1	TM	Transmembrane
288	LI:199639.12:2001MAY17	609	798	forward 1	TM	Non-Cytosolic
288	LI:199639.12:2001MAY17	1	252	forward 2	TM	Cytosolic
288	LI:199639.12:2001MAY17	253	275	forward 2	TM	Transmembrane
288	LI:199639.12:2001MAY17	276	798	forward 2	TM	Non-Cytosolic
289	LI:200058.6:2001MAY17	1	101	forward 1	TM	Cytosolic
289	LI:200058.6:2001MAY17	102	124	forward 1	TM	Transmembrane
289	LI:200058.6:2001MAY17	125	546	forward 1	TM	Non-Cytosolic
289	LI:200058.6:2001MAY17	1	402	forward 2	TM	Non-Cytosolic
289	LI:200058.6:2001MAY17	403	422	forward 2	TM	Transmembrane
289	LI:200058.6:2001MAY17	423	434	forward 2	TM	Cytosolic
289	LI:200058.6:2001MAY17	435	454	forward 2	TM	Transmembrane
289	LI:200058.6:2001MAY17	455	468	forward 2	TM	Non-Cytosolic
289	LI:200058.6:2001MAY17	469	491	forward 2	TM	Transmembrane
289	LI:200058.6:2001MAY17	492	546	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
290	LI:201374.23:2001MAY17	1	177	forward 1	TM	Non-Cytosolic
290	LI:201374.23:2001MAY17	178	200	forward 1	TM	Transmembrane
290	LI:201374.23:2001MAY17	201	202	forward 1	TM	Cytosolic
290	LI:201374.23:2001MAY17	1	58	forward 3	TM	Cytosolic
290	LI:201374.23:2001MAY17	59	81	forward 3	TM	Transmembrane
290	LI:201374.23:2001MAY17	82	201	forward 3	TM	Non-Cytosolic
291	LI:201824.1:2001MAY17	1	488	forward 1	TM	Non-Cytosolic
291	LI:201824.1:2001MAY17	489	511	forward 1	TM	Transmembrane
291	LI:201824.1:2001MAY17	512	713	forward 1	TM	Cytosolic
291	LI:201824.1:2001MAY17	714	736	forward 1	TM	Transmembrane
291	LI:201824.1:2001MAY17	737	804	forward 1	TM	Non-Cytosolic
291	LI:201824.1:2001MAY17	805	824	forward 1	TM	Transmembrane
291	LI:201824.1:2001MAY17	825	836	forward 1	TM	Cytosolic
291	LI:201824.1:2001MAY17	837	856	forward 1	TM	Transmembrane
291	LI:201824.1:2001MAY17	857	870	forward 1	TM	Non-Cytosolic
291	LI:201824.1:2001MAY17	871	893	forward 1	TM	Transmembrane
291	LI:201824.1:2001MAY17	894	1218	forward 1	TM	Cytosolic
291	LI:201824.1:2001MAY17	1219	1249	forward 1	TM	Transmembrane
291	LI:201824.1:2001MAY17	1250	1253	forward 1	TM	Non-Cytosolic
291	LI:201824.1:2001MAY17	1	143	forward 3	TM	Cytosolic
291	LI:201824.1:2001MAY17	144	166	forward 3	TM	Transmembrane
291	LI:201824.1:2001MAY17	167	199	forward 3	TM	Non-Cytosolic
291	LI:201824.1:2001MAY17	200	219	forward 3	TM	Transmembrane
291	LI:201824.1:2001MAY17	220	231	forward 3	TM	Cytosolic
291	LI:201824.1:2001MAY17	232	254	forward 3	TM	Transmembrane
291	LI:201824.1:2001MAY17	255	500	forward 3	TM	Non-Cytosolic
291	LI:201824.1:2001MAY17	501	523	forward 3	TM	Transmembrane
291	LI:201824.1:2001MAY17	524	529	forward 3	TM	Cytosolic
291	LI:201824.1:2001MAY17	530	549	forward 3	TM	Transmembrane
291	LI:201824.1:2001MAY17	550	575	forward 3	TM	Non-Cytosolic
291	LI:201824.1:2001MAY17	576	598	forward 3	TM	Transmembrane
291	LI:201824.1:2001MAY17	599	692	forward 3	TM	Cytosolic
291	LI:201824.1:2001MAY17	693	715	forward 3	TM	Transmembrane
291	LI:201824.1:2001MAY17	716	729	forward 3	TM	Non-Cytosolic
291	LI:201824.1:2001MAY17	730	752	forward 3	TM	Transmembrane
291	LI:201824.1:2001MAY17	753	860	forward 3	TM	Cytosolic
291	LI:201824.1:2001MAY17	861	883	forward 3	TM	Transmembrane
291	LI:201824.1:2001MAY17	884	1226	forward 3	TM	Non-Cytosolic
291	LI:201824.1:2001MAY17	1227	1249	forward 3	TM	Transmembrane
291	LI:201824.1:2001MAY17	1250	1253	forward 3	TM	Cytosolic
292	LI:201989.11:2001MAY17	1	406	forward 1	TM	Non-Cytosolic
292	LI:201989.11:2001MAY17	407	429	forward 1	TM	Transmembrane
292	LI:201989.11:2001MAY17	430	443	forward 1	TM	Cytosolic
292	LI:201989.11:2001MAY17	1	400	forward 3	TM	Non-Cytosolic
292	LI:201989.11:2001MAY17	401	423	forward 3	TM	Transmembrane
292	LI:201989.11:2001MAY17	424	442	forward 3	TM	Cytosolic
293	LI:2035159.1:2001MAY17	1	52	forward 1	TM	Cytosolic
293	LI:2035159.1:2001MAY17	53	72	forward 1	TM	Transmembrane
293	LI:2035159.1:2001MAY17	73	242	forward 1	TM	Non-Cytosolic
293	LI:2035159.1:2001MAY17	1	216	forward 2	TM	Cytosolic
293	LI:2035159.1:2001MAY17	217	236	forward 2	TM	Transmembrane
293	LI:2035159.1:2001MAY17	237	242	forward 2	TM	Non-Cytosolic
294	LI:204818.10:2001MAY17	1	364	forward 1	TM	Non-Cytosolic
294	LI:204818.10:2001MAY17	365	387	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
294	LI:204818.10:2001MAY17	388	482	forward 1	TM	Cytosolic
294	LI:204818.10:2001MAY17	1	229	forward 2	TM	Non-Cytosolic
294	LI:204818.10:2001MAY17	230	252	forward 2	TM	Transmembrane
294	LI:204818.10:2001MAY17	253	365	forward 2	TM	Cytosolic
294	LI:204818.10:2001MAY17	366	388	forward 2	TM	Transmembrane
294	LI:204818.10:2001MAY17	389	481	forward 2	TM	Non-Cytosolic
295	LI:2048337.1:2001MAY17	1	611	forward 2	TM	Non-Cytosolic
295	LI:2048337.1:2001MAY17	612	634	forward 2	TM	Transmembrane
295	LI:2048337.1:2001MAY17	635	658	forward 2	TM	Cytosolic
295	LI:2048337.1:2001MAY17	659	681	forward 2	TM	Transmembrane
295	LI:2048337.1:2001MAY17	682	709	forward 2	TM	Non-Cytosolic
296	LI:2049697.4:2001MAY17	1	390	forward 3	TM	Non-Cytosolic
296	LI:2049697.4:2001MAY17	391	413	forward 3	TM	Transmembrane
296	LI:2049697.4:2001MAY17	414	698	forward 3	TM	Cytosolic
297	LI:2050808.19:2001MAY17	1	105	forward 2	TM	Non-Cytosolic
297	LI:2050808.19:2001MAY17	106	128	forward 2	TM	Transmembrane
297	LI:2050808.19:2001MAY17	129	134	forward 2	TM	Cytosolic
297	LI:2050808.19:2001MAY17	135	157	forward 2	TM	Transmembrane
297	LI:2050808.19:2001MAY17	158	176	forward 2	TM	Non-Cytosolic
297	LI:2050808.19:2001MAY17	177	199	forward 2	TM	Transmembrane
297	LI:2050808.19:2001MAY17	200	412	forward 2	TM	Cytosolic
298	LI:209773.25:2001MAY17	1	4	forward 1	TM	Cytosolic
298	LI:209773.25:2001MAY17	5	27	forward 1	TM	Transmembrane
298	LI:209773.25:2001MAY17	28	363	forward 1	TM	Non-Cytosolic
298	LI:209773.25:2001MAY17	1	6	forward 3	TM	Cytosolic
298	LI:209773.25:2001MAY17	7	29	forward 3	TM	Transmembrane
298	LI:209773.25:2001MAY17	30	362	forward 3	TM	Non-Cytosolic
299	LI:2117881.32:2001MAY17	1	177	forward 1	TM	Non-Cytosolic
299	LI:2117881.32:2001MAY17	178	200	forward 1	TM	Transmembrane
299	LI:2117881.32:2001MAY17	201	386	forward 1	TM	Cytosolic
299	LI:2117881.32:2001MAY17	387	406	forward 1	TM	Transmembrane
299	LI:2117881.32:2001MAY17	407	422	forward 1	TM	Non-Cytosolic
299	LI:2117881.32:2001MAY17	1	288	forward 2	TM	Cytosolic
299	LI:2117881.32:2001MAY17	289	311	forward 2	TM	Transmembrane
299	LI:2117881.32:2001MAY17	312	325	forward 2	TM	Non-Cytosolic
299	LI:2117881.32:2001MAY17	326	348	forward 2	TM	Transmembrane
299	LI:2117881.32:2001MAY17	349	422	forward 2	TM	Cytosolic
299	LI:2117881.32:2001MAY17	1	384	forward 3	TM	Non-Cytosolic
299	LI:2117881.32:2001MAY17	385	404	forward 3	TM	Transmembrane
299	LI:2117881.32:2001MAY17	405	422	forward 3	TM	Cytosolic
300	LI:2118140.9:2001MAY17	1	446	forward 1	TM	Non-Cytosolic
300	LI:2118140.9:2001MAY17	447	469	forward 1	TM	Transmembrane
300	LI:2118140.9:2001MAY17	470	510	forward 1	TM	Cytosolic
300	LI:2118140.9:2001MAY17	511	533	forward 1	TM	Transmembrane
300	LI:2118140.9:2001MAY17	534	566	forward 1	TM	Non-Cytosolic
300	LI:2118140.9:2001MAY17	1	179	forward 2	TM	Non-Cytosolic
300	LI:2118140.9:2001MAY17	180	202	forward 2	TM	Transmembrane
300	LI:2118140.9:2001MAY17	203	411	forward 2	TM	Cytosolic
300	LI:2118140.9:2001MAY17	412	434	forward 2	TM	Transmembrane
300	LI:2118140.9:2001MAY17	435	443	forward 2	TM	Non-Cytosolic
300	LI:2118140.9:2001MAY17	444	466	forward 2	TM	Transmembrane
300	LI:2118140.9:2001MAY17	467	565	forward 2	TM	Cytosolic
300	LI:2118140.9:2001MAY17	1	201	forward 3	TM	Cytosolic
300	LI:2118140.9:2001MAY17	202	219	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
300	LI:2118140.9:2001MAY17	220	233	forward 3	TM	Non-Cytosolic
300	LI:2118140.9:2001MAY17	234	256	forward 3	TM	Transmembrane
300	LI:2118140.9:2001MAY17	257	296	forward 3	TM	Cytosolic
300	LI:2118140.9:2001MAY17	297	319	forward 3	TM	Transmembrane
300	LI:2118140.9:2001MAY17	320	442	forward 3	TM	Non-Cytosolic
300	LI:2118140.9:2001MAY17	443	465	forward 3	TM	Transmembrane
300	LI:2118140.9:2001MAY17	466	565	forward 3	TM	Cytosolic
301	LI:2118151.15:2001MAY17	1	45	forward 2	TM	Cytosolic
301	LI:2118151.15:2001MAY17	46	68	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	69	82	forward 2	TM	Non-Cytosolic
301	LI:2118151.15:2001MAY17	83	102	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	103	360	forward 2	TM	Cytosolic
301	LI:2118151.15:2001MAY17	361	383	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	384	409	forward 2	TM	Non-Cytosolic
301	LI:2118151.15:2001MAY17	410	429	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	430	441	forward 2	TM	Cytosolic
301	LI:2118151.15:2001MAY17	442	464	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	465	467	forward 2	TM	Non-Cytosolic
301	LI:2118151.15:2001MAY17	468	490	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	491	509	forward 2	TM	Cytosolic
301	LI:2118151.15:2001MAY17	510	529	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	530	543	forward 2	TM	Non-Cytosolic
301	LI:2118151.15:2001MAY17	544	566	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	567	755	forward 2	TM	Cytosolic
301	LI:2118151.15:2001MAY17	756	778	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	779	2202	forward 2	TM	Non-Cytosolic
301	LI:2118151.15:2001MAY17	2203	2225	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	2226	2231	forward 2	TM	Cytosolic
301	LI:2118151.15:2001MAY17	2232	2254	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	2255	2268	forward 2	TM	Non-Cytosolic
301	LI:2118151.15:2001MAY17	2269	2291	forward 2	TM	Transmembrane
301	LI:2118151.15:2001MAY17	2292	2293	forward 2	TM	Cytosolic
302	LI:2118324.9:2001MAY17	1	338	forward 1	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	339	361	forward 1	TM	Transmembrane
302	LI:2118324.9:2001MAY17	362	380	forward 1	TM	Cytosolic
302	LI:2118324.9:2001MAY17	381	403	forward 1	TM	Transmembrane
302	LI:2118324.9:2001MAY17	404	412	forward 1	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	413	435	forward 1	TM	Transmembrane
302	LI:2118324.9:2001MAY17	436	580	forward 1	TM	Cytosolic
302	LI:2118324.9:2001MAY17	581	603	forward 1	TM	Transmembrane
302	LI:2118324.9:2001MAY17	604	612	forward 1	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	613	635	forward 1	TM	Transmembrane
302	LI:2118324.9:2001MAY17	636	836	forward 1	TM	Cytosolic
302	LI:2118324.9:2001MAY17	837	855	forward 1	TM	Transmembrane
302	LI:2118324.9:2001MAY17	856	1153	forward 1	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	1154	1176	forward 1	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1177	1200	forward 1	TM	Cytosolic
302	LI:2118324.9:2001MAY17	1201	1223	forward 1	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1224	1242	forward 1	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	1243	1265	forward 1	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1266	1518	forward 1	TM	Cytosolic
302	LI:2118324.9:2001MAY17	1519	1541	forward 1	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1542	1578	forward 1	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	1	4	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
302	LI:2118324.9:2001MAY17	5	27	forward 2	TM	Transmembrane
302	LI:2118324.9:2001MAY17	28	334	forward 2	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	335	357	forward 2	TM	Transmembrane
302	LI:2118324.9:2001MAY17	358	392	forward 2	TM	Cytosolic
302	LI:2118324.9:2001MAY17	393	415	forward 2	TM	Transmembrane
302	LI:2118324.9:2001MAY17	416	491	forward 2	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	492	514	forward 2	TM	Transmembrane
302	LI:2118324.9:2001MAY17	515	534	forward 2	TM	Cytosolic
302	LI:2118324.9:2001MAY17	535	557	forward 2	TM	Transmembrane
302	LI:2118324.9:2001MAY17	558	585	forward 2	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	586	608	forward 2	TM	Transmembrane
302	LI:2118324.9:2001MAY17	609	614	forward 2	TM	Cytosolic
302	LI:2118324.9:2001MAY17	615	637	forward 2	TM	Transmembrane
302	LI:2118324.9:2001MAY17	638	1154	forward 2	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	1155	1177	forward 2	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1178	1224	forward 2	TM	Cytosolic
302	LI:2118324.9:2001MAY17	1225	1247	forward 2	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1248	1578	forward 2	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	1	152	forward 3	TM	Cytosolic
302	LI:2118324.9:2001MAY17	153	175	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	176	206	forward 3	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	207	229	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	230	334	forward 3	TM	Cytosolic
302	LI:2118324.9:2001MAY17	335	357	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	358	410	forward 3	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	411	433	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	434	535	forward 3	TM	Cytosolic
302	LI:2118324.9:2001MAY17	536	558	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	559	592	forward 3	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	593	615	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	616	838	forward 3	TM	Cytosolic
302	LI:2118324.9:2001MAY17	839	861	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	862	890	forward 3	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	891	910	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	911	1094	forward 3	TM	Cytosolic
302	LI:2118324.9:2001MAY17	1095	1117	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1118	1141	forward 3	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	1142	1164	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1165	1225	forward 3	TM	Cytosolic
302	LI:2118324.9:2001MAY17	1226	1248	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1249	1267	forward 3	TM	Non-Cytosolic
302	LI:2118324.9:2001MAY17	1268	1290	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1291	1512	forward 3	TM	Cytosolic
302	LI:2118324.9:2001MAY17	1513	1535	forward 3	TM	Transmembrane
302	LI:2118324.9:2001MAY17	1536	1577	forward 3	TM	Non-Cytosolic
303	LI:2118368.12:2001MAY17	1	50	forward 2	TM	Non-Cytosolic
303	LI:2118368.12:2001MAY17	51	73	forward 2	TM	Transmembrane
303	LI:2118368.12:2001MAY17	74	84	forward 2	TM	Cytosolic
303	LI:2118368.12:2001MAY17	85	107	forward 2	TM	Transmembrane
303	LI:2118368.12:2001MAY17	108	121	forward 2	TM	Non-Cytosolic
303	LI:2118368.12:2001MAY17	122	144	forward 2	TM	Transmembrane
303	LI:2118368.12:2001MAY17	145	171	forward 2	TM	Cytosolic
303	LI:2118368.12:2001MAY17	172	194	forward 2	TM	Transmembrane
303	LI:2118368.12:2001MAY17	195	452	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
303	LI:2118368.12:2001MAY17	1	53	forward 3	TM	Cytosolic
303	LI:2118368.12:2001MAY17	54	76	forward 3	TM	Transmembrane
303	LI:2118368.12:2001MAY17	77	452	forward 3	TM	Non-Cytosolic
304	LI:2119448.5:2001MAY17	1	220	forward 3	TM	Cytosolic
304	LI:2119448.5:2001MAY17	221	243	forward 3	TM	Transmembrane
304	LI:2119448.5:2001MAY17	244	262	forward 3	TM	Non-Cytosolic
304	LI:2119448.5:2001MAY17	263	285	forward 3	TM	Transmembrane
304	LI:2119448.5:2001MAY17	286	393	forward 3	TM	Cytosolic
304	LI:2119448.5:2001MAY17	394	416	forward 3	TM	Transmembrane
304	LI:2119448.5:2001MAY17	417	1120	forward 3	TM	Non-Cytosolic
305	LI:212023.7:2001MAY17	1	69	forward 2	TM	Cytosolic
305	LI:212023.7:2001MAY17	70	92	forward 2	TM	Transmembrane
305	LI:212023.7:2001MAY17	93	106	forward 2	TM	Non-Cytosolic
305	LI:212023.7:2001MAY17	107	129	forward 2	TM	Transmembrane
305	LI:212023.7:2001MAY17	130	140	forward 2	TM	Cytosolic
305	LI:212023.7:2001MAY17	141	158	forward 2	TM	Transmembrane
305	LI:212023.7:2001MAY17	159	172	forward 2	TM	Non-Cytosolic
305	LI:212023.7:2001MAY17	173	195	forward 2	TM	Transmembrane
305	LI:212023.7:2001MAY17	196	491	forward 2	TM	Cytosolic
306	LI:2120556.1:2001MAY17	1	99	forward 3	TM	Cytosolic
306	LI:2120556.1:2001MAY17	100	122	forward 3	TM	Transmembrane
306	LI:2120556.1:2001MAY17	123	386	forward 3	TM	Non-Cytosolic
307	LI:2121577.3:2001MAY17	1	73	forward 1	TM	Cytosolic
308	LI:2123395.11:2001MAY17	1	364	forward 1	TM	Non-Cytosolic
308	LI:2123395.11:2001MAY17	365	387	forward 1	TM	Transmembrane
308	LI:2123395.11:2001MAY17	388	457	forward 1	TM	Cytosolic
308	LI:2123395.11:2001MAY17	458	480	forward 1	TM	Transmembrane
308	LI:2123395.11:2001MAY17	481	588	forward 1	TM	Non-Cytosolic
308	LI:2123395.11:2001MAY17	589	611	forward 1	TM	Transmembrane
308	LI:2123395.11:2001MAY17	612	707	forward 1	TM	Cytosolic
308	LI:2123395.11:2001MAY17	708	730	forward 1	TM	Transmembrane
308	LI:2123395.11:2001MAY17	731	775	forward 1	TM	Non-Cytosolic
308	LI:2123395.11:2001MAY17	776	798	forward 1	TM	Transmembrane
308	LI:2123395.11:2001MAY17	799	883	forward 1	TM	Cytosolic
308	LI:2123395.11:2001MAY17	1	535	forward 2	TM	Non-Cytosolic
308	LI:2123395.11:2001MAY17	536	558	forward 2	TM	Transmembrane
308	LI:2123395.11:2001MAY17	559	578	forward 2	TM	Cytosolic
308	LI:2123395.11:2001MAY17	579	601	forward 2	TM	Transmembrane
308	LI:2123395.11:2001MAY17	602	665	forward 2	TM	Non-Cytosolic
308	LI:2123395.11:2001MAY17	666	688	forward 2	TM	Transmembrane
308	LI:2123395.11:2001MAY17	689	707	forward 2	TM	Cytosolic
308	LI:2123395.11:2001MAY17	708	730	forward 2	TM	Transmembrane
308	LI:2123395.11:2001MAY17	731	749	forward 2	TM	Non-Cytosolic
308	LI:2123395.11:2001MAY17	750	772	forward 2	TM	Transmembrane
308	LI:2123395.11:2001MAY17	773	882	forward 2	TM	Cytosolic
308	LI:2123395.11:2001MAY17	1	369	forward 3	TM	Non-Cytosolic
308	LI:2123395.11:2001MAY17	370	392	forward 3	TM	Transmembrane
308	LI:2123395.11:2001MAY17	393	437	forward 3	TM	Cytosolic
308	LI:2123395.11:2001MAY17	438	460	forward 3	TM	Transmembrane
308	LI:2123395.11:2001MAY17	461	882	forward 3	TM	Non-Cytosolic
309	LI:2123452.9:2001MAY17	1	462	forward 1	TM	Non-Cytosolic
309	LI:2123452.9:2001MAY17	463	485	forward 1	TM	Transmembrane
309	LI:2123452.9:2001MAY17	486	497	forward 1	TM	Cytosolic
309	LI:2123452.9:2001MAY17	498	520	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
309	LI:2123452.9:2001MAY17	521	534	forward 1	TM	Non-Cytosolic
309	LI:2123452.9:2001MAY17	535	552	forward 1	TM	Transmembrane
309	LI:2123452.9:2001MAY17	553	556	forward 1	TM	Cytosolic
309	LI:2123452.9:2001MAY17	557	574	forward 1	TM	Transmembrane
309	LI:2123452.9:2001MAY17	575	583	forward 1	TM	Non-Cytosolic
309	LI:2123452.9:2001MAY17	584	606	forward 1	TM	Transmembrane
309	LI:2123452.9:2001MAY17	607	686	forward 1	TM	Cytosolic
309	LI:2123452.9:2001MAY17	1	468	forward 2	TM	Non-Cytosolic
309	LI:2123452.9:2001MAY17	469	491	forward 2	TM	Transmembrane
309	LI:2123452.9:2001MAY17	492	551	forward 2	TM	Cytosolic
309	LI:2123452.9:2001MAY17	552	574	forward 2	TM	Transmembrane
309	LI:2123452.9:2001MAY17	575	583	forward 2	TM	Non-Cytosolic
309	LI:2123452.9:2001MAY17	584	606	forward 2	TM	Transmembrane
309	LI:2123452.9:2001MAY17	607	657	forward 2	TM	Cytosolic
309	LI:2123452.9:2001MAY17	658	680	forward 2	TM	Transmembrane
309	LI:2123452.9:2001MAY17	681	686	forward 2	TM	Non-Cytosolic
309	LI:2123452.9:2001MAY17	1	389	forward 3	TM	Non-Cytosolic
309	LI:2123452.9:2001MAY17	390	408	forward 3	TM	Transmembrane
309	LI:2123452.9:2001MAY17	409	428	forward 3	TM	Cytosolic
309	LI:2123452.9:2001MAY17	429	448	forward 3	TM	Transmembrane
309	LI:2123452.9:2001MAY17	449	457	forward 3	TM	Non-Cytosolic
309	LI:2123452.9:2001MAY17	458	480	forward 3	TM	Transmembrane
309	LI:2123452.9:2001MAY17	481	484	forward 3	TM	Cytosolic
309	LI:2123452.9:2001MAY17	485	507	forward 3	TM	Transmembrane
309	LI:2123452.9:2001MAY17	508	685	forward 3	TM	Non-Cytosolic
310	LI:2164109.1:2001MAY17	1	20	forward 1	TM	Cytosolic
310	LI:2164109.1:2001MAY17	21	43	forward 1	TM	Transmembrane
310	LI:2164109.1:2001MAY17	44	127	forward 1	TM	Non-Cytosolic
310	LI:2164109.1:2001MAY17	128	150	forward 1	TM	Transmembrane
310	LI:2164109.1:2001MAY17	151	154	forward 1	TM	Cytosolic
310	LI:2164109.1:2001MAY17	1	12	forward 3	TM	Cytosolic
310	LI:2164109.1:2001MAY17	13	35	forward 3	TM	Transmembrane
310	LI:2164109.1:2001MAY17	36	153	forward 3	TM	Non-Cytosolic
311	LI:2168320.1:2001MAY17	1	9	forward 2	TM	Non-Cytosolic
311	LI:2168320.1:2001MAY17	10	32	forward 2	TM	Transmembrane
311	LI:2168320.1:2001MAY17	33	38	forward 2	TM	Cytosolic
311	LI:2168320.1:2001MAY17	39	61	forward 2	TM	Transmembrane
311	LI:2168320.1:2001MAY17	62	123	forward 2	TM	Non-Cytosolic
311	LI:2168320.1:2001MAY17	124	146	forward 2	TM	Transmembrane
311	LI:2168320.1:2001MAY17	147	172	forward 2	TM	Cytosolic
311	LI:2168320.1:2001MAY17	1	9	forward 3	TM	Non-Cytosolic
311	LI:2168320.1:2001MAY17	10	32	forward 3	TM	Transmembrane
311	LI:2168320.1:2001MAY17	33	172	forward 3	TM	Cytosolic
312	LI:2173577.1:2001MAY17	1	30	forward 1	TM	Non-Cytosolic
312	LI:2173577.1:2001MAY17	31	53	forward 1	TM	Transmembrane
312	LI:2173577.1:2001MAY17	54	65	forward 1	TM	Cytosolic
312	LI:2173577.1:2001MAY17	66	88	forward 1	TM	Transmembrane
312	LI:2173577.1:2001MAY17	89	92	forward 1	TM	Non-Cytosolic
312	LI:2173577.1:2001MAY17	93	115	forward 1	TM	Transmembrane
312	LI:2173577.1:2001MAY17	116	194	forward 1	TM	Cytosolic
312	LI:2173577.1:2001MAY17	1	37	forward 2	TM	Cytosolic
312	LI:2173577.1:2001MAY17	38	57	forward 2	TM	Transmembrane
312	LI:2173577.1:2001MAY17	58	66	forward 2	TM	Non-Cytosolic
312	LI:2173577.1:2001MAY17	67	89	forward 2	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
312	LI:2173577.1:2001MAY17	90	193	forward 2	TM	Cytosolic
312	LI:2173577.1:2001MAY17	1	43	forward 3	TM	Cytosolic
312	LI:2173577.1:2001MAY17	44	66	forward 3	TM	Transmembrane
312	LI:2173577.1:2001MAY17	67	75	forward 3	TM	Non-Cytosolic
312	LI:2173577.1:2001MAY17	76	98	forward 3	TM	Transmembrane
312	LI:2173577.1:2001MAY17	99	193	forward 3	TM	Cytosolic
313	LI:2179256.1:2001MAY17	1	41	forward 2	TM	Cytosolic
313	LI:2179256.1:2001MAY17	42	64	forward 2	TM	Transmembrane
313	LI:2179256.1:2001MAY17	65	210	forward 2	TM	Non-Cytosolic
314	LI:2180388.1:2001MAY17	1	118	forward 2	TM	Non-Cytosolic
314	LI:2180388.1:2001MAY17	119	141	forward 2	TM	Transmembrane
314	LI:2180388.1:2001MAY17	142	215	forward 2	TM	Cytosolic
315	LI:2199713.8:2001MAY17	1	553	forward 2	TM	Non-Cytosolic
315	LI:2199713.8:2001MAY17	554	571	forward 2	TM	Transmembrane
315	LI:2199713.8:2001MAY17	572	590	forward 2	TM	Cytosolic
316	LI:2200587.2:2001MAY17	1	4	forward 1	TM	Cytosolic
316	LI:2200587.2:2001MAY17	5	27	forward 1	TM	Transmembrane
316	LI:2200587.2:2001MAY17	28	36	forward 1	TM	Non-Cytosolic
316	LI:2200587.2:2001MAY17	37	56	forward 1	TM	Transmembrane
316	LI:2200587.2:2001MAY17	57	62	forward 1	TM	Cytosolic
316	LI:2200587.2:2001MAY17	63	85	forward 1	TM	Transmembrane
316	LI:2200587.2:2001MAY17	86	88	forward 1	TM	Non-Cytosolic
316	LI:2200587.2:2001MAY17	89	111	forward 1	TM	Transmembrane
316	LI:2200587.2:2001MAY17	112	119	forward 1	TM	Cytosolic
316	LI:2200587.2:2001MAY17	120	142	forward 1	TM	Transmembrane
316	LI:2200587.2:2001MAY17	143	146	forward 1	TM	Non-Cytosolic
316	LI:2200587.2:2001MAY17	147	169	forward 1	TM	Transmembrane
316	LI:2200587.2:2001MAY17	170	176	forward 1	TM	Cytosolic
316	LI:2200587.2:2001MAY17	1	22	forward 2	TM	Non-Cytosolic
316	LI:2200587.2:2001MAY17	23	45	forward 2	TM	Transmembrane
316	LI:2200587.2:2001MAY17	46	53	forward 2	TM	Cytosolic
316	LI:2200587.2:2001MAY17	54	76	forward 2	TM	Transmembrane
316	LI:2200587.2:2001MAY17	77	90	forward 2	TM	Non-Cytosolic
316	LI:2200587.2:2001MAY17	91	113	forward 2	TM	Transmembrane
316	LI:2200587.2:2001MAY17	114	125	forward 2	TM	Cytosolic
316	LI:2200587.2:2001MAY17	126	148	forward 2	TM	Transmembrane
316	LI:2200587.2:2001MAY17	149	176	forward 2	TM	Non-Cytosolic
316	LI:2200587.2:2001MAY17	1	14	forward 3	TM	Non-Cytosolic
316	LI:2200587.2:2001MAY17	15	37	forward 3	TM	Transmembrane
316	LI:2200587.2:2001MAY17	38	43	forward 3	TM	Cytosolic
316	LI:2200587.2:2001MAY17	44	63	forward 3	TM	Transmembrane
316	LI:2200587.2:2001MAY17	64	72	forward 3	TM	Non-Cytosolic
316	LI:2200587.2:2001MAY17	73	95	forward 3	TM	Transmembrane
316	LI:2200587.2:2001MAY17	96	101	forward 3	TM	Cytosolic
316	LI:2200587.2:2001MAY17	102	124	forward 3	TM	Transmembrane
316	LI:2200587.2:2001MAY17	125	143	forward 3	TM	Non-Cytosolic
316	LI:2200587.2:2001MAY17	144	166	forward 3	TM	Transmembrane
316	LI:2200587.2:2001MAY17	167	176	forward 3	TM	Cytosolic
317	LI:2200761.12:2001MAY17	1	3	forward 1	TM	Non-Cytosolic
317	LI:2200761.12:2001MAY17	4	26	forward 1	TM	Transmembrane
317	LI:2200761.12:2001MAY17	27	343	forward 1	TM	Cytosolic
317	LI:2200761.12:2001MAY17	344	366	forward 1	TM	Transmembrane
317	LI:2200761.12:2001MAY17	367	374	forward 1	TM	Non-Cytosolic
317	LI:2200761.12:2001MAY17	1	346	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
317	LI:2200761.12:2001MAY17	347	369	forward 2	TM	Transmembrane
317	LI:2200761.12:2001MAY17	370	374	forward 2	TM	Cytosolic
317	LI:2200761.12:2001MAY17	1	299	forward 3	TM	Non-Cytosolic
317	LI:2200761.12:2001MAY17	300	322	forward 3	TM	Transmembrane
317	LI:2200761.12:2001MAY17	323	342	forward 3	TM	Cytosolic
317	LI:2200761.12:2001MAY17	343	365	forward 3	TM	Transmembrane
317	LI:2200761.12:2001MAY17	366	373	forward 3	TM	Non-Cytosolic
318	LI:2203624.1:2001MAY17	1	139	forward 1	TM	Cytosolic
318	LI:2203624.1:2001MAY17	140	156	forward 1	TM	Transmembrane
318	LI:2203624.1:2001MAY17	157	226	forward 1	TM	Non-Cytosolic
318	LI:2203624.1:2001MAY17	227	249	forward 1	TM	Transmembrane
318	LI:2203624.1:2001MAY17	250	376	forward 1	TM	Cytosolic
319	LI:220495.9:2001MAY17	1	40	forward 2	TM	Non-Cytosolic
319	LI:220495.9:2001MAY17	41	63	forward 2	TM	Transmembrane
319	LI:220495.9:2001MAY17	64	163	forward 2	TM	Cytosolic
319	LI:220495.9:2001MAY17	164	183	forward 2	TM	Transmembrane
319	LI:220495.9:2001MAY17	184	192	forward 2	TM	Non-Cytosolic
319	LI:220495.9:2001MAY17	193	210	forward 2	TM	Transmembrane
319	LI:220495.9:2001MAY17	211	247	forward 2	TM	Cytosolic
319	LI:220495.9:2001MAY17	248	270	forward 2	TM	Transmembrane
319	LI:220495.9:2001MAY17	271	284	forward 2	TM	Non-Cytosolic
319	LI:220495.9:2001MAY17	285	307	forward 2	TM	Transmembrane
319	LI:220495.9:2001MAY17	308	451	forward 2	TM	Cytosolic
319	LI:220495.9:2001MAY17	452	474	forward 2	TM	Transmembrane
319	LI:220495.9:2001MAY17	475	931	forward 2	TM	Non-Cytosolic
319	LI:220495.9:2001MAY17	932	954	forward 2	TM	Transmembrane
319	LI:220495.9:2001MAY17	955	973	forward 2	TM	Cytosolic
319	LI:220495.9:2001MAY17	974	996	forward 2	TM	Transmembrane
319	LI:220495.9:2001MAY17	997	1034	forward 2	TM	Non-Cytosolic
319	LI:220495.9:2001MAY17	1	25	forward 3	TM	Non-Cytosolic
319	LI:220495.9:2001MAY17	26	48	forward 3	TM	Transmembrane
319	LI:220495.9:2001MAY17	49	453	forward 3	TM	Cytosolic
319	LI:220495.9:2001MAY17	454	472	forward 3	TM	Transmembrane
319	LI:220495.9:2001MAY17	473	491	forward 3	TM	Non-Cytosolic
319	LI:220495.9:2001MAY17	492	514	forward 3	TM	Transmembrane
319	LI:220495.9:2001MAY17	515	574	forward 3	TM	Cytosolic
319	LI:220495.9:2001MAY17	575	597	forward 3	TM	Transmembrane
319	LI:220495.9:2001MAY17	598	606	forward 3	TM	Non-Cytosolic
319	LI:220495.9:2001MAY17	607	629	forward 3	TM	Transmembrane
319	LI:220495.9:2001MAY17	630	931	forward 3	TM	Cytosolic
319	LI:220495.9:2001MAY17	932	954	forward 3	TM	Transmembrane
319	LI:220495.9:2001MAY17	955	1033	forward 3	TM	Non-Cytosolic
320	LI:2205532.1:2001MAY17	1	28	forward 1	TM	Non-Cytosolic
320	LI:2205532.1:2001MAY17	29	51	forward 1	TM	Transmembrane
320	LI:2205532.1:2001MAY17	52	70	forward 1	TM	Cytosolic
320	LI:2205532.1:2001MAY17	71	90	forward 1	TM	Transmembrane
320	LI:2205532.1:2001MAY17	91	99	forward 1	TM	Non-Cytosolic
320	LI:2205532.1:2001MAY17	100	122	forward 1	TM	Transmembrane
320	LI:2205532.1:2001MAY17	123	155	forward 1	TM	Cytosolic
320	LI:2205532.1:2001MAY17	156	178	forward 1	TM	Transmembrane
320	LI:2205532.1:2001MAY17	179	210	forward 1	TM	Non-Cytosolic
320	LI:2205532.1:2001MAY17	211	230	forward 1	TM	Transmembrane
320	LI:2205532.1:2001MAY17	231	250	forward 1	TM	Cytosolic
320	LI:2205532.1:2001MAY17	251	273	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
320	LI:2205532.1:2001MAY17	274	367	forward 1	TM	Non-Cytosolic
320	LI:2205532.1:2001MAY17	368	390	forward 1	TM	Transmembrane
320	LI:2205532.1:2001MAY17	391	407	forward 1	TM	Cytosolic
320	LI:2205532.1:2001MAY17	1	30	forward 2	TM	Cytosolic
320	LI:2205532.1:2001MAY17	31	53	forward 2	TM	Transmembrane
320	LI:2205532.1:2001MAY17	54	96	forward 2	TM	Non-Cytosolic
320	LI:2205532.1:2001MAY17	97	119	forward 2	TM	Transmembrane
320	LI:2205532.1:2001MAY17	120	243	forward 2	TM	Cytosolic
320	LI:2205532.1:2001MAY17	244	266	forward 2	TM	Transmembrane
320	LI:2205532.1:2001MAY17	267	275	forward 2	TM	Non-Cytosolic
320	LI:2205532.1:2001MAY17	276	293	forward 2	TM	Transmembrane
320	LI:2205532.1:2001MAY17	294	406	forward 2	TM	Cytosolic
320	LI:2205532.1:2001MAY17	1	35	forward 3	TM	Cytosolic
320	LI:2205532.1:2001MAY17	36	58	forward 3	TM	Transmembrane
320	LI:2205532.1:2001MAY17	59	82	forward 3	TM	Non-Cytosolic
320	LI:2205532.1:2001MAY17	83	102	forward 3	TM	Transmembrane
320	LI:2205532.1:2001MAY17	103	106	forward 3	TM	Cytosolic
320	LI:2205532.1:2001MAY17	107	129	forward 3	TM	Transmembrane
320	LI:2205532.1:2001MAY17	130	148	forward 3	TM	Non-Cytosolic
320	LI:2205532.1:2001MAY17	149	171	forward 3	TM	Transmembrane
320	LI:2205532.1:2001MAY17	172	244	forward 3	TM	Cytosolic
320	LI:2205532.1:2001MAY17	245	267	forward 3	TM	Transmembrane
320	LI:2205532.1:2001MAY17	268	406	forward 3	TM	Non-Cytosolic
321	LI:2206277.1:2001MAY17	1	246	forward 1	TM	Cytosolic
321	LI:2206277.1:2001MAY17	247	269	forward 1	TM	Transmembrane
321	LI:2206277.1:2001MAY17	270	283	forward 1	TM	Non-Cytosolic
321	LI:2206277.1:2001MAY17	284	306	forward 1	TM	Transmembrane
321	LI:2206277.1:2001MAY17	307	367	forward 1	TM	Cytosolic
322	LI:2207765.8:2001MAY17	1	6	forward 3	TM	Cytosolic
322	LI:2207765.8:2001MAY17	7	29	forward 3	TM	Transmembrane
322	LI:2207765.8:2001MAY17	30	384	forward 3	TM	Non-Cytosolic
323	LI:2208404.4:2001MAY17	1	44	forward 3	TM	Non-Cytosolic
323	LI:2208404.4:2001MAY17	45	64	forward 3	TM	Transmembrane
323	LI:2208404.4:2001MAY17	65	114	forward 3	TM	Cytosolic
324	LI:2208715.3:2001MAY17	1	237	forward 1	TM	Cytosolic
325	LI:2208766.2:2001MAY17	1	28	forward 1	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	29	48	forward 1	TM	Transmembrane
325	LI:2208766.2:2001MAY17	49	272	forward 1	TM	Cytosolic
325	LI:2208766.2:2001MAY17	273	295	forward 1	TM	Transmembrane
325	LI:2208766.2:2001MAY17	296	309	forward 1	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	310	332	forward 1	TM	Transmembrane
325	LI:2208766.2:2001MAY17	333	369	forward 1	TM	Cytosolic
325	LI:2208766.2:2001MAY17	370	387	forward 1	TM	Transmembrane
325	LI:2208766.2:2001MAY17	388	396	forward 1	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	397	419	forward 1	TM	Transmembrane
325	LI:2208766.2:2001MAY17	420	535	forward 1	TM	Cytosolic
325	LI:2208766.2:2001MAY17	536	558	forward 1	TM	Transmembrane
325	LI:2208766.2:2001MAY17	559	577	forward 1	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	578	597	forward 1	TM	Transmembrane
325	LI:2208766.2:2001MAY17	598	731	forward 1	TM	Cytosolic
325	LI:2208766.2:2001MAY17	732	751	forward 1	TM	Transmembrane
325	LI:2208766.2:2001MAY17	752	779	forward 1	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	780	802	forward 1	TM	Transmembrane
325	LI:2208766.2:2001MAY17	803	835	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
325	LI:2208766.2:2001MAY17	1	43	forward 2	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	44	66	forward 2	TM	Transmembrane
325	LI:2208766.2:2001MAY17	67	78	forward 2	TM	Cytosolic
325	LI:2208766.2:2001MAY17	79	101	forward 2	TM	Transmembrane
325	LI:2208766.2:2001MAY17	102	197	forward 2	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	198	220	forward 2	TM	Transmembrane
325	LI:2208766.2:2001MAY17	221	272	forward 2	TM	Cytosolic
325	LI:2208766.2:2001MAY17	273	295	forward 2	TM	Transmembrane
325	LI:2208766.2:2001MAY17	296	309	forward 2	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	310	332	forward 2	TM	Transmembrane
325	LI:2208766.2:2001MAY17	333	518	forward 2	TM	Cytosolic
325	LI:2208766.2:2001MAY17	519	541	forward 2	TM	Transmembrane
325	LI:2208766.2:2001MAY17	542	550	forward 2	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	551	573	forward 2	TM	Transmembrane
325	LI:2208766.2:2001MAY17	574	690	forward 2	TM	Cytosolic
325	LI:2208766.2:2001MAY17	691	713	forward 2	TM	Transmembrane
325	LI:2208766.2:2001MAY17	714	727	forward 2	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	728	750	forward 2	TM	Transmembrane
325	LI:2208766.2:2001MAY17	751	834	forward 2	TM	Cytosolic
325	LI:2208766.2:2001MAY17	1	267	forward 3	TM	Non-Cytosolic
325	LI:2208766.2:2001MAY17	268	290	forward 3	TM	Transmembrane
325	LI:2208766.2:2001MAY17	291	296	forward 3	TM	Cytosolic
325	LI:2208766.2:2001MAY17	297	319	forward 3	TM	Transmembrane
325	LI:2208766.2:2001MAY17	320	834	forward 3	TM	Non-Cytosolic
326	LI:2209636.3:2001MAY17	1	154	forward 1	TM	Cytosolic
326	LI:2209636.3:2001MAY17	155	177	forward 1	TM	Transmembrane
326	LI:2209636.3:2001MAY17	178	207	forward 1	TM	Non-Cytosolic
326	LI:2209636.3:2001MAY17	208	230	forward 1	TM	Transmembrane
326	LI:2209636.3:2001MAY17	231	375	forward 1	TM	Cytosolic
326	LI:2209636.3:2001MAY17	376	395	forward 1	TM	Transmembrane
326	LI:2209636.3:2001MAY17	396	443	forward 1	TM	Non-Cytosolic
326	LI:2209636.3:2001MAY17	444	466	forward 1	TM	Transmembrane
326	LI:2209636.3:2001MAY17	467	472	forward 1	TM	Cytosolic
326	LI:2209636.3:2001MAY17	473	495	forward 1	TM	Transmembrane
326	LI:2209636.3:2001MAY17	496	498	forward 1	TM	Non-Cytosolic
326	LI:2209636.3:2001MAY17	499	521	forward 1	TM	Transmembrane
326	LI:2209636.3:2001MAY17	522	527	forward 1	TM	Cytosolic
326	LI:2209636.3:2001MAY17	528	550	forward 1	TM	Transmembrane
326	LI:2209636.3:2001MAY17	551	616	forward 1	TM	Non-Cytosolic
326	LI:2209636.3:2001MAY17	1	20	forward 3	TM	Cytosolic
326	LI:2209636.3:2001MAY17	21	43	forward 3	TM	Transmembrane
326	LI:2209636.3:2001MAY17	44	196	forward 3	TM	Non-Cytosolic
326	LI:2209636.3:2001MAY17	197	219	forward 3	TM	Transmembrane
326	LI:2209636.3:2001MAY17	220	319	forward 3	TM	Cytosolic
326	LI:2209636.3:2001MAY17	320	342	forward 3	TM	Transmembrane
326	LI:2209636.3:2001MAY17	343	425	forward 3	TM	Non-Cytosolic
326	LI:2209636.3:2001MAY17	426	448	forward 3	TM	Transmembrane
326	LI:2209636.3:2001MAY17	449	467	forward 3	TM	Cytosolic
326	LI:2209636.3:2001MAY17	468	490	forward 3	TM	Transmembrane
326	LI:2209636.3:2001MAY17	491	499	forward 3	TM	Non-Cytosolic
326	LI:2209636.3:2001MAY17	500	522	forward 3	TM	Transmembrane
326	LI:2209636.3:2001MAY17	523	616	forward 3	TM	Cytosolic
327	LI:221864.68:2001MAY17	1	183	forward 1	TM	Cytosolic
328	LI:229267.1:2001MAY17	1	294	forward 3	TM	Non-Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
328	LI:229267.1:2001MAY17	295	317	forward 3	TM	Transmembrane
328	LI:229267.1:2001MAY17	318	570	forward 3	TM	Cytosolic
328	LI:229267.1:2001MAY17	571	593	forward 3	TM	Transmembrane
328	LI:229267.1:2001MAY17	594	927	forward 3	TM	Non-Cytosolic
329	LI:229648.2:2001MAY17	1	539	forward 2	TM	Non-Cytosolic
329	LI:229648.2:2001MAY17	540	562	forward 2	TM	Transmembrane
329	LI:229648.2:2001MAY17	563	751	forward 2	TM	Cytosolic
329	LI:229648.2:2001MAY17	752	774	forward 2	TM	Transmembrane
329	LI:229648.2:2001MAY17	775	779	forward 2	TM	Non-Cytosolic
329	LI:229648.2:2001MAY17	780	802	forward 2	TM	Transmembrane
329	LI:229648.2:2001MAY17	803	814	forward 2	TM	Cytosolic
329	LI:229648.2:2001MAY17	815	837	forward 2	TM	Transmembrane
329	LI:229648.2:2001MAY17	838	846	forward 2	TM	Non-Cytosolic
329	LI:229648.2:2001MAY17	847	869	forward 2	TM	Transmembrane
329	LI:229648.2:2001MAY17	870	891	forward 2	TM	Cytosolic
329	LI:229648.2:2001MAY17	1	657	forward 3	TM	Non-Cytosolic
329	LI:229648.2:2001MAY17	658	680	forward 3	TM	Transmembrane
329	LI:229648.2:2001MAY17	681	755	forward 3	TM	Cytosolic
329	LI:229648.2:2001MAY17	756	778	forward 3	TM	Transmembrane
329	LI:229648.2:2001MAY17	779	833	forward 3	TM	Non-Cytosolic
329	LI:229648.2:2001MAY17	834	856	forward 3	TM	Transmembrane
329	LI:229648.2:2001MAY17	857	891	forward 3	TM	Cytosolic
330	LI:231016.1:2001MAY17	1	14	forward 3	TM	Non-Cytosolic
330	LI:231016.1:2001MAY17	15	37	forward 3	TM	Transmembrane
330	LI:231016.1:2001MAY17	38	57	forward 3	TM	Cytosolic
330	LI:231016.1:2001MAY17	58	80	forward 3	TM	Transmembrane
330	LI:231016.1:2001MAY17	81	84	forward 3	TM	Non-Cytosolic
330	LI:231016.1:2001MAY17	85	107	forward 3	TM	Transmembrane
330	LI:231016.1:2001MAY17	108	201	forward 3	TM	Cytosolic
330	LI:231016.1:2001MAY17	202	224	forward 3	TM	Transmembrane
330	LI:231016.1:2001MAY17	225	360	forward 3	TM	Non-Cytosolic
331	LI:231140.5:2001MAY17	1	146	forward 2	TM	Non-Cytosolic
331	LI:231140.5:2001MAY17	147	169	forward 2	TM	Transmembrane
331	LI:231140.5:2001MAY17	170	223	forward 2	TM	Cytosolic
331	LI:231140.5:2001MAY17	224	246	forward 2	TM	Transmembrane
331	LI:231140.5:2001MAY17	247	250	forward 2	TM	Non-Cytosolic
331	LI:231140.5:2001MAY17	1	127	forward 3	TM	Cytosolic
331	LI:231140.5:2001MAY17	128	150	forward 3	TM	Transmembrane
331	LI:231140.5:2001MAY17	151	159	forward 3	TM	Non-Cytosolic
331	LI:231140.5:2001MAY17	160	178	forward 3	TM	Transmembrane
331	LI:231140.5:2001MAY17	179	249	forward 3	TM	Cytosolic
332	LI:231695.14:2001MAY17	1	148	forward 1	TM	Non-Cytosolic
332	LI:231695.14:2001MAY17	149	171	forward 1	TM	Transmembrane
332	LI:231695.14:2001MAY17	172	212	forward 1	TM	Cytosolic
333	LI:232846.24:2001MAY17	1	1167	forward 1	TM	Non-Cytosolic
333	LI:232846.24:2001MAY17	1168	1187	forward 1	TM	Transmembrane
333	LI:232846.24:2001MAY17	1188	1193	forward 1	TM	Cytosolic
333	LI:232846.24:2001MAY17	1194	1216	forward 1	TM	Transmembrane
333	LI:232846.24:2001MAY17	1217	1848	forward 1	TM	Non-Cytosolic
333	LI:232846.24:2001MAY17	1	1311	forward 2	TM	Non-Cytosolic
333	LI:232846.24:2001MAY17	1312	1334	forward 2	TM	Transmembrane
333	LI:232846.24:2001MAY17	1335	1449	forward 2	TM	Cytosolic
333	LI:232846.24:2001MAY17	1450	1472	forward 2	TM	Transmembrane
333	LI:232846.24:2001MAY17	1473	1848	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
333	LI:232846.24:2001MAY17	1	906	forward 3	TM	Non-Cytosolic
333	LI:232846.24:2001MAY17	907	929	forward 3	TM	Transmembrane
333	LI:232846.24:2001MAY17	930	1166	forward 3	TM	Cytosolic
333	LI:232846.24:2001MAY17	1167	1189	forward 3	TM	Transmembrane
333	LI:232846.24:2001MAY17	1190	1848	forward 3	TM	Non-Cytosolic
334	LI:233411.11:2001MAY17	1	1003	forward 1	TM	Non-Cytosolic
334	LI:233411.11:2001MAY17	1004	1026	forward 1	TM	Transmembrane
334	LI:233411.11:2001MAY17	1027	1055	forward 1	TM	Cytosolic
334	LI:233411.11:2001MAY17	1056	1078	forward 1	TM	Transmembrane
334	LI:233411.11:2001MAY17	1079	1092	forward 1	TM	Non-Cytosolic
334	LI:233411.11:2001MAY17	1093	1115	forward 1	TM	Transmembrane
334	LI:233411.11:2001MAY17	1116	1236	forward 1	TM	Cytosolic
334	LI:233411.11:2001MAY17	1	261	forward 2	TM	Non-Cytosolic
334	LI:233411.11:2001MAY17	262	284	forward 2	TM	Transmembrane
334	LI:233411.11:2001MAY17	285	360	forward 2	TM	Cytosolic
334	LI:233411.11:2001MAY17	361	383	forward 2	TM	Transmembrane
334	LI:233411.11:2001MAY17	384	1236	forward 2	TM	Non-Cytosolic
334	LI:233411.11:2001MAY17	1	345	forward 3	TM	Non-Cytosolic
334	LI:233411.11:2001MAY17	346	368	forward 3	TM	Transmembrane
334	LI:233411.11:2001MAY17	369	374	forward 3	TM	Cytosolic
334	LI:233411.11:2001MAY17	375	397	forward 3	TM	Transmembrane
334	LI:233411.11:2001MAY17	398	887	forward 3	TM	Non-Cytosolic
334	LI:233411.11:2001MAY17	888	910	forward 3	TM	Transmembrane
334	LI:233411.11:2001MAY17	911	922	forward 3	TM	Cytosolic
334	LI:233411.11:2001MAY17	923	945	forward 3	TM	Transmembrane
334	LI:233411.11:2001MAY17	946	959	forward 3	TM	Non-Cytosolic
334	LI:233411.11:2001MAY17	960	982	forward 3	TM	Transmembrane
334	LI:233411.11:2001MAY17	983	1050	forward 3	TM	Cytosolic
334	LI:233411.11:2001MAY17	1051	1073	forward 3	TM	Transmembrane
334	LI:233411.11:2001MAY17	1074	1092	forward 3	TM	Non-Cytosolic
334	LI:233411.11:2001MAY17	1093	1115	forward 3	TM	Transmembrane
334	LI:233411.11:2001MAY17	1116	1126	forward 3	TM	Cytosolic
334	LI:233411.11:2001MAY17	1127	1149	forward 3	TM	Transmembrane
334	LI:233411.11:2001MAY17	1150	1203	forward 3	TM	Non-Cytosolic
334	LI:233411.11:2001MAY17	1204	1223	forward 3	TM	Transmembrane
334	LI:233411.11:2001MAY17	1224	1235	forward 3	TM	Cytosolic
335	LI:233545.13:2001MAY17	1	506	forward 3	TM	Non-Cytosolic
335	LI:233545.13:2001MAY17	507	529	forward 3	TM	Transmembrane
335	LI:233545.13:2001MAY17	530	630	forward 3	TM	Cytosolic
336	LI:234671.101:2001MAY17	1	103	forward 1	TM	Cytosolic
336	LI:234671.101:2001MAY17	104	126	forward 1	TM	Transmembrane
336	LI:234671.101:2001MAY17	127	418	forward 1	TM	Non-Cytosolic
336	LI:234671.101:2001MAY17	1	288	forward 2	TM	Non-Cytosolic
336	LI:234671.101:2001MAY17	289	311	forward 2	TM	Transmembrane
336	LI:234671.101:2001MAY17	312	323	forward 2	TM	Cytosolic
336	LI:234671.101:2001MAY17	324	343	forward 2	TM	Transmembrane
336	LI:234671.101:2001MAY17	344	352	forward 2	TM	Non-Cytosolic
336	LI:234671.101:2001MAY17	353	375	forward 2	TM	Transmembrane
336	LI:234671.101:2001MAY17	376	418	forward 2	TM	Cytosolic
337	LI:236098.14:2001MAY17	1	34	forward 1	TM	Cytosolic
337	LI:236098.14:2001MAY17	35	57	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	58	71	forward 1	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	72	91	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	92	97	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
337	LI:236098.14:2001MAY17	98	117	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	118	127	forward 1	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	128	150	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	151	520	forward 1	TM	Cytosolic
337	LI:236098.14:2001MAY17	521	543	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	544	562	forward 1	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	563	585	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	586	591	forward 1	TM	Cytosolic
337	LI:236098.14:2001MAY17	592	614	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	615	628	forward 1	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	629	651	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	652	858	forward 1	TM	Cytosolic
337	LI:236098.14:2001MAY17	859	881	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	882	900	forward 1	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	901	923	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	924	976	forward 1	TM	Cytosolic
337	LI:236098.14:2001MAY17	977	999	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	1000	1008	forward 1	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	1009	1031	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	1032	1051	forward 1	TM	Cytosolic
337	LI:236098.14:2001MAY17	1052	1074	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	1075	1088	forward 1	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	1089	1111	forward 1	TM	Transmembrane
337	LI:236098.14:2001MAY17	1112	1124	forward 1	TM	Cytosolic
337	LI:236098.14:2001MAY17	1	19	forward 2	TM	Cytosolic
337	LI:236098.14:2001MAY17	20	39	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	40	65	forward 2	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	66	88	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	89	133	forward 2	TM	Cytosolic
337	LI:236098.14:2001MAY17	134	156	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	157	170	forward 2	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	171	188	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	189	215	forward 2	TM	Cytosolic
337	LI:236098.14:2001MAY17	216	235	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	236	244	forward 2	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	245	267	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	268	518	forward 2	TM	Cytosolic
337	LI:236098.14:2001MAY17	519	541	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	542	550	forward 2	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	551	573	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	574	593	forward 2	TM	Cytosolic
337	LI:236098.14:2001MAY17	594	616	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	617	635	forward 2	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	636	658	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	659	799	forward 2	TM	Cytosolic
337	LI:236098.14:2001MAY17	800	822	forward 2	TM	Transmembrane
337	LI:236098.14:2001MAY17	823	1124	forward 2	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	1	66	forward 3	TM	Cytosolic
337	LI:236098.14:2001MAY17	67	89	forward 3	TM	Transmembrane
337	LI:236098.14:2001MAY17	90	159	forward 3	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	160	182	forward 3	TM	Transmembrane
337	LI:236098.14:2001MAY17	183	245	forward 3	TM	Cytosolic
337	LI:236098.14:2001MAY17	246	268	forward 3	TM	Transmembrane
337	LI:236098.14:2001MAY17	269	389	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
337	LI:236098.14:2001MAY17	390	412	forward 3	TM	Transmembrane
337	LI:236098.14:2001MAY17	413	528	forward 3	TM	Cytosolic
337	LI:236098.14:2001MAY17	529	551	forward 3	TM	Transmembrane
337	LI:236098.14:2001MAY17	552	565	forward 3	TM	Non-Cytosolic
337	LI:236098.14:2001MAY17	566	583	forward 3	TM	Transmembrane
337	LI:236098.14:2001MAY17	584	587	forward 3	TM	Cytosolic
337	LI:236098.14:2001MAY17	588	610	forward 3	TM	Transmembrane
337	LI:236098.14:2001MAY17	611	1124	forward 3	TM	Non-Cytosolic
338	LI:236196.15:2001MAY17	1	267	forward 1	TM	Cytosolic
338	LI:236196.15:2001MAY17	268	287	forward 1	TM	Transmembrane
338	LI:236196.15:2001MAY17	288	301	forward 1	TM	Non-Cytosolic
338	LI:236196.15:2001MAY17	302	324	forward 1	TM	Transmembrane
338	LI:236196.15:2001MAY17	325	328	forward 1	TM	Cytosolic
338	LI:236196.15:2001MAY17	329	348	forward 1	TM	Transmembrane
338	LI:236196.15:2001MAY17	349	500	forward 1	TM	Non-Cytosolic
338	LI:236196.15:2001MAY17	501	523	forward 1	TM	Transmembrane
338	LI:236196.15:2001MAY17	524	589	forward 1	TM	Cytosolic
338	LI:236196.15:2001MAY17	590	612	forward 1	TM	Transmembrane
338	LI:236196.15:2001MAY17	613	613	forward 1	TM	Non-Cytosolic
338	LI:236196.15:2001MAY17	1	201	forward 2	TM	Cytosolic
338	LI:236196.15:2001MAY17	202	224	forward 2	TM	Transmembrane
338	LI:236196.15:2001MAY17	225	261	forward 2	TM	Non-Cytosolic
338	LI:236196.15:2001MAY17	262	281	forward 2	TM	Transmembrane
338	LI:236196.15:2001MAY17	282	300	forward 2	TM	Cytosolic
338	LI:236196.15:2001MAY17	301	323	forward 2	TM	Transmembrane
338	LI:236196.15:2001MAY17	324	502	forward 2	TM	Non-Cytosolic
338	LI:236196.15:2001MAY17	503	525	forward 2	TM	Transmembrane
338.	LI:236196.15:2001MAY17	526	545	forward 2	TM	Cytosolic
338	LI:236196.15:2001MAY17	546	568	forward 2	TM	Transmembrane
338	LI:236196.15:2001MAY17	569	613	forward 2	TM	Non-Cytosolic
338	LI:236196.15:2001MAY17	1	266	forward 3	TM	Cytosolic
338	LI:236196.15:2001MAY17	267	284	forward 3	TM	Transmembrane
338	LI:236196.15:2001MAY17	285	293	forward 3	TM	Non-Cytosolic
338	LI:236196.15:2001MAY17	294	316	forward 3	TM	Transmembrane
338	LI:236196.15:2001MAY17	317	483	forward 3	TM	Cytosolic
338	LI:236196.15:2001MAY17	484	506	forward 3	TM	Transmembrane
338	LI:236196.15:2001MAY17	507	558	forward 3	TM	Non-Cytosolic
338	LI:236196.15:2001MAY17	559	581	forward 3	TM	Transmembrane
338	LI:236196.15:2001MAY17	582	613	forward 3	TM	Cytosolic
339	LI:237086.1:2001MAY17	1	320	forward 2	TM	Non-Cytosolic
339	LI:237086.1:2001MAY17	321	343	forward 2	TM	Transmembrane
339	LI:237086.1:2001MAY17	344	379	forward 2	TM	Cytosolic
339	LI:237086.1:2001MAY17	1	182	forward 3	TM	Non-Cytosolic
339	LI:237086.1:2001MAY17	183	205	forward 3	TM	Transmembrane
339	LI:237086.1:2001MAY17	206	358	forward 3	TM	Cytosolic
339	LI:237086.1:2001MAY17	359	378	forward 3	TM	Transmembrane
339	LI:237086.1:2001MAY17	379	379	forward 3	TM	Non-Cytosolic
340	LI:238585.30:2001MAY17	1	108	forward 2	TM	Cytosolic
340	LI:238585.30:2001MAY17	109	131	forward 2	TM	Transmembrane
340	LI:238585.30:2001MAY17	132	134	forward 2	TM	Non-Cytosolic
340	LI:238585.30:2001MAY17	135	157	forward 2	TM	Transmembrane
340	LI:238585.30:2001MAY17	158	183	forward 2	TM	Cytosolic
340	LI:238585.30:2001MAY17	1	41	forward 3	TM	Non-Cytosolic
340	LI:238585.30:2001MAY17	42	64	forward 3	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
340	LI:238585.30:2001MAY17	65	102	forward 3	TM	Cytosolic
340	LI:238585.30:2001MAY17	103	125	forward 3	TM	Transmembrane
340	LI:238585.30:2001MAY17	126	139	forward 3	TM	Non-Cytosolic
340	LI:238585.30:2001MAY17	140	162	forward 3	TM	Transmembrane
340	LI:238585.30:2001MAY17	163	183	forward 3	TM	Cytosolic
341	LI:238672.6:2001MAY17	1	228	forward 3	TM	Non-Cytosolic
341	LI:238672.6:2001MAY17	229	251	forward 3	TM	Transmembrane
341	LI:238672.6:2001MAY17	252	279	forward 3	TM	Cytosolic
341	LI:238672.6:2001MAY17	280	301	forward 3	TM	Transmembrane
341	LI:238672.6:2001MAY17	302	320	forward 3	TM	Non-Cytosolic
341	LI:238672.6:2001MAY17.	321	343	forward 3	TM	Transmembrane
341	LI:238672.6:2001MAY17	344	373	forward 3	TM	Cytosolic
342	LI:239579.9:2001MAY17	1	685	forward 1	TM	Non-Cytosolic
342	LI:239579.9:2001MAY17	686	708	forward 1	TM	Transmembrane
342	LI:239579.9:2001MAY17	709	736	forward 1	TM	Cytosolic
342	LI:239579.9:2001MAY17	1	62	forward 2	TM	Cytosolic
342	LI:239579.9:2001MAY17	63	85	forward 2	TM	Transmembrane
342	LI:239579.9:2001MAY17	86	491	forward 2	TM	Non-Cytosolic
342	LI:239579.9:2001MAY17	492	514	forward 2	TM	Transmembrane
342	LI:239579.9:2001MAY17	515	687	forward 2	TM	Cytosolic
342	LI:239579.9:2001MAY17	688	710	forward 2	TM	Transmembrane
342	LI:239579.9:2001MAY17	711	736	forward 2	TM	Non-Cytosolic
342	LI:239579.9:2001MAY17	1	489	forward 3	TM	Non-Cytosolic
342	LI:239579.9:2001MAY17	490	512	forward 3	TM	Transmembrane
342	LI:239579.9:2001MAY17	513	531	forward 3	TM	Cytosolic
342	LI:239579.9:2001MAY17	532	554	forward 3	TM	Transmembrane
342	LI:239579.9:2001MAY17	555	568	forward 3	TM	Non-Cytosolic
342	LI:239579.9:2001MAY17	569	591	forward 3	TM	Transmembrane
342	LI:239579.9:2001MAY17	592	685	forward 3	TM	Cytosolic
342	LI:239579.9:2001MAY17	686	708	forward 3	TM	Transmembrane
342	LI:239579.9:2001MAY17	709	735	forward 3	TM	Non-Cytosolic
343	LI:239720.1:2001MAY17	1	986	forward 2	TM	Non-Cytosolic
343	LI:239720.1:2001MAY17	987	1009	forward 2	TM	Transmembrane
343	LI:239720.1:2001MAY17	1010	1210	forward 2	TM	Cytosolic
344	LI:240037.6:2001MAY17	1	306	forward 3	TM	Non-Cytosolic
344	LI:240037.6:2001MAY17	307	329	forward 3	TM	Transmembrane
344	LI:240037.6:2001MAY17	330	346	forward 3	TM	Cytosolic
345	LI:243900.7:2001MAY17	1	289	forward 2	TM	Cytosolic
345	LI:243900.7:2001MAY17	290	309	forward 2	TM	Transmembrane
345	LI:243900.7:2001MAY17	310	313	forward 2	TM	Non-Cytosolic
345	LI:243900.7:2001MAY17	314	336	forward 2	TM	Transmembrane
345	LI:243900.7:2001MAY17	337	401	forward 2	TM	Cytosolic
345	LI:243900.7:2001MAY17	1	308	forward 3	TM	Non-Cytosolic
345	LI:243900.7:2001MAY17	309	331	forward 3	TM	Transmembrane
345	LI:243900.7:2001MAY17	332	400	forward 3	TM	Cytosolic
346	LI:244378.1:2001MAY17	1	57	forward 1	TM	Non-Cytosolic
346	LI:244378.1:2001MAY17	58	75	forward 1	TM	Transmembrane
346	LI:244378.1:2001MAY17	76	87	forward 1	TM	Cytosolic
346	LI:244378.1:2001MAY17	88	110	forward 1	TM	Transmembrane
346	LI:244378.1:2001MAY17	111	119	forward 1	TM	Non-Cytosolic
346	LI:244378.1:2001MAY17	120	142	forward 1	TM	Transmembrane
346	LI:244378.1:2001MAY17	143	160	forward 1	TM	Cytosolic
346	LI:244378.1:2001MAY17	161	178	forward 1	TM	Transmembrane
346	LI:244378.1:2001MAY17	179	826	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
346	LI:244378.1:2001MAY17	1	47	forward 2	TM	Non-Cytosolic
346	LI:244378.1:2001MAY17	48	70	forward 2	TM	Transmembrane
346	LI:244378.1:2001MAY17	71	101	forward 2	TM	Cytosolic
346	LI:244378.1:2001MAY17	102	124	forward 2	TM	Transmembrane
346	LI:244378.1:2001MAY17	125	258	forward 2	TM	Non-Cytosolic
346	LI:244378.1:2001MAY17	259	278	forward 2	TM	Transmembrane
346	LI:244378.1:2001MAY17	279	538	forward 2	TM	Cytosolic
346	LI:244378.1:2001MAY17	539	561	forward 2	TM	Transmembrane
346	LI:244378.1:2001MAY17	562	826	forward 2	TM	Non-Cytosolic
346	LI:244378.1:2001MAY17	1	31	forward 3	TM	Non-Cytosolic
346	LI:244378.1:2001MAY17	32	54	forward 3	TM	Transmembrane
346	LI:244378.1:2001MAY17	55	85	forward 3	TM	Cytosolic
346	LI:244378.1:2001MAY17	86	105	forward 3	TM	Transmembrane
346	LI:244378.1:2001MAY17	106	825	forward 3	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	1	107	forward 1	TM	Cytosolic
347	LI:245500.3:2001MAY17	108	130	forward 1	TM	Transmembrane
347	LI:245500.3:2001MAY17	131	144	forward 1	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	145	167	forward 1	TM	Transmembrane
347	LI:245500.3:2001MAY17	168	232	forward 1	TM	Cytosolic
347	LI:245500.3:2001MAY17	233	255	forward 1	TM	Transmembrane
347	LI:245500.3:2001MAY17	256	267	forward 1	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	268	290	forward 1	TM	Transmembrane
347	LI:245500.3:2001MAY17	291	340	forward 1	TM	Cytosolic
347	LI:245500.3:2001MAY17	341	363	forward 1	TM	Transmembrane
347	LI:245500.3:2001MAY17	364	372	forward 1	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	373	395	forward 1	TM	Transmembrane
347	LI:245500.3:2001MAY17	396	414	forward 1	TM	Cytosolic
347	LI:245500.3:2001MAY17	415	437	forward 1	TM	Transmembrane
347	LI:245500.3:2001MAY17	438	935	forward 1	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	936	958	forward 1	TM	Transmembrane
347	LI:245500.3:2001MAY17	959	1018	forward 1	TM	Cytosolic
347	LI:245500.3:2001MAY17	1019	1041	forward 1	TM	Transmembrane
347	LI:245500.3:2001MAY17	1042	1052	forward 1	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	1	19	forward 2	TM	Cytosolic
347	LI:245500.3:2001MAY17	20	39	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	40	48	forward 2	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	49	71	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	72	116	forward 2	TM	Cytosolic
347	LI:245500.3:2001MAY17	117	136	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	137	145	forward 2	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	146	168	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	169	243	forward 2	TM	Cytosolic
347	LI:245500.3:2001MAY17	244	266	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	267	337	forward 2	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	338	360	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	361	366	forward 2	TM	Cytosolic
347	LI:245500.3:2001MAY17	367	389	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	390	392	forward 2	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	393	410	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	411	439	forward 2	TM	Cytosolic
347	LI:245500.3:2001MAY17	440	459	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	460	491	forward 2	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	492	514	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	515	677	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
347	LI:245500.3:2001MAY17	678	700	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	701	727	forward 2	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	728	750	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	751	761	forward 2	TM	Cytosolic
347	LI:245500.3:2001MAY17	762	784	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	785	803	forward 2	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	804	826	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	827	939	forward 2	TM	Cytosolic
347	LI:245500.3:2001MAY17	940	959	forward 2	TM	Transmembrane
347	LI:245500.3:2001MAY17	960	1052	forward 2	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	1	295	forward 3	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	296	318	forward 3	TM	Transmembrane
347	LI:245500.3:2001MAY17	319	329	forward 3	TM	Cytosolic
347	LI:245500.3:2001MAY17	330	352	forward 3	TM	Transmembrane
347	LI:245500.3:2001MAY17	353	386	forward 3	TM	Non-Cytosolic
347	LI:245500.3:2001MAY17	387	409	forward 3	TM	Transmembrane
347	LI:245500.3:2001MAY17	410	429	forward 3	TM	Cytosolic
347	LI:245500.3:2001MAY17	430	452	forward 3	TM	Transmembrane
347	LI:245500.3:2001MAY17	453	1052	forward 3	TM	Non-Cytosolic
348	LI:245982.24:2001MAY17	1	748	forward 3	TM	Non-Cytosolic
348	LI:245982.24:2001MAY17	749	771	forward 3	TM	Transmembrane
348	LI:245982.24:2001MAY17	772	788	forward 3	TM	Cytosolic
349	LI:246054.1:2001MAY17	1	214	forward 1	TM	Non-Cytosolic
349	LI:246054.1:2001MAY17	215	237	forward 1	TM	Transmembrane
349	LI:246054.1:2001MAY17	238	243	forward 1	TM	Cytosolic
349	LI:246054.1:2001MAY17	244	266	forward 1	TM	Transmembrane
349	LI:246054.1:2001MAY17	267	509	forward 1	TM	Non-Cytosolic
349	LI:246054.1:2001MAY17	510	532	forward 1	TM	Transmembrane
349	LI:246054.1:2001MAY17	533	627	forward 1	TM	Cytosolic
349	LI:246054.1:2001MAY17	1	257	forward 2	TM	Non-Cytosolic
349	LI:246054.1:2001MAY17	258	280	forward 2	TM	Transmembrane
349	LI:246054.1:2001MAY17	281	306	forward 2	TM	Cytosolic
349	LI:246054.1:2001MAY17	307	329	forward 2	TM	Transmembrane
349	LI:246054.1:2001MAY17	330	627	forward 2	TM	Non-Cytosolic
349	LI:246054.1:2001MAY17	1	506	forward 3	TM	Non-Cytosolic
349	LI:246054.1:2001MAY17	507	529	forward 3	TM	Transmembrane
349	LI:246054.1:2001MAY17	530	597	forward 3	TM	Cytosolic
349	LI:246054.1:2001MAY17	598	620	forward 3	TM	Transmembrane
349	LI:246054.1:2001MAY17	621	627	forward 3	TM	Non-Cytosolic
350	LI:256051.229:2001MAY17	1	229	forward 1	TM	Non-Cytosolic
350	LI:256051.229:2001MAY17	230	252	forward 1	TM	Transmembrane
350	LI:256051.229:2001MAY17	253	257	forward 1	TM	Cytosolic
350	LI:256051.229:2001MAY17	1	225	forward 2	TM	Cytosolic
350	LI:256051.229:2001MAY17	226	248	forward 2	TM	Transmembrane
350	LI:256051.229:2001MAY17	249	256	forward 2	TM	Non-Cytosolic
351	LI:260629.7:2001MAY17	1	4	forward 1	TM	Cytosolic
351	LI:260629.7:2001MAY17	5	27	forward 1	TM	Transmembrane
351	LI:260629.7:2001MAY17	28	48	forward 1	TM	Non-Cytosolic
351	LI:260629.7:2001MAY17	1	14	forward 2	TM	Non-Cytosolic
351	LI:260629.7:2001MAY17	15	32	forward 2	TM	Transmembrane
351	LI:260629.7:2001MAY17	33	48	forward 2	TM	Cytosolic
352	LI:272723.1:2001MAY17	1	116	forward 2	TM	Non-Cytosolic
352	LI:272723.1:2001MAY17	117	139	forward 2	TM	Transmembrane
352	LI:272723.1:2001MAY17	140	255	forward 2	TM	Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
352	LI:272723.1:2001MAY17	256	278	forward 2	TM	Transmembrane
352	LI:272723.1:2001MAY17	279	287	forward 2	TM	Non-Cytosolic
353	LI:272766.1:2001MAY17	1	270	forward 3	TM	Non-Cytosolic
353	LI:272766.1:2001MAY17	271	293	forward 3	TM	Transmembrane
353	LI:272766.1:2001MAY17	294	318	forward 3	TM	Cytosolic
354	LI:275726.1:2001MAY17	1	197	forward 3	TM	Cytosolic
355	LI:276815.1:2001MAY17	1	20	forward 2	TM	Cytosolic
355	LI:276815.1:2001MAY17	21	43	forward 2	TM	Transmembrane
355	LI:276815.1:2001MAY17	44	199	forward 2	TM	Non-Cytosolic
355	LI:276815.1:2001MAY17	1	20	forward 3	TM	Cytosolic
355	LI:276815.1:2001MAY17	21	43	forward 3	TM	Transmembrane
355	LI:276815.1:2001MAY17	44	198	forward 3	TM	Non-Cytosolic
356	LI:283562.5:2001MAY17	1	289	forward 1	TM	Cytosolic
356	LI:283562.5:2001MAY17	290	312	forward 1	TM	Transmembrane
356	LI:283562.5:2001MAY17	313	1092	forward 1	TM	Non-Cytosolic
356	LI:283562.5:2001MAY17	1093	1115	forward 1	TM	Transmembrane
356	LI:283562.5:2001MAY17	1116	1125	forward 1	TM	Cytosolic
356	LI:283562.5:2001MAY17	1	1091	forward 3	TM	Non-Cytosolic
356	LI:283562.5:2001MAY17	1092	1114	forward 3	TM	Transmembrane
356	LI:283562.5:2001MAY17	1115	1124	forward 3	TM	Cytosolic
357	LI:289066.15:2001MAY17	1	175	forward 1	TM	Cytosolic
357	LI:289066.15:2001MAY17	176	198	forward 1	TM	Transmembrane
357	LI:289066.15:2001MAY17	199	925	forward 1	TM	Non-Cytosolic
357	LI:289066.15:2001MAY17	926	948	forward 1	TM	Transmembrane
357	LI:289066.15:2001MAY17	949	968	forward 1	TM	Cytosolic
357	LI:289066.15:2001MAY17	969	991	forward 1	TM	Transmembrane
357	LI:289066.15:2001MAY17	992	1022	forward 1	TM	Non-Cytosolic
357	LI:289066.15:2001MAY17	1023	1045	forward 1	TM	Transmembrane
357	LI:289066.15:2001MAY17	1046	1083	forward 1	TM	Cytosolic
357	LI:289066.15:2001MAY17	1	12	forward 2	TM	Cytosolic
357	LI:289066.15:2001MAY17	13	30	forward 2	TM	Transmembrane
357	LI:289066.15:2001MAY17	31	39	forward 2	TM	Non-Cytosolic
357	LI:289066.15:2001MAY17	40	59	forward 2	TM	Transmembrane
357	LI:289066.15:2001MAY17	60	189	forward 2	TM	Cytosolic
357	LI:289066.15:2001MAY17	190	212	forward 2	TM	Transmembrane
357	LI:289066.15:2001MAY17	213	226	forward 2	TM	Non-Cytosolic
357	LI:289066.15:2001MAY17	227	249	forward 2	TM	Transmembrane
357	LI:289066.15:2001MAY17	250	303	forward 2	TM	Cytosolic
357	LI:289066.15:2001MAY17	304	326	forward 2	TM	Transmembrane
357	LI:289066.15:2001MAY17	327	932	forward 2	TM	Non-Cytosolic
357	LI:289066.15:2001MAY17	933	955	forward 2	TM	Transmembrane
357	LI:289066.15:2001MAY17	956	975	forward 2	TM	Cytosolic
357	LI:289066.15:2001MAY17	976	998	forward 2	TM	Transmembrane
357	LI:289066.15:2001MAY17	999	1026	forward 2	TM	Non-Cytosolic
357	LI:289066.15:2001MAY17	1027	1049	forward 2	TM	Transmembrane
357	LI:289066.15:2001MAY17	1050	1083	forward 2	TM	Cytosolic
357	LI:289066.15:2001MAY17	1	90	forward 3	TM	Cytosolic
357	LI:289066.15:2001MAY17	91	113	forward 3	TM	Transmembrane
357	LI:289066.15:2001MAY17	114	174	forward 3	TM	Non-Cytosolic
357	LI:289066.15:2001MAY17	175	197	forward 3	TM	Transmembrane
357	LI:289066.15:2001MAY17	198	220	forward 3	TM	Cytosolic
357	LI:289066.15:2001MAY17	221	243	forward 3	TM	Transmembrane
357	LI:289066.15:2001MAY17	244	833	forward 3	TM	Non-Cytosolic
357	LI:289066.15:2001MAY17	834	856	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
357	LI:289066.15:2001MAY17	857	975	forward 3	TM	Cytosolic
357	LI:289066.15:2001MAY17	976	998	forward 3	TM	Transmembrane
357	LI:289066.15:2001MAY17	999	1017	forward 3	TM	Non-Cytosolic
357	LI:289066.15:2001MAY17	1018	1040	forward 3	TM	Transmembrane
357	LI:289066.15:2001MAY17	1041	1083	forward 3	TM	Cytosolic
358	LI:331040.17:2001MAY17	1	207	forward 1	TM	Non-Cytosolic
358	LI:331040.17:2001MAY17	208	230	forward 1	TM	Transmembrane
358	LI:331040.17:2001MAY17	231	314	forward 1	TM	Cytosolic
358	LI:331040.17:2001MAY17	1	239	forward 3	TM	Non-Cytosolic
358	LI:331040.17:2001MAY17	240	262	forward 3	TM	Transmembrane
358	LI:331040.17:2001MAY17	263	282	forward 3	TM	Cytosolic
358	LI:331040.17:2001MAY17	283	305	forward 3	TM	Transmembrane
358	LI:331040.17:2001MAY17	306	313	forward 3	TM	Non-Cytosolic
359	LI:332414.5:2001MAY17	1	534	forward 1	TM	Non-Cytosolic
359	LI:332414.5:2001MAY17	535	557	forward 1	TM	Transmembrane
359	LI:332414.5:2001MAY17	558	574	forward 1	TM	Cytosolic
359	LI:332414.5:2001MAY17	1	167	forward 2	TM	Cytosolic
359	LI:332414.5:2001MAY17	168	190	forward 2	TM	Transmembrane
359	LI:332414.5:2001MAY17	191	574	forward 2	TM	Non-Cytosolic
359	LI:332414.5:2001MAY17	1	534	forward 3	TM	Non-Cytosolic
359	LI:332414.5:2001MAY17	535	557	forward 3	TM	Transmembrane
359	LI:332414.5:2001MAY17	558	573	forward 3	TM	Cytosolic
360	LI:332730.16:2001MAY17	1	427	forward 1	TM	Cytosolic
360	LI:332730.16:2001MAY17	428	450	forward 1	TM	Transmembrane
360	LI:332730.16:2001MAY17	451	963	forward 1	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	964	986	forward 1	TM	Transmembrane
360	LI:332730.16:2001MAY17	987	1176	forward 1	TM	Cytosolic
360	LI:332730.16:2001MAY17	1177	1199	forward 1	TM	Transmembrane
360	LI:332730.16:2001MAY17	1200	1218	forward 1	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	1219	1241	forward 1	TM	Transmembrane
360	LI:332730.16:2001MAY17	1242	1328	forward 1	TM	Cytosolic
360	LI:332730.16:2001MAY17	1329	1351	forward 1	TM	Transmembrane
360	LI:332730.16:2001MAY17	1352	1383	forward 1	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	1384	1406	forward 1	TM	Transmembrane
360	LI:332730.16:2001MAY17	1407	1438	forward 1	TM	Cytosolic
360	LI:332730.16:2001MAY17	1439	1461	forward 1	TM	Transmembrane
360	LI:332730.16:2001MAY17	1462	1465	forward 1	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	1466	1485	forward 1	TM	Transmembrane
360	LI:332730.16:2001MAY17	1486	1516	forward 1	TM	Cytosolic
360	LI:332730.16:2001MAY17	1517	1539	forward 1	TM	Transmembrane
360	LI:332730.16:2001MAY17	1540	1738	forward 1	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	1	951	forward 2	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	952	974	forward 2	TM	Transmembrane
360	LI:332730.16:2001MAY17	975	1175	forward 2	TM	Cytosolic
360	LI:332730.16:2001MAY17	1176	1198	forward 2	TM	Transmembrane
360	LI:332730.16:2001MAY17	1199	1217	forward 2	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	1218	1240	forward 2	TM	Transmembrane
360	LI:332730.16:2001MAY17	1241	1531	forward 2	TM	Cytosolic
360	LI:332730.16:2001MAY17	1532	1554	forward 2	TM	Transmembrane
360	LI:332730.16:2001MAY17	1555	1618	forward 2	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	1619	1638	forward 2	TM	Transmembrane
360	LI:332730.16:2001MAY17	1639	1649	forward 2	TM	Cytosolic
360	LI:332730.16:2001MAY17	1650	1672	forward 2	TM	Transmembrane
360	LI:332730.16:2001MAY17	1673	1706	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
360	LI:332730.16:2001MAY17	1707	1724	forward 2	TM	Transmembrane
360	LI:332730.16:2001MAY17	1725	1738	forward 2	TM	Cytosolic
360	LI:332730.16:2001MAY17	1	952	forward 3	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	953	975	forward 3	TM	Transmembrane
360	LI:332730.16:2001MAY17	976	1120	forward 3	TM	Cytosolic
360	LI:332730.16:2001MAY17	1121	1143	forward 3	TM	Transmembrane
360	LI:332730.16:2001MAY17	1144	1146	forward 3	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	1147	1169	forward 3	TM	Transmembrane
360	LI:332730.16:2001MAY17	1170	1175	forward 3	TM	Cytosolic
360	LI:332730.16:2001MAY17	1176	1198	forward 3	TM	Transmembrane
360	LI:332730.16:2001MAY17	1199	1217	forward 3	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	1218	1240	forward 3	TM	Transmembrane
360	LI:332730.16:2001MAY17	1241	1447	forward 3	TM	Cytosolic
360	LI:332730.16:2001MAY17	1448	1470	forward 3	TM	Transmembrane
360	LI:332730.16:2001MAY17	1471	1479	forward 3	TM	Non-Cytosolic
360	LI:332730.16:2001MAY17	1480	1499	forward 3	TM	Transmembrane
360	LI:332730.16:2001MAY17	1500	1519	forward 3	TM	Cytosolic
360	LI:332730.16:2001MAY17	1520	1542	forward 3	TM	Transmembrane
360	LI:332730.16:2001MAY17	1543	1738	forward 3	TM	Non-Cytosolic
361	LI:333849.21:2001MAY17	1	188	forward 1	TM	Cytosolic
362	LI:337038.15:2001MAY17	1	660	forward 1	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	661	683	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	684	793	forward 1	TM	Cytosolic
362	LI:337038.15:2001MAY17	794	816	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	817	928	forward 1	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	929	951	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	952	957	forward 1	TM	Cytosolic
362	LI:337038.15:2001MAY17	958	980	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	981	989	forward 1	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	990	1009	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1010	1029	forward 1	TM	Cytosolic
362	LI:337038.15:2001MAY17	1030	1052	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1053	1119	forward 1	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1120	1142	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1143	1174	forward 1	TM	Cytosolic
362	LI:337038.15:2001MAY17	1175	1197	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1198	1211	forward 1	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1212	1231	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1232	1357	forward 1	TM	Cytosolic
362	LI:337038.15:2001MAY17	1358	1380	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1381	1394	forward 1	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1395	1417	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1418	1429	forward 1	TM	Cytosolic
362	LI:337038.15:2001MAY17	1430	1452	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1453	1515	forward 1	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1516	1538	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1539	1550	forward 1	TM	Cytosolic
362	LI:337038.15:2001MAY17	1551	1573	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1574	1582	forward 1	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1583	1601	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1602	1656	forward 1	TM	Cytosolic
362	LI:337038.15:2001MAY17	1657	1679	forward 1	TM	Transmembrane
362	LI:337038.15:2001MAY17	1680	1698	forward 1	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1699	1721	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
362	LI:337038.15:2001MAY17	1722	1749	forward 1	TM	Cytosolic
362	LI:337038.15:2001MAY17	1	660	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	661	683	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	684	703	forward 2	TM	Cytosolic
362	LI:337038.15:2001MAY17	704	721	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	722	735	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	736	758	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	759	764	forward 2	TM	Cytosolic
362	LI:337038.15:2001MAY17	765	785	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	786	804	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	805	827	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	828	839	forward 2	TM	Cytosolic
362	LI:337038.15:2001MAY17	840	862	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	863	935	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	936	953	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	954	959	forward 2	TM	Cytosolic
362	LI:337038.15:2001MAY17	960	982	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	983	1027	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1028	1050	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1051	1095	forward 2	TM	Cytosolic
362	LI:337038.15:2001MAY17	1096	1118	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1119	1132	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1133	1152	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1153	1325	forward 2	TM	Cytosolic
362	LI:337038.15:2001MAY17	1326	1345	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1346	1359	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1360	1382	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1383	1401	forward 2	TM	Cytosolic
362	LI:337038.15:2001MAY17	1402	1424	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1425	1438	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1439	1461	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1462	1467	forward 2	TM	Cytosolic
362	LI:337038.15:2001MAY17	1468	1487	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1488	1491	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1492	1509	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1510	1515	forward 2	TM	Cytosolic
362	LI:337038.15:2001MAY17	1516	1538	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1539	1552	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1553	1575	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1576	1610	forward 2	TM	Cytosolic
362	LI:337038.15:2001MAY17	1611	1633	forward 2	TM	Transmembrane
362	LI:337038.15:2001MAY17	1634	1749	forward 2	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1	206	forward 3	TM	Cytosolic
362	LI:337038.15:2001MAY17	207	229	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	230	764	forward 3	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	765	787	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	788	942	forward 3	TM	Cytosolic
362	LI:337038.15:2001MAY17	943	965	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	966	1030	forward 3	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1031	1050	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	1051	1172	forward 3	TM	Cytosolic
362	LI:337038.15:2001MAY17	1173	1192	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	1193	1242	forward 3	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1243	1265	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
362	LI:337038.15:2001MAY17	1266	1393	forward 3	TM	Cytosolic
362	LI:337038.15:2001MAY17	1394	1416	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	1417	1430	forward 3	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1431	1453	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	1454	1472	forward 3	TM	Cytosolic
362	LI:337038.15:2001MAY17	1473	1495	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	1496	1516	forward 3	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1517	1539	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	1540	1551	forward 3	TM	Cytosolic
362	LI:337038.15:2001MAY17	1552	1574	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	1575	1607	forward 3	TM	Non-Cytosolic
362	LI:337038.15:2001MAY17	1608	1630	forward 3	TM	Transmembrane
362	LI:337038.15:2001MAY17	1631	1749	forward 3	TM	Cytosolic
363	LI:337606.6:2001MAY17	1	73	forward 1	TM	Cytosolic
363	LI:337606.6:2001MAY17	74	96	forward 1	TM	Transmembrane
363	LI:337606.6:2001MAY17	97	210	forward 1	TM	Non-Cytosolic
363	LI:337606.6:2001MAY17	1	168	forward 3	TM	Cytosolic
363	LI:337606.6:2001MAY17	169	191	forward 3	TM	Transmembrane
363	LI:337606.6:2001MAY17	192	209	forward 3	TM	Non-Cytosolic
364	LI:338032.10:2001MAY17	1	4	forward 1	TM	Non-Cytosolic
364	LI:338032.10:2001MAY17	5	27	forward 1	TM	Transmembrane
364	LI:338032.10:2001MAY17	28	131	forward 1	TM	Cytosolic
365	LI:339265.16:2001MAY17	1	1231	forward 1	TM	Non-Cytosolic
365	LI:339265.16:2001MAY17	1232	1254	forward 1	TM	Transmembrane
365	LI:339265.16:2001MAY17	1255	1274	forward 1	TM	Cytosolic
365	LI:339265.16:2001MAY17	1	224	forward 3	TM	Non-Cytosolic
365	LI:339265.16:2001MAY17	225	247	forward 3	TM	Transmembrane
365	LI:339265.16:2001MAY17	248	341	forward 3	TM	Cytosolic
365	LI:339265.16:2001MAY17	342	364	forward 3	TM	Transmembrane
365	LI:339265.16:2001MAY17	365	1274	forward 3	TM	Non-Cytosolic
366	LI:344646.4:2001MAY17	1	452	forward 1	TM	Non-Cytosolic
366	LI:344646.4:2001MAY17	453	475	forward 1	TM	Transmembrane
366	LI:344646.4:2001MAY17	476	598	forward 1	TM	Cytosolic
366	LI:344646.4:2001MAY17	1	104	forward 2	TM	Cytosolic
366	LI:344646.4:2001MAY17	105	127	forward 2	TM	Transmembrane
366	LI:344646.4:2001MAY17	128	141	forward 2	TM	Non-Cytosolic
366	LI:344646.4:2001MAY17	142	164	forward 2	TM	Transmembrane
366	LI:344646.4:2001MAY17	165	250	forward 2	TM	Cytosolic
366	LI:344646.4:2001MAY17	251	273	forward 2	TM	Transmembrane
366	LI:344646.4:2001MAY17	274	598	forward 2	TM	Non-Cytosolic
366	LI:344646.4:2001MAY17	1	289	forward 3	TM	Cytosolic
366	LI:344646.4:2001MAY17	290	312	forward 3	TM	Transmembrane
366	LI:344646.4:2001MAY17	313	345	forward 3	TM	Non-Cytosolic
366	LI:344646.4:2001MAY17	346	365	forward 3	TM	Transmembrane
366	LI:344646.4:2001MAY17	366	523	forward 3	TM	Cytosolic
366	LI:344646.4:2001MAY17	524	546	forward 3	TM	Transmembrane
366	LI:344646.4:2001MAY17	547	598	forward 3	TM	Non-Cytosolic
367	LI:347393.7:2001MAY17	1	384	forward 2	TM	Non-Cytosolic
367	LI:347393.7:2001MAY17	385	407	forward 2	TM	Transmembrane
367	LI:347393.7:2001MAY17	408	449	forward 2	TM	Cytosolic
368	LI:348107.36:2001MAY17	1	140	forward 2	TM	Non-Cytosolic
368	LI:348107.36:2001MAY17	141	163	forward 2	TM	Transmembrane
368	LI:348107.36:2001MAY17	164	166	forward 2	TM	Cytosolic
369	LI:351120.6:2001MAY17	1	196	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
369	LI:351120.6:2001MAY17	197	219	forward 1	TM	Transmembrane
369	LI:351120.6:2001MAY17	220	303	forward 1	TM	Cytosolic
369	LI:351120.6:2001MAY17	304	326	forward 1	TM	Transmembrane
369	LI:351120.6:2001MAY17	327	357	forward 1	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	358	380	forward 1	TM	Transmembrane
369	LI:351120.6:2001MAY17	381	392	forward 1	TM	Cytosolic
369	LI:351120.6:2001MAY17	393	415	forward 1	TM	Transmembrane
369	LI:351120.6:2001MAY17	416	458	forward 1	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	459	481	forward 1	TM	Transmembrane
369	LI:351120.6:2001MAY17	482	554	forward 1	TM	Cytosolic
369	LI:351120.6:2001MAY17	555	577	forward 1	TM	Transmembrane
369	LI:351120.6:2001MAY17	578	586	forward 1	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	587	609	forward 1	TM	Transmembrane
369	LI:351120.6:2001MAY17	610	737	forward 1	TM	Cytosolic
369	LI:351120.6:2001MAY17	738	760	forward 1	TM	Transmembrane
369	LI:351120.6:2001MAY17	761	1098	forward 1	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	1	270	forward 2	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	271	290	forward 2	TM	Transmembrane
369	LI:351120.6:2001MAY17	291	344	forward 2	TM	Cytosolic
369	LI:351120.6:2001MAY17	345	367	forward 2	TM	Transmembrane
369	LI:351120.6:2001MAY17	368	381	forward 2	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	382	404	forward 2	TM	Transmembrane
369	LI:351120.6:2001MAY17	405	416	forward 2	TM	Cytosolic
369	LI:351120.6:2001MAY17	417	434	forward 2	TM	Transmembrane
369	LI:351120.6:2001MAY17	435	448	forward 2	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	449	471	forward 2	TM	Transmembrane
369	LI:351120.6:2001MAY17	472	491	forward 2	TM	Cytosolic
369	LI:351120.6:2001MAY17	492	511	forward 2	TM	Transmembrane
369	LI:351120.6:2001MAY17	512	525	forward 2	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	526	548	forward 2	TM	Transmembrane
369	LI:351120.6:2001MAY17	549	641	forward 2	TM	Cytosolic
369	LI:351120.6:2001MAY17	642	664	forward 2	TM	Transmembrane
369	LI:351120.6:2001MAY17	665	698	forward 2	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	699	721	forward 2	TM	Transmembrane
369	LI:351120.6:2001MAY17	722	737	forward 2	TM	Cytosolic
369	LI:351120.6:2001MAY17	738	760	forward 2	TM	Transmembrane
369	LI:351120.6:2001MAY17	761	1098	forward 2	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	1	87	forward 3	TM	Cytosolic
369	LI:351120.6:2001MAY17	88	107	forward 3	TM	Transmembrane
369	LI:351120.6:2001MAY17	108	121	forward 3	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	122	141	forward 3	TM	Transmembrane
369	LI:351120.6:2001MAY17	142	309	forward 3	TM	Cytosolic
369	LI:351120.6:2001MAY17	310	329	forward 3	TM	Transmembrane
369	LI:351120.6:2001MAY17	330	357	forward 3	TM	Non-Cytosolic
369	LI:351120.6:2001MAY17	358	380	forward 3	TM	Transmembrane
369	LI:351120.6:2001MAY17	381	392	forward 3	TM	Cytosolic
369	LI:351120.6:2001MAY17	393	415	forward 3	TM	Transmembrane
369	LI:351120.6:2001MAY17	416	1097	forward 3	TM	Non-Cytosolic
370	LI:358762.41:2001MAY17	1	177	forward 1	TM	Non-Cytosolic
370	LI:358762.41:2001MAY17	178	200	forward 1	TM	Transmembrane
370	LI:358762.41:2001MAY17	201	206	forward 1	TM	Cytosolic
370	LI:358762.41:2001MAY17	207	229	forward 1	TM	Transmembrane
370	LI:358762.41:2001MAY17	230	561	forward 1	TM	Non-Cytosolic
370	LI:358762.41:2001MAY17	1	160	forward 2	TM	Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
370	LI:358762.41:2001MAY17	161	183	forward 2	TM	Transmembrane
370	LI:358762.41:2001MAY17	184	216	forward 2	TM	Non-Cytosolic
370	LI:358762.41:2001MAY17	217	239	forward 2	TM	Transmembrane
370	LI:358762.41:2001MAY17	240	441	forward 2	TM	Cytosolic
370	LI:358762.41:2001MAY17	442	464	forward 2	TM	Transmembrane
370	LI:358762.41:2001MAY17	465	561	forward 2	TM	Non-Cytosolic
370	LI:358762.41:2001MAY17	1	14	forward 3	TM	Non-Cytosolic
370	LI:358762.41:2001MAY17	15	37	forward 3	TM	Transmembrane
370	LI:358762.41:2001MAY17	38	172	forward 3	TM	Cytosolic
370	LI:358762.41:2001MAY17	173	195	forward 3	TM	Transmembrane
370	LI:358762.41:2001MAY17	196	209	forward 3	TM	Non-Cytosolic
370	LI:358762.41:2001MAY17	210	229	forward 3	TM	Transmembrane
370	LI:358762.41:2001MAY17	230	433	forward 3	TM	Cytosolic
370	LI:358762.41:2001MAY17	434	453	forward 3	TM	Transmembrane
370	LI:358762.41:2001MAY17	454	472	forward 3	TM	Non-Cytosolic
370	LI:358762.41:2001MAY17	473	495	forward 3	TM	Transmembrane
370	LI:358762.41:2001MAY17	496	560	forward 3	TM	Cytosolic
371	LI:363003.48:2001MAY17	1	192	forward 3	TM	Non-Cytosolic
371	LI:363003.48:2001MAY17	193	215	forward 3	TM	Transmembrane
371	LI:363003.48:2001MAY17	216	256	forward 3	TM	Cytosolic
371	LI:363003.48:2001MAY17	257	279	forward 3	TM	Transmembrane
371	LI:363003.48:2001MAY17	280	288	forward 3	TM	Non-Cytosolic
371	LI:363003.48:2001MAY17	289	311	forward 3	TM	Transmembrane
371	LI:363003.48:2001MAY17	312	323	forward 3	TM	Cytosolic
371	LI:363003.48:2001MAY17	324	346	forward 3	TM	Transmembrane
371	LI:363003.48:2001MAY17	347	347	forward 3	TM	Non-Cytosolic
372	LI:370899.6:2001MAY17	1	523	forward 1	TM	Non-Cytosolic
372	LI:370899.6:2001MAY17	524	546	forward 1	TM	Transmembrane
372	LI:370899.6:2001MAY17	547	579	forward 1	TM	Cytosolic
372	LI:370899.6:2001MAY17	580	602	forward 1	TM	Transmembrane
372	LI:370899.6:2001MAY17	603	621	forward 1	TM	Non-Cytosolic
372	LI:370899.6:2001MAY17	622	644	forward 1	TM	Transmembrane
372	LI:370899.6:2001MAY17	645	664	forward 1	TM	Cytosolic
372	LI:370899.6:2001MAY17	665	687	forward 1	TM	Transmembrane
372	LI:370899.6:2001MAY17	688	1216	forward 1	TM	Non-Cytosolic
372	LI:370899.6:2001MAY17	1	553	forward 2	TM	Non-Cytosolic
372	LI:370899.6:2001MAY17	554	576	forward 2	TM	Transmembrane
372	LI:370899.6:2001MAY17	577	617	forward 2	TM	Cytosolic
372	LI:370899.6:2001MAY17	618	640	forward 2	TM	Transmembrane
372	LI:370899.6:2001MAY17	641	659	forward 2	TM	Non-Cytosolic
372	LI:370899.6:2001MAY17	660	682	forward 2	TM	Transmembrane
372	LI:370899.6:2001MAY17	683	711	forward 2	TM	Cytosolic
372	LI:370899.6:2001MAY17	712	734	forward 2	TM	Transmembrane
372	LI:370899.6:2001MAY17	735	1216	forward 2	TM	Non-Cytosolic
372	LI:370899.6:2001MAY17	1	522	forward 3	TM	Non-Cytosolic
372	LI:370899.6:2001MAY17	523	545	forward 3	TM	Transmembrane
372	LI:370899.6:2001MAY17	546	714	forward 3	TM	Cytosolic
372	LI:370899.6:2001MAY17	715	737	forward 3	TM	Transmembrane
372	LI:370899.6:2001MAY17	738	1215	forward 3	TM	Non-Cytosolic
373	LI:376470.1:2001MAY17	1	126	forward 3	TM	Cytosolic
373	LI:376470.1:2001MAY17	127	149	forward 3	TM	Transmembrane
373	LI:376470.1:2001MAY17	150	180	forward 3	TM	Non-Cytosolic
374	LI:400961.18:2001MAY17	1	303	forward 1	TM	Non-Cytosolic
374	LI:400961.18:2001MAY17	304	326	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
374	LI:400961.18:2001MAY17	327	489	forward 1	TM	Cytosolic
374	LI:400961.18:2001MAY17	490	512	forward 1	TM	Transmembrane
374	LI:400961.18:2001MAY17	513	607	forward 1	TM	Non-Cytosolic
374	LI:400961.18:2001MAY17	1	186	forward 3	TM	Non-Cytosolic
374	LI:400961.18:2001MAY17	187	206	forward 3	TM	Transmembrane
374	LI:400961.18:2001MAY17	207	210	forward 3	TM	Cytosolic
374	LI:400961.18:2001MAY17	211	233	forward 3	TM	Transmembrane
374	LI:400961.18:2001MAY17	234	606	forward 3	TM	Non-Cytosolic
375	LI:404482.20:2001MAY17	1	421	forward 1	TM	Non-Cytosolic
375	LI:404482.20:2001MAY17	422	444	forward 1	TM	Transmembrane
375	LI:404482.20:2001MAY17	445	653	forward 1	TM	Cytosolic
375	LI:404482.20:2001MAY17	654	676	forward 1	TM	Transmembrane
375	LI:404482.20:2001MAY17	677	719	forward 1	TM	Non-Cytosolic
375	LI:404482.20:2001MAY17	720	742	forward 1	TM	Transmembrane
375	LI:404482.20:2001MAY17	743	1018	forward 1	TM	Cytosolic
375	LI:404482.20:2001MAY17	1019	1038	forward 1	TM	Transmembrane
375	LI:404482.20:2001MAY17	1039	1052	forward 1	TM	Non-Cytosolic
375	LI:404482.20:2001MAY17	1053	1075	forward 1	TM	Transmembrane
375	LI:404482.20:2001MAY17	1076	1081	forward 1	TM	Cytosolic
375	LI:404482.20:2001MAY17	1082	1100	forward 1	TM	Transmembrane
375	LI:404482.20:2001MAY17	1101	1201	forward 1	TM	Non-Cytosolic
375	LI:404482.20:2001MAY17	1	250	forward 2	TM	Cytosolic
375	LI:404482.20:2001MAY17	251	273	forward 2	TM	Transmembrane
375	LI:404482.20:2001MAY17	274	1041	forward 2	TM	Non-Cytosolic
375	LI:404482.20:2001MAY17	1042	1061	forward 2	TM	Transmembrane
375	LI:404482.20:2001MAY17	1062	1201	forward 2	TM	Cytosolic
375	LI:404482.20:2001MAY17	1	930	forward 3	TM	Non-Cytosolic
375	LI:404482.20:2001MAY17	931	953	forward 3	TM	Transmembrane
375	LI:404482.20:2001MAY17	954	1016	forward 3	TM	Cytosolic
375	LI:404482.20:2001MAY17	1017	1039	forward 3	TM	Transmembrane
375	LI:404482.20:2001MAY17	1040	1048	forward 3	TM	Non-Cytosolic
375	LI:404482.20:2001MAY17	1049	1071	forward 3	TM	Transmembrane
375	LI:404482.20:2001MAY17	1072	1102	forward 3	TM	Cytosolic
375	LI:404482.20:2001MAY17	1103	1125	forward 3	TM	Transmembrane
375	LI:404482.20:2001MAY17	1126	1200	forward 3	TM	Non-Cytosolic
376	LI:405985.1:2001MAY17	1	364	forward 1	TM	Non-Cytosolic
376	LI:405985.1:2001MAY17	365	387	forward 1	TM	Transmembrane
376	LI:405985.1:2001MAY17	388	424	forward 1	TM	Cytosolic
376	LI:405985.1:2001MAY17	1	64	forward 2	TM	Cytosolic
376	LI:405985.1:2001MAY17	65	87	forward 2	TM	Transmembrane
376	LI:405985.1:2001MAY17	88	424	forward 2	TM	Non-Cytosolic
377	LI:406389.1:2001MAY17	1	37	forward 2	TM	Cytosolic
377	LI:406389.1:2001MAY17	38	60	forward 2	TM	Transmembrane
377	LI:406389.1:2001MAY17	61	160	forward 2	TM	Non-Cytosolic
377	LI:406389.1:2001MAY17	161	183	forward 2	TM	Transmembrane
377	LI:406389.1:2001MAY17	184	199	forward 2	TM	Cytosolic
377	LI:406389.1:2001MAY17	200	222	forward 2	TM	Transmembrane
377	LI:406389.1:2001MAY17	223	622	forward 2	TM	Non-Cytosolic
378	LI:406833.1:2001MAY17	1	448	forward 1	TM	Non-Cytosolic
378	LI:406833.1:2001MAY17	449	471	forward 1	TM	Transmembrane
378	LI:406833.1:2001MAY17	472	500	forward 1	TM	Cytosolic
378	LI:406833.1:2001MAY17	501	523	forward 1	TM	Transmembrane
378	LI:406833.1:2001MAY17	524	975	forward 1	TM	Non-Cytosolic
378	LI:406833.1:2001MAY17	1	902	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
378	LI:406833.1:2001MAY17	903	925	forward 2	TM	Transmembrane
378	LI:406833.1:2001MAY17	926	945	forward 2	TM	Cytosolic
378	LI:406833.1:2001MAY17	946	968	forward 2	TM	Transmembrane
378	LI:406833.1:2001MAY17	969	975	forward 2	TM	Non-Cytosolic
378	LI:406833.1:2001MAY17	1	901	forward 3	TM	Non-Cytosolic
378	LI:406833.1:2001MAY17	902	924	forward 3	TM	Transmembrane
378	LI:406833.1:2001MAY17	925	943	forward 3	TM	Cytosolic
378	LI:406833.1:2001MAY17	944	961	forward 3	TM	Transmembrane
378	LI:406833.1:2001MAY17	962	975	forward 3	TM	Non-Cytosolic
379	LI:407921.3:2001MAY17	1	1805	forward 2	TM	Non-Cytosolic
379	LI:407921.3:2001MAY17	1806	1828	forward 2	TM	Transmembrane
379	LI:407921.3:2001MAY17	1829	1863	forward 2	TM	Cytosolic
380	LI:409078.54:2001MAY17	1	28	forward 3	TM	Non-Cytosolic
380	LI:409078.54:2001MAY17	29	51	forward 3	TM	Transmembrane
380	LI:409078.54:2001MAY17	52	80	forward 3	TM	Cytosolic
380	LI:409078.54:2001MAY17	81	103	forward 3	TM	Transmembrane
380	LI:409078.54:2001MAY17	104	1242	forward 3	TM	Non-Cytosolic
381	LI:423601.6:2001MAY17	1	314	forward 3	TM	Non-Cytosolic
381	LI:423601.6:2001MAY17	315	337	forward 3	TM	Transmembrane
381	LI:423601.6:2001MAY17	338	345	forward 3	TM	Cytosolic
381	LI:423601.6:2001MAY17	346	364	forward 3	TM	Transmembrane
381	LI:423601.6:2001MAY17	365	378	forward 3	TM	Non-Cytosolic
381	LI:423601.6:2001MAY17	379	401	forward 3	TM	Transmembrane
381	LI:423601.6:2001MAY17	402	414	forward 3	TM	Cytosolic
382	LI:425024.5:2001MAY17	1	173	forward 2	TM	Non-Cytosolic
382	LI:425024.5:2001MAY17	174	196	forward 2	TM	Transmembrane
382	LI:425024.5:2001MAY17	197	215	forward 2	TM	Cytosolic
382	LI:425024.5:2001MAY17	216	238	forward 2	TM	Transmembrane
382	LI:425024.5:2001MAY17	239	242	forward 2	TM	Non-Cytosolic
382	LI:425024.5:2001MAY17	243	260	forward 2	TM	Transmembrane
382	LI:425024.5:2001MAY17	261	266	forward 2	TM	Cytosolic
382	LI:425024.5:2001MAY17	267	289	forward 2	TM	Transmembrane
382	LI:425024.5:2001MAY17	290	583	forward 2	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	1	252	forward 1	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	253	275	forward 1	TM	Transmembrane
383	LI:427909.29:2001MAY17	276	463	forward 1	TM	Cytosolic
383	LI:427909.29:2001MAY17	464	483	forward 1	TM	Transmembrane
383	LI:427909.29:2001MAY17	484	545	forward 1	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	546	568	forward 1	TM	Transmembrane
383	LI:427909.29:2001MAY17	569	580	forward 1	TM	Cytosolic
383	LI:427909.29:2001MAY17	581	603	forward 1	TM	Transmembrane
383	LI:427909.29:2001MAY17	604	617	forward 1	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	618	637	forward 1	TM	Transmembrane
383	LI:427909.29:2001MAY17	638	657	forward 1	TM	Cytosolic
383	LI:427909.29:2001MAY17	658	680	forward 1	TM	Transmembrane
383	LI:427909.29:2001MAY17	681	725	forward 1	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	726	748	forward 1	TM	Transmembrane
383	LI:427909.29:2001MAY17	749	780	forward 1	TM	Cytosolic
383	LI:427909.29:2001MAY17	781	803	forward 1	TM	Transmembrane
383	LI:427909.29:2001MAY17	804	858	forward 1	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	859	881	forward 1	TM	Transmembrane
383	LI:427909.29:2001MAY17	882	1201	forward 1	TM	Cytosolic
383	LI:427909.29:2001MAY17	1202	1224	forward 1	TM	Transmembrane
383	LI:427909.29:2001MAY17	1225	1255	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
383	LI:427909.29:2001MAY17	1	283	forward 2	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	284	306	forward 2	TM	Transmembrane
383	LI:427909.29:2001MAY17	307	318	forward 2	TM	Cytosolic
383	LI:427909.29:2001MAY17	319	341	forward 2	TM	Transmembrane
383	LI:427909.29:2001MAY17	342	460	forward 2	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	461	483	forward 2	TM	Transmembrane
383	LI:427909.29:2001MAY17	484	582	forward 2	TM	Cytosolic
383	LI:427909.29:2001MAY17	583	605	forward 2	TM	Transmembrane
383	LI:427909.29:2001MAY17	606	624	forward 2	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	625	642	forward 2	TM	Transmembrane
383	LI:427909.29:2001MAY17	643	662	forward 2	TM	Cytosolic
383	LI:427909.29:2001MAY17	663	685	forward 2	TM	Transmembrane
383	LI:427909.29:2001MAY17	686	688	forward 2	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	689	711	forward 2	TM	Transmembrane
383	LI:427909.29:2001MAY17	712	729	forward 2	TM	Cytosolic
383	LI:427909.29:2001MAY17	730	752	forward 2	TM	Transmembrane
383	LI:427909.29:2001MAY17	753	780	forward 2	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	781	803	forward 2	TM	Transmembrane
383	LI:427909.29:2001MAY17	804	929	forward 2	TM	Cytosolic
383	LI:427909.29:2001MAY17	930	949	forward 2	TM	Transmembrane
383	LI:427909.29:2001MAY17	950	1254	forward 2	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	1	319	forward 3	TM	Cytosolic
383	LI:427909.29:2001MAY17	320	339	forward 3	TM	Transmembrane
383	LI:427909.29:2001MAY17	340	622	forward 3	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	623	640	forward 3	TM	Transmembrane
383	LI:427909.29:2001MAY17	641	675	forward 3	TM	Cytosolic
383	LI:427909.29:2001MAY17	676	698	forward 3	TM	Transmembrane
383	LI:427909.29:2001MAY17	699	728	forward 3	TM	Non-Cytosolic
383	LI:427909.29:2001MAY17	729	751	forward 3	TM	Transmembrane
383	LI:427909.29:2001MAY17	752	833	forward 3	TM	Cytosolic
383	LI:427909.29:2001MAY17	834	856	forward 3	TM	Transmembrane
383	LI:427909.29:2001MAY17	857	1254	forward 3	TM	Non-Cytosolic
384	LI:428198.20:2001MAY17	1	171	forward 2	TM	Cytosolic
384	LI:428198.20:2001MAY17	172	194	forward 2	TM	Transmembrane
384	LI:428198.20:2001MAY17	195	820	forward 2	TM	Non-Cytosolic
384	LI:428198.20:2001MAY17	821	840	forward 2	TM	Transmembrane
384	LI:428198.20:2001MAY17	841	860	forward 2	TM	Cytosolic
384	LI:428198.20:2001MAY17	861	883	forward 2	TM	Transmembrane
384	LI:428198.20:2001MAY17	884	892	forward 2	TM	Non-Cytosolic
384	LI:428198.20:2001MAY17	893	915	forward 2	TM	Transmembrane
384	LI:428198.20:2001MAY17	916	958	forward 2	TM	Cytosolic
384	LI:428198.20:2001MAY17	1	910	forward 3	TM	Non-Cytosolic
384	LI:428198.20:2001MAY17	911	933	forward 3	TM	Transmembrane
384	LI:428198.20:2001MAY17	934	958	forward 3	TM	Cytosolic
385	LI:429738.6:2001MAY17	1	19	forward 1	TM	Cytosolic
385	LI:429738.6:2001MAY17	20	42	forward 1	TM	Transmembrane
385	LI:429738.6:2001MAY17	43	45	forward 1	TM	Non-Cytosolic
385	LI:429738.6:2001MAY17	46	63	forward 1	TM	Transmembrane
385	LI:429738.6:2001MAY17	64	343	forward 1	TM	Cytosolic
385	LI:429738.6:2001MAY17	344	366	forward 1	TM	Transmembrane
385	LI:429738.6:2001MAY17	367	380	forward 1	TM	Non-Cytosolic
385	LI:429738.6:2001MAY17	381	403	forward 1	TM	Transmembrane
385	LI:429738.6:2001MAY17	404	416	forward 1	TM	Cytosolic
385	LI:429738.6:2001MAY17	1	19	forward 2	TM	Non-Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
385	LI:429738.6:2001MAY17	20	42	forward 2	TM	Transmembrane
385	LI:429738.6:2001MAY17	43	336	forward 2	TM	Cytosolic
385	LI:429738.6:2001MAY17	337	359	forward 2	TM	Transmembrane
385	LI:429738.6:2001MAY17	360	363	forward 2	TM	Non-Cytosolic
385	LI:429738.6:2001MAY17	364	386	forward 2	TM	Transmembrane
385	LI:429738.6:2001MAY17	387	392	forward 2	TM	Cytosolic
385	LI:429738.6:2001MAY17	393	415	forward 2	TM	Transmembrane
385	LI:429738.6:2001MAY17	416	416	forward 2	TM	Non-Cytosolic
385	LI:429738.6:2001MAY17	1	19	forward 3	TM	Cytosolic
385	LI:429738.6:2001MAY17	20	42	forward 3	TM	Transmembrane
385	LI:429738.6:2001MAY17	43	333	forward 3	TM	Non-Cytosolic
385	LI:429738.6:2001MAY17	334	356	forward 3	TM	Transmembrane
385	LI:429738.6:2001MAY17	357	360	forward 3	TM	Cytosolic
385	LI:429738.6:2001MAY17	361	383	forward 3	TM	Transmembrane
385	LI:429738.6:2001MAY17	384	387	forward 3	TM	Non-Cytosolic
385	LI:429738.6:2001MAY17	388	410	forward 3	TM	Transmembrane
385	LI:429738.6:2001MAY17	411	415	forward 3	TM	Cytosolic
386	LI:449437.1:2001MAY17	1	73	forward 2	TM	Cytosolic
386	LI:449437.1:2001MAY17	74	96	forward 2	TM	Transmembrane
386	LI:449437.1:2001MAY17	97	115	forward 2	TM	Non-Cytosolic
386	LI:449437.1:2001MAY17	116	133	forward 2	TM	Transmembrane
386	LI:449437.1:2001MAY17	134	237	forward 2	TM	Cytosolic
386	LI:449437.1:2001MAY17	238	260	forward 2	TM	Transmembrane
386	LI:449437.1:2001MAY17	261	279	forward 2	TM	Non-Cytosolic
387	LI:459269.25:2001MAY17	1	326	forward 2	TM	Non-Cytosolic
387	LI:459269.25:2001MAY17	327	349	forward 2	TM	Transmembrane
387	LI:459269.25:2001MAY17	350	640	forward 2	TM	Cytosolic
388	LI:464206.1:2001MAY17	1	80	forward 2	TM	Cytosolic
388	LI:464206.1:2001MAY17	81	103	forward 2	TM	Transmembrane
388	LI:464206.1:2001MAY17	104	942	forward 2	TM	Non-Cytosolic
388	LI:464206.1:2001MAY17	1	694	forward 3	TM	Non-Cytosolic
388	LI:464206.1:2001MAY17	695	717	forward 3	TM	Transmembrane
388	LI:464206.1:2001MAY17	718	723	forward 3	TM	Cytosolic
388	LI:464206.1:2001MAY17	724	746	forward 3	TM	Transmembrane
388	LI:464206.1:2001MAY17	747	942	forward 3	TM	Non-Cytosolic
389	LI:465821.2:2001MAY17	1	446	forward 1	TM	Non-Cytosolic
389	LI:465821.2:2001MAY17	447	466	forward 1	TM	Transmembrane
389	LI:465821.2:2001MAY17	467	477	forward 1	TM	Cytosolic
389	LI:465821.2:2001MAY17	478	500	forward 1	TM	Transmembrane
389	LI:465821.2:2001MAY17	501	654	forward 1	TM	Non-Cytosolic
389	LI:465821.2:2001MAY17	1	439	forward 2	TM	Non-Cytosolic
389	LI:465821.2:2001MAY17	440	459	forward 2	TM	Transmembrane
389	LI:465821.2:2001MAY17	460	470	forward 2	TM	Cytosolic
389	LI:465821.2:2001MAY17	471	493	forward 2	TM	Transmembrane
389	LI:465821.2:2001MAY17	494	653	forward 2	TM	Non-Cytosolic
389	LI:465821.2:2001MAY17	1	469	forward 3	TM	Non-Cytosolic
389	LI:465821.2:2001MAY17	470	492	forward 3	TM	Transmembrane
389	LI:465821.2:2001MAY17	493	653	forward 3	TM	Cytosolic
390	LI:474414.28:2001MAY17	1	349	forward 1	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	350	372	forward 1	TM	Transmembrane
390	LI:474414.28:2001MAY17	373	391	forward 1	TM	Cytosolic
390	LI:474414.28:2001MAY17	392	414	forward 1	TM	Transmembrane
390	LI:474414.28:2001MAY17	415	1028	forward 1	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	1029	1051	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
390	LI:474414.28:2001MAY17	1052	1133	forward 1	TM	Cytosolic
390	LI:474414.28:2001MAY17	1134	1156	forward 1	TM	Transmembrane
390	LI:474414.28:2001MAY17	1157	1405	forward 1	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	1	12	forward 2	TM	Cytosolic
390	LI:474414.28:2001MAY17	13	35	forward 2	TM	Transmembrane
390	LI:474414.28:2001MAY17	36	44	forward 2	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	45	67	forward 2	TM	Transmembrane
390	LI:474414.28:2001MAY17	68	437	forward 2	TM	Cytosolic
390	LI:474414.28:2001MAY17	438	457	forward 2	TM	Transmembrane
390	LI:474414.28:2001MAY17	458	466	forward 2	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	467	489	forward 2	TM	Transmembrane
390	LI:474414.28:2001MAY17	490	501	forward 2	TM	Cytosolic
390	LI:474414.28:2001MAY17	502	521	forward 2	TM	Transmembrane
390	LI:474414.28:2001MAY17	522	1405	forward 2	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	1	302	forward 3	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	303	325	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	326	345	forward 3	TM	Cytosolic
390	LI:474414.28:2001MAY17	346	368	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	369	394	forward 3	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	395	417	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	418	437	forward 3	TM	Cytosolic
390	LI:474414.28:2001MAY17	438	455	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	456	467	forward 3	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	468	490	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	491	496	forward 3	TM	Cytosolic
390	LI:474414.28:2001MAY17	497	514	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	515	629	forward 3	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	630	652	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	653	920	forward 3	TM	Cytosolic
390	LI:474414.28:2001MAY17	921	943	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	944	1027	forward 3	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	1028	1050	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	1051	1259	forward 3	TM	Cytosolic
390	LI:474414.28:2001MAY17	1260	1282	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	1283	1296	forward 3	TM	Non-Cytosolic
390	LI:474414.28:2001MAY17	1297	1316	forward 3	TM	Transmembrane
390	LI:474414.28:2001MAY17	1317	1405	forward 3	TM	Cytosolic
391	LI:474435.14:2001MAY17	1	137	forward 2	TM	Non-Cytosolic
391	LI:474435.14:2001MAY17	138	160	forward 2	TM	Transmembrane
391	LI:474435.14:2001MAY17	161	180	forward 2	TM	Cytosolic
391	LI:474435.14:2001MAY17	181	203	forward 2	TM	Transmembrane
391	LI:474435.14:2001MAY17	204	472	forward 2	TM	Non-Cytosolic
391	LI:474435.14:2001MAY17	473	495	forward 2	TM	Transmembrane
391	LI:474435.14:2001MAY17	496	542	forward 2	TM	Cytosolic
391	LI:474435.14:2001MAY17	543	565	forward 2	TM	Transmembrane
391	LI:474435.14:2001MAY17	566	1160	forward 2	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	1	3	forward 1	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	4	21	forward 1	TM	Transmembrane
392	LI:474458.11:2001MAY17	22	203	forward 1	TM	Cytosolic
392	LI:474458.11:2001MAY17	204	226	forward 1	TM	Transmembrane
392	LI:474458.11:2001MAY17	227	249	forward 1	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	250	269	forward 1	TM	Transmembrane
392	LI:474458.11:2001MAY17	270	275	forward 1	TM	Cytosolic
392	LI:474458.11:2001MAY17	276	298	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
392	LI:474458.11:2001MAY17	299	567	forward 1	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	568	590	forward 1	TM	Transmembrane
392	LI:474458.11:2001MAY17	591	617	forward 1	TM	Cytosolic
392	LI:474458.11:2001MAY17	618	640	forward 1	TM	Transmembrane
392	LI:474458.11:2001MAY17	641	854	forward 1	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	1	572	forward 2	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	573	595	forward 2	TM	Transmembrane
392	LI:474458.11:2001MAY17	596	606	forward 2	TM	Cytosolic
392	LI:474458.11:2001MAY17	607	629	forward 2	TM	Transmembrane
392	LI:474458.11:2001MAY17	630	854	forward 2	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	1	116	forward 3	TM	Cytosolic
392	LI:474458.11:2001MAY17	117	139	forward 3	TM	Transmembrane
392	LI:474458.11:2001MAY17	140	185	forward 3	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	186	208	forward 3	TM	Transmembrane
392	LI:474458.11:2001MAY17	209	214	forward 3	TM	Cytosolic
392	LI:474458.11:2001MAY17	215	234	forward 3	TM	Transmembrane
392	LI:474458.11:2001MAY17	235	248	forward 3	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	249	268	forward 3	TM	Transmembrane
392	LI:474458.11:2001MAY17	269	304	forward 3	TM	Cytosolic
392	LI:474458.11:2001MAY17	305	327	forward 3	TM	Transmembrane
392	LI:474458.11:2001MAY17	328	336	forward 3	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	337	359	forward 3	TM	Transmembrane
392	LI:474458.11:2001MAY17	360	415	forward 3	TM	Cytosolic
392	LI:474458.11:2001MAY17	416	433	forward 3	TM	Transmembrane
392	LI:474458.11:2001MAY17	434	567	forward 3	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	568	590	forward 3	TM	Transmembrane
392	LI:474458.11:2001MAY17	591	752	forward 3	TM	Cytosolic
392	LI:474458.11:2001MAY17	753	775	forward 3	TM	Transmembrane
392	LI:474458.11:2001MAY17	776	819	forward 3	TM	Non-Cytosolic
392	LI:474458.11:2001MAY17	820	842	forward 3	TM	Transmembrane
392	LI:474458.11:2001MAY17	843	854	forward 3	TM	Cytosolic
393	LI:477127.18:2001MAY17	1	659	forward 1	TM	Non-Cytosolic
393	LI:477127.18:2001MAY17	660	682	forward 1	TM	Transmembrane
393	LI:477127.18:2001MAY17	683	752	forward 1	TM	Cytosolic
393	LI:477127.18:2001MAY17	753	775	forward 1	TM	Transmembrane
393	LI:477127.18:2001MAY17	776	1102	forward 1	TM	Non-Cytosolic
393	LI:477127.18:2001MAY17	1	664	forward 2	TM	Non-Cytosolic
393	LI:477127.18:2001MAY17	665	687	forward 2	TM	Transmembrane
393	LI:477127.18:2001MAY17	688	750	forward 2	TM	Cytosolic
393	LI:477127.18:2001MAY17	751	773	forward 2	TM	Transmembrane
393	LI:477127.18:2001MAY17	774	1102	forward 2	TM	Non-Cytosolic
393	LI:477127.18:2001MAY17	1	135	forward 3	TM	Cytosolic
393	LI:477127.18:2001MAY17	136	158	forward 3	TM	Transmembrane
393	LI:477127.18:2001MAY17	159	1102	forward 3	TM	Non-Cytosolic
394	LI:480375.55:2001MAY17	1	740	forward 3	TM	Non-Cytosolic
394	LI:480375.55:2001MAY17	741	763	forward 3	TM	Transmembrane
394	LI:480375.55:2001MAY17	764	805	forward 3	TM	Cytosolic
395	LI:480467.24:2001MAY17	1	146	forward 3	TM	Cytosolic
395	LI:480467.24:2001MAY17	147	164	forward 3	TM	Transmembrane
395	LI:480467.24:2001MAY17	165	191	forward 3	TM	Non-Cytosolic
395	LI:480467.24:2001MAY17	192	214	forward 3	TM	Transmembrane
395	LI:480467.24:2001MAY17	215	220	forward 3	TM	Cytosolic
395	LI:480467.24:2001MAY17	221	238	forward 3	TM	Transmembrane
395	LI:480467.24:2001MAY17	239	325	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
395	LI:480467.24:2001MAY17	326	343	forward 3	TM	Transmembrane
395	LI:480467.24:2001MAY17	344	457	forward 3	TM	Cytosolic
396	LI:480587.1:2001MAY17	1	95	forward 1	TM	Cytosolic
396	LI:480587.1:2001MAY17	96	118	forward 1	TM	Transmembrane
396	LI:480587.1:2001MAY17	119	157	forward 1	TM	Non-Cytosolic
396	LI:480587.1:2001MAY17	158	175	forward 1	TM	Transmembrane
396	LI:480587.1:2001MAY17	176	238	forward 1	TM	Cytosolic
396	LI:480587.1:2001MAY17	239	261	forward 1	TM	Transmembrane
396	LI:480587.1:2001MAY17	262	273	forward 1	TM	Non-Cytosolic
396	LI:480587.1:2001MAY17	274	296	forward 1	TM	Transmembrane
396	LI:480587.1:2001MAY17	297	308	forward 1	TM	Cytosolic
396	LI:480587.1:2001MAY17	309	331	forward 1	TM	Transmembrane
396	LI:480587.1:2001MAY17	332	886	forward 1	TM	Non-Cytosolic
396	LI:480587.1:2001MAY17	887	909	forward 1	TM	Transmembrane
396	LI:480587.1:2001MAY17	910	942	forward 1	TM	Cytosolic
396	LI:480587.1:2001MAY17	943	965	forward 1	TM	Transmembrane
396	LI:480587.1:2001MAY17	966	1035	forward 1	TM	Non-Cytosolic
396	LI:480587.1:2001MAY17	1036	1058	forward 1	TM	Transmembrane
396	LI:480587.1:2001MAY17	1059	1070	forward 1	TM	Cytosolic
396	LI:480587.1:2001MAY17	1071	1093	forward 1	TM	Transmembrane
396	LI:480587.1:2001MAY17	1094	1097	forward 1	TM	Non-Cytosolic
396	LI:480587.1:2001MAY17	1098	1120	forward 1	TM	Transmembrane
396	LI:480587.1:2001MAY17	1121	1236	forward 1	TM	Cytosolic
396	LI:480587.1:2001MAY17	1	275	forward 3	TM	Cytosolic
396	LI:480587.1:2001MAY17	276	298	forward 3	TM	Transmembrane
396	LI:480587.1:2001MAY17	299	307	forward 3	TM	Non-Cytosolic
396	LI:480587.1:2001MAY17	308	330	forward 3	TM	Transmembrane
396	LI:480587.1:2001MAY17	331	424	forward 3	TM	Cytosolic
396	LI:480587.1:2001MAY17	425	447	forward 3	TM	Transmembrane
396	LI:480587.1:2001MAY17	448	938	forward 3	TM	Non-Cytosolic
396	LI:480587.1:2001MAY17	939	961	forward 3	TM	Transmembrane
396	LI:480587.1:2001MAY17	962	1073	forward 3	TM	Cytosolic
396	LI:480587.1:2001MAY17	1074	1096	forward 3	TM	Transmembrane
396	LI:480587.1:2001MAY17	1097	1235	forward 3	TM	Non-Cytosolic
397	LI:480798.13:2001MAY17	1	392	forward 1	TM	Non-Cytosolic
397	LI:480798.13:2001MAY17	393	410	forward 1	TM	Transmembrane
397	LI:480798.13:2001MAY17	411	557	forward 1	TM	Cytosolic
397	LI:480798.13:2001MAY17	558	580	forward 1	TM	Transmembrane
397	LI:480798.13:2001MAY17	581	678	forward 1	TM	Non-Cytosolic
397	LI:480798.13:2001MAY17	679	701	forward 1	TM	Transmembrane
397	LI:480798.13:2001MAY17	702	741	forward 1	TM	Cytosolic
397	LI:480798.13:2001MAY17	1	362	forward 2	TM	Non-Cytosolic
397	LI:480798.13:2001MAY17	363	380	forward 2	TM	Transmembrane
397	LI:480798.13:2001MAY17	381	386	forward 2	TM	Cytosolic
397	LI:480798.13:2001MAY17	387	409	forward 2	TM	Transmembrane
397	LI:480798.13:2001MAY17	410	418	forward 2	TM	Non-Cytosolic
397	LI:480798.13:2001MAY17	419	441	forward 2	TM	Transmembrane
397	LI:480798.13:2001MAY17	442	670	forward 2	TM	Cytosolic
397	LI:480798.13:2001MAY17	671	693	forward 2	TM	Transmembrane
397	LI:480798.13:2001MAY17	694	741	forward 2	TM	Non-Cytosolic
397	LI:480798.13:2001MAY17	1	360	forward 3	TM	Non-Cytosolic
397	LI:480798.13:2001MAY17	361	380	forward 3	TM	Transmembrane
397	LI:480798.13:2001MAY17	381	391	forward 3	TM	Cytosolic
397	LI:480798.13:2001MAY17	392	411	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
397	LI:480798.13:2001MAY17	412	420	forward 3	TM	Non-Cytosolic
397	LI:480798.13:2001MAY17	421	443	forward 3	TM	Transmembrane
397	LI:480798.13:2001MAY17	444	476	forward 3	TM	Cytosolic
397	LI:480798.13:2001MAY17	477	499	forward 3	TM	Transmembrane
397	LI:480798.13:2001MAY17	500	559	forward 3	TM	Non-Cytosolic
397	LI:480798.13:2001MAY17	560	579	forward 3	TM	Transmembrane
397	LI:480798.13:2001MAY17	580	637	forward 3	TM	Cytosolic
397	LI:480798.13:2001MAY17	638	656	forward 3	TM	Transmembrane
397	LI:480798.13:2001MAY17	657	670	forward 3	TM	Non-Cytosolic
397	LI:480798.13:2001MAY17	671	693	forward 3	TM	Transmembrane
397	LI:480798.13:2001MAY17	694	740	forward 3	TM	Cytosolic
398	LI:481203.14:2001MAY17	1	160	forward 2	TM	Cytosolic
398	LI:481203.14:2001MAY17	161	183	forward 2	TM	Transmembrane
398	LI:481203.14:2001MAY17	184	1084	forward 2	TM	Non-Cytosolic
399	LI:481237.11:2001MAY17	1	711	forward 2	TM	Non-Cytosolic
399	LI:481237.11:2001MAY17	712	731	forward 2	TM	Transmembrane
399	LI:481237.11:2001MAY17	732	811	forward 2	TM	Cytosolic
399	LI:481237.11:2001MAY17	812	831	forward 2	TM	Transmembrane
399	LI:481237.11:2001MAY17	832	844	forward 2	TM	Non-Cytosolic
400	LI:481368.12:2001MAY17	1	15	forward 2	TM	Cytosolic
400	LI:481368.12:2001MAY17	16	38	forward 2	TM	Transmembrane
400	LI:481368.12:2001MAY17	39	956	forward 2	TM	Non-Cytosolic
401	LI:482301.8:2001MAY17	1	358	forward 1	TM	Non-Cytosolic
401	LI:482301.8:2001MAY17	359	381	forward 1	TM	Transmembrane
401	LI:482301.8:2001MAY17	382	409	forward 1	TM	Cytosolic
401	LI:482301.8:2001MAY17	410	432	forward 1	TM	Transmembrane
401	LI:482301.8:2001MAY17	433	589	forward 1	TM	Non-Cytosolic
401	LI:482301.8:2001MAY17	590	609	forward 1	TM	Transmembrane
401	LI:482301.8:2001MAY17	610	626	forward 1	TM	Cytosolic
401	LI:482301.8:2001MAY17	1	361	forward 2	TM	Non-Cytosolic
401	LI:482301.8:2001MAY17	362	384	forward 2	TM	Transmembrane
401	LI:482301.8:2001MAY17	385	536	forward 2	TM	Cytosolic
401	LI:482301.8:2001MAY17	537	559	forward 2	TM	Transmembrane
401	LI:482301.8:2001MAY17	560	597	forward 2	TM	Non-Cytosolic
401	LI:482301.8:2001MAY17	598	620	forward 2	TM	Transmembrane
401	LI:482301.8:2001MAY17	621	625	forward 2	TM	Cytosolic
401	LI:482301.8:2001MAY17	1	153	forward 3	TM	Non-Cytosolic
401	LI:482301.8:2001MAY17	154	176	forward 3	TM	Transmembrane
401	LI:482301.8:2001MAY17	177	333	forward 3	TM	Cytosolic
401	LI:482301.8:2001MAY17	334	356	forward 3	TM	Transmembrane
401	LI:482301.8:2001MAY17	357	360	forward 3	TM	Non-Cytosolic
401	LI:482301.8:2001MAY17	361	383	forward 3	TM	Transmembrane
401	LI:482301.8:2001MAY17	384	387	forward 3	TM	Cytosolic
401	LI:482301.8:2001MAY17	388	410	forward 3	TM	Transmembrane
401	LI:482301.8:2001MAY17	411	625	forward 3	TM	Non-Cytosolic
402	LI:482482.29:2001MAY17	1	168	forward 1	TM	Cytosolic
402	LI:482482.29:2001MAY17	169	191	forward 1	TM	Transmembrane
402	LI:482482.29:2001MAY17	192	386	forward 1	TM	Non-Cytosolic
402	LI:482482.29:2001MAY17	1	119	forward 3	TM	Cytosolic
402	LI:482482.29:2001MAY17	120	142	forward 3	TM	Transmembrane
402	LI:482482.29:2001MAY17	143	385	forward 3	TM	Non-Cytosolic
403	LI:758877.26:2001MAY17	1	201	forward 1	TM	Non-Cytosolic
403	LI:758877.26:2001MAY17	202	224	forward 1	TM	Transmembrane
403	LI:758877.26:2001MAY17	225	265	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
403	LI:758877.26:2001MAY17	266	288	forward 1	TM	Transmembrane
403	LI:758877.26:2001MAY17	289	711	forward 1	TM	Non-Cytosolic
403	LI:758877.26:2001MAY17	1	205	forward 2	TM	Cytosolic
403	LI:758877.26:2001MAY17	206	228	forward 2	TM	Transmembrane
403	LI:758877.26:2001MAY17	229	263	forward 2	TM	Non-Cytosolic
403	LI:758877.26:2001MAY17	264	286	forward 2	TM	Transmembrane
403	LI:758877.26:2001MAY17	287	290	forward 2	TM	Cytosolic
403	LI:758877.26:2001MAY17	291	313	forward 2	TM	Transmembrane
403	LI:758877.26:2001MAY17	314	327	forward 2	TM	Non-Cytosolic
403	LI:758877.26:2001MAY17	328	350	forward 2	TM	Transmembrane
403	LI:758877.26:2001MAY17	351	485	forward 2	TM	Cytosolic
403	LI:758877.26:2001MAY17	486	508	forward 2	TM	Transmembrane
403	LI:758877.26:2001MAY17	509	586	forward 2	TM	Non-Cytosolic
403	LI:758877.26:2001MAY17	587	609	forward 2	TM	Transmembrane
403	LI:758877.26:2001MAY17	610	711	forward 2	TM	Cytosolic
403	LI:758877.26:2001MAY17	1	490	forward 3	TM	Non-Cytosolic
403	LI:758877.26:2001MAY17	491	513	forward 3	TM	Transmembrane
403	LI:758877.26:2001MAY17	514	571	forward 3	TM	Cytosolic
403	LI:758877.26:2001MAY17	572	594	forward 3	TM	Transmembrane
403	LI:758877.26:2001MAY17	595	640	forward 3	TM	Non-Cytosolic
403	LI:758877.26:2001MAY17	641	663	forward 3	TM	Transmembrane
403	LI:758877.26:2001MAY17	664	710	forward 3	TM	Cytosolic
404	LI:791042.1:2001MAY17	1	455	forward 3	TM	Non-Cytosolic
404	LI:791042.1:2001MAY17	456	478	forward 3	TM	Transmembrane
404	LI:791042.1:2001MAY17	479	497	forward 3	TM	Cytosolic
404	LI:791042.1:2001MAY17	498	520	forward 3	TM	Transmembrane
404	LI:791042.1:2001MAY17	521	550	forward 3	TM	Non-Cytosolic
405	LI:808999.26:2001MAY17	1	1475	forward 3	TM	Non-Cytosolic
405	LI:808999.26:2001MAY17	1476	1498	forward 3	TM	Transmembrane
405	LI:808999.26:2001MAY17	1499	1523	forward 3	TM	Cytosolic
405	LI:808999.26:2001MAY17	1524	1546	forward 3	TM	Transmembrane
405	LI:808999.26:2001MAY17	1547	1565	forward 3	TM	Non-Cytosolic
405	LI:808999.26:2001MAY17	1566	1588	forward 3	TM	Transmembrane
405	LI:808999.26:2001MAY17	1589	1846	forward 3	TM	Cytosolic
406	LI:815715.10:2001MAY17	1	355	forward 1	TM	Non-Cytosolic
406	LI:815715.10:2001MAY17	356	378	forward 1	TM	Transmembrane
406	LI:815715.10:2001MAY17	379	387	forward 1	TM	Cytosolic
406	LI:815715.10:2001MAY17	1	14	forward 2	TM	Non-Cytosolic
406	LI:815715.10:2001MAY17	15	37	forward 2	TM	Transmembrane
406	LI:815715.10:2001MAY17	38	305	forward 2	TM	Cytosolic
406	LI:815715.10:2001MAY17	306	328	forward 2	TM	Transmembrane
406	LI:815715.10:2001MAY17	329	337	forward 2	TM	Non-Cytosolic
406	LI:815715.10:2001MAY17	338	360	forward 2	TM	Transmembrane
406	LI:815715.10:2001MAY17	361	366	forward 2	TM	Cytosolic
406	LI:815715.10:2001MAY17	367	384	forward 2	TM	Transmembrane
406	LI:815715.10:2001MAY17	385	386	forward 2	TM	Non-Cytosolic
406	LI:815715.10:2001MAY17	1	92	forward 3	TM	Cytosolic
406	LI:815715.10:2001MAY17	93	115	forward 3	TM	Transmembrane
406	LI:815715.10:2001MAY17	116	358	forward 3	TM	Non-Cytosolic
406	LI:815715.10:2001MAY17	359	381	forward 3	TM	Transmembrane
406	LI:815715.10:2001MAY17	382	386	forward 3	TM	Cytosolic
407	LI:902980.16:2001MAY17	1	448	forward 1	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	449	471	forward 1	TM	Transmembrane
407	LI:902980.16:2001MAY17	472	553	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
407	LI:902980.16:2001MAY17	554	576	forward 1	TM	Transmembrane
407	LI:902980.16:2001MAY17	577	585	forward 1	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	586	608	forward 1	TM	Transmembrane
407	LI:902980.16:2001MAY17	609	655	forward 1	TM	Cytosolic
407	LI:902980.16:2001MAY17	656	678	forward 1	TM	Transmembrane
407	LI:902980.16:2001MAY17	679	1196	forward 1	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	1	415	forward 2	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	416	438	forward 2	TM	Transmembrane
407	LI:902980.16:2001MAY17	439	559	forward 2	TM	Cytosolic
407	LI:902980.16:2001MAY17	560	582	forward 2	TM	Transmembrane
407	LI:902980.16:2001MAY17	583	596	forward 2	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	597	619	forward 2	TM	Transmembrane
407	LI:902980.16:2001MAY17	620	639	forward 2	TM	Cytosolic
407	LI:902980.16:2001MAY17	640	662	forward 2	TM	Transmembrane
407	LI:902980.16:2001MAY17	663	699	forward 2	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	700	721	forward 2	TM	Transmembrane
407	LI:902980.16:2001MAY17	722	816	forward 2	TM	Cytosolic
407	LI:902980.16:2001MAY17	817	834	forward 2	TM	Transmembrane
407	LI:902980.16:2001MAY17	835	853	forward 2	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	854	876	forward 2	TM	Transmembrane
407	LI:902980.16:2001MAY17	877	882	forward 2	TM	Cytosolic
407	LI:902980.16:2001MAY17	883	905	forward 2	TM	Transmembrane
407	LI:902980.16:2001MAY17	906	1196	forward 2	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	1	558	forward 3	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	559	581	forward 3	TM	Transmembrane
407	LI:902980.16:2001MAY17	582	655	forward 3	TM	Cytosolic
407	LI:902980.16:2001MAY17	656	678	forward 3	TM	Transmembrane
407	LI:902980.16:2001MAY17	679	840	forward 3	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	841	863	forward 3	TM	Transmembrane
407	LI:902980.16:2001MAY17	864	869	forward 3	TM	Cytosolic
407	LI:902980.16:2001MAY17	870	892	forward 3	TM	Transmembrane
407	LI:902980.16:2001MAY17	893	1002	forward 3	TM	Non-Cytosolic
407	LI:902980.16:2001MAY17	1003	1025	forward 3	TM	Transmembrane
407	LI:902980.16:2001MAY17	1026	1044	forward 3	TM	Cytosolic
407	LI:902980.16:2001MAY17	1045	1067	forward 3	TM	Transmembrane
407	LI:902980.16:2001MAY17	1068	1196	forward 3	TM	Non-Cytosolic
408	LI:903196.25:2001MAY17	1	829	forward 2	TM	Non-Cytosolic
408	LI:903196.25:2001MAY17	830	852	forward 2	TM	Transmembrane
408	LI:903196.25:2001MAY17	853	864	forward 2	TM	Cytosolic
408	LI:903196.25:2001MAY17	865	884	forward 2	TM	Transmembrane
408	LI:903196.25:2001MAY17	885	920	forward 2	TM	Non-Cytosolic
408	LI:903196.25:2001MAY17	921	943	forward 2	TM	Transmembrane
408	LI:903196.25:2001MAY17	944	1224	forward 2	TM	Cytosolic
409	LI:903914.10:2001MAY17	1	415	forward 2	TM	Non-Cytosolic
409	LI:903914.10:2001MAY17	416	435	forward 2	TM	Transmembrane
409	LI:903914.10:2001MAY17	436	664	forward 2	TM	Cytosolic
409	LI:903914.10:2001MAY17	665	687	forward 2	TM	Transmembrane
409	LI:903914.10:2001MAY17	688	701	forward 2	TM	Non-Cytosolic
409	LI:903914.10:2001MAY17	702	724	forward 2	TM	Transmembrane
409	LI:903914.10:2001MAY17	725	743	forward 2	TM	Cytosolic
409	LI:903914.10:2001MAY17	744	766	forward 2	TM	Transmembrane
409	LI:903914.10:2001MAY17	767	1664	forward 2	TM	Non-Cytosolic
409	LI:903914.10:2001MAY17	1	668	forward 3	TM	Non-Cytosolic
409	LI:903914.10:2001MAY17	669	691	forward 3	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
409	LI:903914.10:2001MAY17	692	841	forward 3	TM	Cytosolic
409	LI:903914.10:2001MAY17	842	864	forward 3	TM	Transmembrane
409	LI:903914.10:2001MAY17	865	1579	forward 3	TM	Non-Cytosolic
409	LI:903914.10:2001MAY17	1580	1602	forward 3	TM	Transmembrane
409	LI:903914.10:2001MAY17	1603	1663	forward 3	TM	Cytosolic
410	LG:006764.2:2001JUN22	1	139	forward 1	TM	Cytosolic
410	LG:006764.2:2001JUN22	140	162	forward 1	TM	Transmembrane
410	LG:006764.2:2001JUN22	163	181	forward 1	TM	Non-Cytosolic
410	LG:006764.2:2001JUN22	182	204	forward 1	TM	Transmembrane
410	LG:006764.2:2001JUN22	205	479	forward 1	TM	Cytosolic
410	LG:006764.2:2001JUN22	480	502	forward 1	TM	Transmembrane
410	LG:006764.2:2001JUN22	503	511	forward 1	TM	Non-Cytosolic
410	LG:006764.2:2001JUN22	512	534	forward 1	TM	Transmembrane
410	LG:006764.2:2001JUN22	535	539	forward 1	TM	Cytosolic
410	LG:006764.2:2001JUN22	1	441	forward 2	TM	Non-Cytosolic
410	LG:006764.2:2001JUN22	442	464	forward 2	TM	Transmembrane
410	LG:006764.2:2001JUN22	465	484	forward 2	TM	Cytosolic
410	LG:006764.2:2001JUN22	485	507	forward 2	TM	Transmembrane
410	LG:006764.2:2001JUN22	508	538	forward 2	TM	Non-Cytosolic
410	LG:006764.2:2001JUN22	1	86	forward 3	TM	Non-Cytosolic
410	LG:006764.2:2001JUN22	87	109	forward 3	TM	Transmembrane
410	LG:006764.2:2001JUN22	110	142	forward 3	TM	Cytosolic
410	LG:006764.2:2001JUN22	143	165	forward 3	TM	Transmembrane
410	LG:006764.2:2001JUN22	166	184	forward 3	TM	Non-Cytosolic
410	LG:006764.2:2001JUN22	185	207	forward 3	TM	Transmembrane
410	LG:006764.2:2001JUN22	208	472	forward 3	TM	Cytosolic
410	LG:006764.2:2001JUN22	473	495	forward 3	TM	Transmembrane
410	LG:006764.2:2001JUN22	496	509	forward 3	TM	Non-Cytosolic
410	LG:006764.2:2001JUN22	510	532	forward 3	TM	Transmembrane
410	LG:006764.2:2001JUN22	533	538	forward 3	TM	Cytosolic
411	LG:014704.8:2001JUN22	1	30	forward 1	TM	Non-Cytosolic
411	LG:014704.8:2001JUN22	31	53	forward 1	TM	Transmembrane
411	LG:014704.8:2001JUN22	54	72	forward 1	TM	Cytosolic
411	LG:014704.8:2001JUN22	73	95	forward 1	TM	Transmembrane
411	LG:014704.8:2001JUN22	96	467	forward 1	TM	Non-Cytosolic
411	LG:014704.8:2001JUN22	468	485	forward 1	TM	Transmembrane
411	LG:014704.8:2001JUN22	486	517	forward 1	TM	Cytosolic
411	LG:014704.8:2001JUN22	518	540	forward 1	TM	Transmembrane
411	LG:014704.8:2001JUN22	541	568	forward 1	TM	Non-Cytosolic
411	LG:014704.8:2001JUN22	569	591	forward 1	TM	Transmembrane
411	LG:014704.8:2001JUN22	592	647	forward 1	TM	Cytosolic
411	LG:014704.8:2001JUN22	1	505	forward 2	TM	Non-Cytosolic
411	LG:014704.8:2001JUN22	506	523	forward 2	TM	Transmembrane
411	LG:014704.8:2001JUN22	524	560	forward 2	TM	Cytosolic
411	LG:014704.8:2001JUN22	561	583	forward 2	TM	Transmembrane
411	LG:014704.8:2001JUN22	584	646	forward 2	TM	Non-Cytosolic
411	LG:014704.8:2001JUN22	1	133	forward 3	TM	Cytosolic
411	LG:014704.8:2001JUN22	134	151	forward 3	TM	Transmembrane
411	LG:014704.8:2001JUN22	152	165	forward 3	TM	Non-Cytosolic
411	LG:014704.8:2001JUN22	166	184	forward 3	TM	Transmembrane
411	LG:014704.8:2001JUN22	185	196	forward 3	TM	Cytosolic
411	LG:014704.8:2001JUN22	197	219	forward 3	TM	Transmembrane
411	LG:014704.8:2001JUN22	220	233	forward 3	TM	Non-Cytosolic
411	LG:014704.8:2001JUN22	234	256	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
411	LG:014704.8:2001JUN22	257	305	forward 3	TM	Cytosolic
411	LG:014704.8:2001JUN22	306	328	forward 3	TM	Transmembrane
411	LG:014704.8:2001JUN22	329	350	forward 3	TM	Non-Cytosolic
411	LG:014704.8:2001JUN22	351	373	forward 3	TM	Transmembrane
411	LG:014704.8:2001JUN22	374	393	forward 3	TM	Cytosolic
411	LG:014704.8:2001JUN22	394	413	forward 3	TM	Transmembrane
411	LG:014704.8:2001JUN22	414	467	forward 3	TM	Non-Cytosolic
411	LG:014704.8:2001JUN22	468	485	forward 3	TM	Transmembrane
411	LG:014704.8:2001JUN22	486	491	forward 3	TM	Cytosolic
411	LG:014704.8:2001JUN22	492	514	forward 3	TM	Transmembrane
411	LG:014704.8:2001JUN22	515	564	forward 3	TM	Non-Cytosolic
411	LG:014704.8:2001JUN22	565	584	forward 3	TM	Transmembrane
411	LG:014704.8:2001JUN22	585	646	forward 3	TM	Cytosolic
412	LG:1447607.7:2001JUN22	1	72	forward 1	TM	Cytosolic
412	LG:1447607.7:2001JUN22	73	95	forward 1	TM	Transmembrane
412	LG:1447607.7:2001JUN22	96	336	forward 1	TM	Non-Cytosolic
412	LG:1447607.7:2001JUN22	337	359	forward 1	TM	Transmembrane
412	LG:1447607.7:2001JUN22	360	406	forward 1	TM	Cytosolic
412	LG:1447607.7:2001JUN22	407	429	forward 1	TM	Transmembrane
412	LG:1447607.7:2001JUN22	430	760	forward 1	TM	Non-Cytosolic
412	LG:1447607.7:2001JUN22	1	20	forward 2	TM	Cytosolic
412	LG:1447607.7:2001JUN22	21	43	forward 2	TM	Transmembrane
412	LG:1447607.7:2001JUN22	44	72	forward 2	TM	Non-Cytosolic
412	LG:1447607.7:2001JUN22	73	92	forward 2	TM	Transmembrane
412	LG:1447607.7:2001JUN22	93	276	forward 2	TM	Cytosolic
412	LG:1447607.7:2001JUN22	277	299	forward 2	TM	Transmembrane
412	LG:1447607.7:2001JUN22	300	323	forward 2	TM	Non-Cytosolic
412	LG:1447607.7:2001JUN22	324	346	forward 2	TM	Transmembrane
412	LG:1447607.7:2001JUN22	347	407	forward 2	TM	Cytosolic
412	LG:1447607.7:2001JUN22	408	430	forward 2	TM	Transmembrane
412	LG:1447607.7:2001JUN22	431	449	forward 2	TM	Non-Cytosolic
412	LG:1447607.7:2001JUN22	450	472	forward 2	TM	Transmembrane
412	LG:1447607.7:2001JUN22	473	694	forward 2	TM	Cytosolic
412	LG:1447607.7:2001JUN22	695	717	forward 2	TM	Transmembrane
412	LG:1447607.7:2001JUN22	718	759	forward 2	TM	Non-Cytosolic
412	LG:1447607.7:2001JUN22	1	19	forward 3	TM	Cytosolic
412	LG:1447607.7:2001JUN22	20	39	forward 3	TM	Transmembrane
412	LG:1447607.7:2001JUN22	40	334	forward 3	TM	Non-Cytosolic
412	LG:1447607.7:2001JUN22	335	357	forward 3	TM	Transmembrane
412	LG:1447607.7:2001JUN22	358	381	forward 3	TM	Cytosolic
412	LG:1447607.7:2001JUN22	382	404	forward 3	TM	Transmembrane
412	LG:1447607.7:2001JUN22	405	423	forward 3	TM	Non-Cytosolic
412	LG:1447607.7:2001JUN22	424	446	forward 3	TM	Transmembrane
412	LG:1447607.7:2001JUN22	447	699	forward 3	TM	Cytosolic
412	LG:1447607.7:2001JUN22	700	722	forward 3	TM	Transmembrane
412	LG:1447607.7:2001JUN22	723	759	forward 3	TM	Non-Cytosolic
413	LG:1455032.3:2001JUN22	1	151	forward 1	TM	Cytosolic
413	LG:1455032.3:2001JUN22	152	174	forward 1	TM	Transmembrane
413	LG:1455032.3:2001JUN22	175	244	forward 1	TM	Non-Cytosolic
413	LG:1455032.3:2001JUN22	245	264	forward 1	TM	Transmembrane
413	LG:1455032.3:2001JUN22	265	396	forward 1	TM	Cytosolic
413	LG:1455032.3:2001JUN22	1	134	forward 2	TM	Cytosolic
413	LG:1455032.3:2001JUN22	135	157	forward 2	TM	Transmembrane
413	LG:1455032.3:2001JUN22	158	166	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
413	LG:1455032.3:2001JUN22	167	184	forward 2	TM	Transmembrane
413	LG:1455032.3:2001JUN22	185	396	forward 2	TM	Cytosolic
413	LG:1455032.3:2001JUN22	1	164	forward 3	TM	Cytosolic
413	LG:1455032.3:2001JUN22	165	187	forward 3	TM	Transmembrane
413	LG:1455032.3:2001JUN22	188	274	forward 3	TM	Non-Cytosolic
413	LG:1455032.3:2001JUN22	275	297	forward 3	TM	Transmembrane
413	LG:1455032.3:2001JUN22	298	395	forward 3	TM	Cytosolic
414	LG:1501898.18:2001JUN22	1	6	forward 3	TM	Cytosolic
414	LG:1501898.18:2001JUN22	7	29	forward 3	TM	Transmembrane
414	LG:1501898.18:2001JUN22	30	357	forward 3	TM	Non-Cytosolic
415	LG:1502692.5:2001JUN22	1	178	forward 1	TM	Non-Cytosolic
415	LG:1502692.5:2001JUN22	179	201	forward 1	TM	Transmembrane
415	LG:1502692.5:2001JUN22	202	213	forward 1	TM	Cytosolic
415	LG:1502692.5:2001JUN22	214	236	forward 1	TM	Transmembrane
415	LG:1502692.5:2001JUN22	237	255	forward 1	TM	Non-Cytosolic
415	LG:1502692.5:2001JUN22	256	273	forward 1	TM	Transmembrane
415	LG:1502692.5:2001JUN22	274	327	forward 1	TM	Cytosolic
415	LG:1502692.5:2001JUN22	328	347	forward 1	TM	Transmembrane
415	LG:1502692.5:2001JUN22	348	359	forward 1	TM	Non-Cytosolic
415	LG:1502692.5:2001JUN22	1	129	forward 2	TM	Cytosolic
415	LG:1502692.5:2001JUN22	130	152	forward 2	TM	Transmembrane
415	LG:1502692.5:2001JUN22	153	224	forward 2	TM	Non-Cytosolic
415	LG:1502692.5:2001JUN22	225	247	forward 2	TM	Transmembrane
415	LG:1502692.5:2001JUN22	248	258	forward 2	TM	Cytosolic
415	LG:1502692.5:2001JUN22	259	276	forward 2	TM	Transmembrane
415	LG:1502692.5:2001JUN22	277	330	forward 2	TM	Non-Cytosolic
415	LG:1502692.5:2001JUN22	331	350	forward 2	TM	Transmembrane
415	LG:1502692.5:2001JUN22	351	359	forward 2	TM	Cytosolic
415	LG:1502692.5:2001JUN22	1	44	forward 3	TM	Cytosolic
415	LG:1502692.5:2001JUN22	45	67	forward 3	TM	Transmembrane
415	LG:1502692.5:2001JUN22	68	166	forward 3	TM	Non-Cytosolic
415	LG:1502692.5:2001JUN22	167	189	forward 3	TM	Transmembrane
415	LG:1502692.5:2001JUN22	190	209	forward 3	TM	Cytosolic
415	LG:1502692.5:2001JUN22	210	232	forward 3	TM	Transmembrane
415	LG:1502692.5:2001JUN22	233	358	forward 3	TM	Non-Cytosolic
416	LG:208949.8:2001JUN22	1	177	forward 1	TM	Cytosolic
416	LG:208949.8:2001JUN22	178	200	forward 1	TM	Transmembrane
416	LG:208949.8:2001JUN22	201	219	forward 1	TM	Non-Cytosolic
416	LG:208949.8:2001JUN22	220	237	forward 1	TM	Transmembrane
416	LG:208949.8:2001JUN22	238	253	forward 1	TM	Cytosolic
416	LG:208949.8:2001JUN22	1	161	forward 2	TM	Cytosolic
416	LG:208949.8:2001JUN22	162	184	forward 2	TM	Transmembrane
416	LG:208949.8:2001JUN22	185	253	forward 2	TM	Non-Cytosolic
416	LG:208949.8:2001JUN22	1	223	forward 3	TM	Cytosolic
416	LG:208949.8:2001JUN22	224	246	forward 3	TM	Transmembrane
416	LG:208949.8:2001JUN22	247	252	forward 3	TM	Non-Cytosolic
417	LG:240501.10:2001JUN22	1	112	forward 1	TM	Cytosolic
417	LG:240501.10:2001JUN22	113	135	forward 1	TM	Transmembrane
417	LG:240501.10:2001JUN22	136	138	forward 1	TM	Non-Cytosolic
417	LG:240501.10:2001JUN22	139	161	forward 1	TM	Transmembrane
417	LG:240501.10:2001JUN22	162	167	forward 1	TM	Cytosolic
417	LG:240501.10:2001JUN22	168	185	forward 1	TM	Transmembrane
417	LG:240501.10:2001JUN22	186	215	forward 1	TM	Non-Cytosolic
417	LG:240501.10:2001JUN22	216	235	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
417	LG:240501.10:2001JUN22	236	241	forward 1	TM	Cytosolic
417	LG:240501.10:2001JUN22	242	264	forward 1	TM	Transmembrane
417	LG:240501.10:2001JUN22	265	267	forward 1	TM	Non-Cytosolic
417	LG:240501.10:2001JUN22	268	290	forward 1	TM	Transmembrane
417	LG:240501.10:2001JUN22	291	413	forward 1	TM	Cytosolic
417	LG:240501.10:2001JUN22	1	106	forward 2	TM	Cytosolic
417	LG:240501.10:2001JUN22	107	129	forward 2	TM	Transmembrane
417	LG:240501.10:2001JUN22	130	138	forward 2	TM	Non-Cytosolic
417	LG:240501.10:2001JUN22	139	161	forward 2	TM	Transmembrane
417	LG:240501.10:2001JUN22	162	215	forward 2	TM	Cytosolic
417	LG:240501.10:2001JUN22	216	233	forward 2	TM	Transmembrane
417	LG:240501.10:2001JUN22	234	413	forward 2	TM	Non-Cytosolic
417	LG:240501.10:2001JUN22	1	67	forward 3	TM	Cytosolic
417	LG:240501.10:2001JUN22	68	90	forward 3	TM	Transmembrane
417	LG:240501.10:2001JUN22	91	109	forward 3	TM	Non-Cytosolic
417	LG:240501.10:2001JUN22	110	132	forward 3	TM	Transmembrane
417	LG:240501.10:2001JUN22	133	138	forward 3	TM	Cytosolic
417	LG:240501.10:2001JUN22	139	161	forward 3	TM	Transmembrane
417	LG:240501.10:2001JUN22	162	215	forward 3	TM	Non-Cytosolic
417	LG:240501.10:2001JUN22	216	234	forward 3	TM	Transmembrane
417	LG:240501.10:2001JUN22	235	240	forward 3	TM	Cytosolic
417	LG:240501.10:2001JUN22	241	263	forward 3	TM	Transmembrane
417	LG:240501.10:2001JUN22	264	322	forward 3	TM	Non-Cytosolic
417	LG:240501.10:2001JUN22	323	345	forward 3	TM	Transmembrane
417	LG:240501.10:2001JUN22	346	412	forward 3	TM	Cytosolic
418	LG:329228.27:2001JUN22	1	261	forward 1	TM	Non-Cytosolic
418	LG:329228.27:2001JUN22	262	284	forward 1	TM	Transmembrane
418	LG:329228.27:2001JUN22	285	290	forward 1	TM	Cytosolic
418	LG:329228.27:2001JUN22	291	313	forward 1	TM	Transmembrane
418	LG:329228.27:2001JUN22	314	509	forward 1	TM	Non-Cytosolic
418	LG:329228.27:2001JUN22	1	263	forward 2	TM	Cytosolic
418	LG:329228.27:2001JUN22	264	286	forward 2	TM	Transmembrane
418	LG:329228.27:2001JUN22	287	509	forward 2	TM	Non-Cytosolic
418	LG:329228.27:2001JUN22	1	220	forward 3	TM	Non-Cytosolic
418	LG:329228.27:2001JUN22	221	243	forward 3	TM	Transmembrane
418	LG:329228.27:2001JUN22	244	254	forward 3	TM	Cytosolic
418	LG:329228.27:2001JUN22	255	274	forward 3	TM	Transmembrane
418	LG:329228.27:2001JUN22	275	508	forward 3	TM	Non-Cytosolic
419	LG:337056.11:2001JUN22	1	20	forward 2	TM	Cytosolic
419	LG:337056.11:2001JUN22	21	43	forward 2	TM	Transmembrane
419	LG:337056.11:2001JUN22	44	62	forward 2	TM	Non-Cytosolic
419	LG:337056.11:2001JUN22	63	85	forward 2	TM	Transmembrane
419	LG:337056.11:2001JUN22	86	131	forward 2	TM	Cytosolic
419	LG:337056.11:2001JUN22	132	154	forward 2	TM	Transmembrane
419	LG:337056.11:2001JUN22	155	227	forward 2	TM	Non-Cytosolic
420	LG:346663.9:2001JUN22	1	303	forward 1	TM	Non-Cytosolic
420	LG:346663.9:2001JUN22	304	326	forward 1	TM	Transmembrane
420	LG:346663.9:2001JUN22	327	337	forward 1	TM	Cytosolic
420	LG:346663.9:2001JUN22	338	360	forward 1	TM	Transmembrane
420	LG:346663.9:2001JUN22	361	388	forward 1	TM	Non-Cytosolic
420	LG:346663.9:2001JUN22	389	406	forward 1	TM	Transmembrane
420	LG:346663.9:2001JUN22	407	417	forward 1	TM	Cytosolic
420	LG:346663.9:2001JUN22	418	440	forward 1	TM	Transmembrane
420	LG:346663.9:2001JUN22	441	445	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
420	LG:346663.9:2001JUN22	1	310	forward 2	TM	Non-Cytosolic
420	LG:346663.9:2001JUN22	311	333	forward 2	TM	Transmembrane
420	LG:346663.9:2001JUN22	334	445	forward 2	TM	Cytosolic
420	LG:346663.9:2001JUN22	1	302	forward 3	TM	Cytosolic
420	LG:346663.9:2001JUN22	303	325	forward 3	TM	Transmembrane
420	LG:346663.9:2001JUN22	326	334	forward 3	TM	Non-Cytosolic
420	LG:346663.9:2001JUN22	335	357	forward 3	TM	Transmembrane
420	LG:346663.9:2001JUN22	358	363	forward 3	TM	Cytosolic
420	LG:346663.9:2001JUN22	364	386	forward 3	TM	Transmembrane
420	LG:346663.9:2001JUN22	387	400	forward 3	TM	Non-Cytosolic
420	LG:346663.9:2001JUN22	401	423	forward 3	TM	Transmembrane
420	LG:346663.9:2001JUN22	424	445	forward 3	TM	Cytosolic
421	LG:7685586.2:2001JUN22	1	152	forward 1	TM	Non-Cytosolic
421	LG:7685586.2:2001JUN22	153	175	forward 1	TM	Transmembrane
421	LG:7685586.2:2001JUN22	176	195	forward 1	TM	Cytosolic
421	LG:7685586.2:2001JUN22	1	142	forward 3	TM	Cytosolic
421	LG:7685586.2:2001JUN22	143	165	forward 3	TM	Transmembrane
421	LG:7685586.2:2001JUN22	166	194	forward 3	TM	Non-Cytosolic
422	LG:407730.13:2001JUN22	1	14	forward 1	TM	Non-Cytosolic
422	LG:407730.13:2001JUN22	15	34	forward 1	TM	Transmembrane
422	LG:407730.13:2001JUN22	35	163	forward 1	TM	Cytosolic
422	LG:407730.13:2001JUN22	1	14	forward 3	TM	Non-Cytosolic
422	LG:407730.13:2001JUN22	15	37	forward 3	TM	Transmembrane
422	LG:407730.13:2001JUN22	38	162	forward 3	TM	Cytosolic
423	LG:025465.5:2001JUN22	1	421	forward 1	TM	Non-Cytosolic
423	LG:025465.5:2001JUN22	422	444	forward 1	TM	Transmembrane
423	LG:025465.5:2001JUN22	445	500	forward 1	TM	Cytosolic
423	LG:025465.5:2001JUN22	501	523	forward 1	TM	Transmembrane
423	LG:025465.5:2001JUN22	524	708	forward 1	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	1	432	forward 1	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	433	455	forward 1	TM	Transmembrane
424	LG:054509.14:2001JUN22	456	567	forward 1	TM	Cytosolic
424	LG:054509.14:2001JUN22	568	590	forward 1	TM	Transmembrane
424	LG:054509.14:2001JUN22	591	642	forward 1	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	643	665	forward 1	TM	Transmembrane
424	LG:054509.14:2001JUN22	666	717	forward 1	TM	Cytosolic
424	LG:054509.14:2001JUN22	718	740	forward 1	TM	Transmembrane
424	LG:054509.14:2001JUN22	741	752	forward 1	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	753	775	forward 1	TM	Transmembrane
424	LG:054509.14:2001JUN22	776	938	forward 1	TM	Cytosolic
424	LG:054509.14:2001JUN22	939	961	forward 1	TM	Transmembrane
424	LG:054509.14:2001JUN22	962	975	forward 1	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	976	998	forward 1	TM	Transmembrane
424	LG:054509.14:2001JUN22	999	1004	forward 1	TM	Cytosolic
424	LG:054509.14:2001JUN22	1005	1027	forward 1	TM	Transmembrane
424	LG:054509.14:2001JUN22	1028	1066	forward 1	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	1067	1089	forward 1	TM	Transmembrane
424	LG:054509.14:2001JUN22	1090	1134	forward 1	TM	Cytosolic
424	LG:054509.14:2001JUN22	1	2	forward 2	TM	Cytosolic
424	LG:054509.14:2001JUN22	3	20	forward 2	TM	Transmembrane
424	LG:054509.14:2001JUN22	21	61	forward 2	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	62	84	forward 2	TM	Transmembrane
424	LG:054509.14:2001JUN22	85	90	forward 2	TM	Cytosolic
424	LG:054509.14:2001JUN22	91	113	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
424	LG:054509.14:2001JUN22	114	188	forward 2	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	189	206	forward 2	TM	Transmembrane
424	LG:054509.14:2001JUN22	207	466	forward 2	TM	Cytosolic
424	LG:054509.14:2001JUN22	467	489	forward 2	TM	Transmembrane
424	LG:054509.14:2001JUN22	490	737	forward 2	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	738	760	forward 2	TM	Transmembrane
424	LG:054509.14:2001JUN22	761	813	forward 2	TM	Cytosolic
424	LG:054509.14:2001JUN22	814	833	forward 2	TM	Transmembrane
424	LG:054509.14:2001JUN22	834	842	forward 2	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	843	865	forward 2	TM	Transmembrane
424	LG:054509.14:2001JUN22	866	946	forward 2	TM	Cytosolic
424	LG:054509.14:2001JUN22	947	969	forward 2	TM	Transmembrane
424	LG:054509.14:2001JUN22	970	1004	forward 2	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	1005	1027	forward 2	TM	Transmembrane
424	LG:054509.14:2001JUN22	1028	1066	forward 2	TM	Cytosolic
424	LG:054509.14:2001JUN22	1067	1089	forward 2	TM	Transmembrane
424	LG:054509.14:2001JUN22	1090	1134	forward 2	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	1	435	forward 3	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	436	454	forward 3	TM	Transmembrane
424	LG:054509.14:2001JUN22	455	466	forward 3	TM	Cytosolic
424	LG:054509.14:2001JUN22	467	489	forward 3	TM	Transmembrane
424	LG:054509.14:2001JUN22	490	503	forward 3	TM	Non-Cytosolic
424	LG:054509.14:2001JUN22	504	523	forward 3	TM	Transmembrane
424	LG:054509.14:2001JUN22	524	717	forward 3	TM	Cytosolic
424	LG:054509.14:2001JUN22	718	740	forward 3	TM	Transmembrane
424	LG:054509.14:2001JUN22	741	1133	forward 3	TM	Non-Cytosolic
425	LG:1067876.1:2001JUN22	1	105	forward 2	TM	Non-Cytosolic
425	LG:1067876.1:2001JUN22	106	128	forward 2	TM	Transmembrane
425	LG:1067876.1:2001JUN22	129	215	forward 2	TM	Cytosolic
426	LG:1327699.55:2001JUN22	1	32	forward 1	TM	Cytosolic
426	LG:1327699.55:2001JUN22	33	55	forward 1	TM	Transmembrane
426	LG:1327699.55:2001JUN22	56	64	forward 1	TM	Non-Cytosolic
426	LG:1327699.55:2001JUN22	65	87	forward 1	TM	Transmembrane
426	LG:1327699.55:2001JUN22	88	90	forward 1	TM	Cytosolic
427	LG:1482904.10:2001JUN22	1	323	forward 1	TM	Non-Cytosolic
427	LG:1482904.10:2001JUN22	324	341	forward 1	TM	Transmembrane
427	LG:1482904.10:2001JUN22	342	420	forward 1	TM	Cytosolic
427	LG:1482904.10:2001JUN22	421	443	forward 1	TM	Transmembrane
427	LG:1482904.10:2001JUN22	444	849	forward 1	TM	Non-Cytosolic
427	LG:1482904.10:2001JUN22	850	869	forward 1	TM	Transmembrane
427	LG:1482904.10:2001JUN22	870	1015	forward 1	TM	Cytosolic
427	LG:1482904.10:2001JUN22	1	959	forward 2	TM	Non-Cytosolic
427	LG:1482904.10:2001JUN22	960	982	forward 2	TM	Transmembrane
427	LG:1482904.10:2001JUN22	983	1014	forward 2	TM	Cytosolic
427	LG:1482904.10:2001JUN22	1	676	forward 3	TM	Non-Cytosolic
427	LG:1482904.10:2001JUN22	677	699	forward 3	TM	Transmembrane
427	LG:1482904.10:2001JUN22	700	918	forward 3	TM	Cytosolic
427	LG:1482904.10:2001JUN22	919	941	forward 3	TM	Transmembrane
427	LG:1482904.10:2001JUN22	942	960	forward 3	TM	Non-Cytosolic
427	LG:1482904.10:2001JUN22	961	983	forward 3	TM	Transmembrane
427	LG:1482904.10:2001JUN22	984	1014	forward 3	TM	Cytosolic
428	LG:222317.4:2001JUN22	1	4	forward 2	TM	Cytosolic
428	LG:222317.4:2001JUN22	5	27	forward 2	TM	Transmembrane
428	LG:222317.4:2001JUN22	28	85	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
428	LG:222317.4:2001JUN22	1	23	forward 3	TM	Non-Cytosolic
428	LG:222317.4:2001JUN22	24	46	forward 3	TM	Transmembrane
428	LG:222317.4:2001JUN22	47	84	forward 3	TM	Cytosolic
429	LG:332701.3:2001JUN22	1	1342	forward 1	TM	Non-Cytosolic
429	LG:332701.3:2001JUN22	1343	1365	forward 1	TM	Transmembrane
429	LG:332701.3:2001JUN22	1366	1542	forward 1	TM .	Cytosolic
429	LG:332701.3:2001JUN22	1	125	forward 2	TM	Non-Cytosolic
429	LG:332701.3:2001JUN22	126	148	forward 2	TM	Transmembrane
429	LG:332701.3:2001JUN22	149	178	forward 2	TM	Cytosolic
429	LG:332701.3:2001JUN22	179	201	forward 2	TM	Transmembrane
429	LG:332701.3:2001JUN22	202	224	forward 2	TM	Non-Cytosolic
429	LG:332701.3:2001JUN22	225	247	forward 2	TM	Transmembrane
429	LG:332701.3:2001JUN22	248	259	forward 2	TM	Cytosolic
429	LG:332701.3:2001JUN22	260	282	forward 2	TM	Transmembrane
429	LG:332701.3:2001JUN22	283	286	forward 2	TM	Non-Cytosolic
429	LG:332701.3:2001JUN22	287	309	forward 2	TM	Transmembrane
429	LG:332701.3:2001JUN22	310	507	forward 2	TM	Cytosolic
429	LG:332701.3:2001JUN22	508	530	forward 2	TM	Transmembrane
429	LG:332701.3:2001JUN22	531	983	forward 2	TM	Non-Cytosolic
429	LG:332701.3:2001JUN22	984	1006	forward 2	TM	Transmembrane
429	LG:332701.3:2001JUN22	1007	1054	forward 2	TM	Cytosolic
429	LG:332701.3:2001JUN22	1055	1077	forward 2	TM	Transmembrane
429	LG:332701.3:2001JUN22	1078	1541	forward 2	TM	Non-Cytosolic
429	LG:332701.3:2001JUN22	1	223	forward 3	TM	Non-Cytosolic
429	LG:332701.3:2001JUN22	224	246	forward 3	TM	Transmembrane
429	LG:332701.3:2001JUN22	247	507	forward 3	TM	Cytosolic
429	LG:332701.3:2001JUN22	508	530	forward 3	TM	Transmembrane
429	LG:332701.3:2001JUN22	531	1541	forward 3	TM	Non-Cytosolic
430	LG:369881.5:2001JUN22	1	311	forward 3	TM	Non-Cytosolic
430	LG:369881.5:2001JUN22	312	334	forward 3	TM	Transmembrane
430	LG:369881.5:2001JUN22	335	346	forward 3	TM	Cytosolic
430	LG:369881.5:2001JUN22	347	369	forward 3	TM	Transmembrane
430	LG:369881.5:2001JUN22	370	383	forward 3	TM	Non-Cytosolic
430	LG:369881.5:2001JUN22	384	406	forward 3	TM	Transmembrane
430	LG:369881.5:2001JUN22	407	435	forward 3	TM	Cytosolic
431	LG:404381.2:2001JUN22	1	34	forward 2	TM	Cytosolic
431	LG:404381.2:2001JUN22	35	57	forward 2	TM	Transmembrane
431	LG:404381.2:2001JUN22	58	66	forward 2	TM	Non-Cytosolic
431	LG:404381.2:2001JUN22	67	89	forward 2	TM	Transmembrane
431	LG:404381.2:2001JUN22	90	100	forward 2	TM	Cytosolic
431	LG:404381.2:2001JUN22	101	123	forward 2	TM	Transmembrane
431	LG:404381.2:2001JUN22	124	132	forward 2	TM	Non-Cytosolic
431	LG:404381.2:2001JUN22	133	155	forward 2	TM	Transmembrane
431	LG:404381.2:2001JUN22	156	192	forward 2	TM	Cytosolic
431	LG:404381.2:2001JUN22	193	215	forward 2	TM	Transmembrane
431	LG:404381.2:2001JUN22	216	271	forward 2	TM	Non-Cytosolic
431	LG:404381.2:2001JUN22	272	294	forward 2	TM	Transmembrane
431	LG:404381.2:2001JUN22	295	302	forward 2	TM	Cytosolic
431	LG:404381.2:2001JUN22	303	325	forward 2	TM	Transmembrane
431	LG:404381.2:2001JUN22	326	339	forward 2	TM	Non-Cytosolic
431	LG:404381.2:2001JUN22	340	359	forward 2	TM	Transmembrane
431	LG:404381.2:2001JUN22	360	466	forward 2	TM	Cytosolic
432	LG:405709.2:2001JUN22	1	75	forward 2	TM	Cytosolic
432	LG:405709.2:2001JUN22	76	94	forward 2	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
432	LG:405709.2:2001JUN22	95	113	forward 2	TM	Non-Cytosolic
432	LG:405709.2:2001JUN22	1	113	forward 3	TM	Cytosolic
433	LG:406664.17:2001JUN22	1	73	forward 1	TM	Cytosolic
434	LG:7670681.1:2001JUN22	1	187	forward 2	TM	Non-Cytosolic
434	LG:7670681.1:2001JUN22	188	210	forward 2	TM	Transmembrane
434	LG:7670681.1:2001JUN22	211	216	forward 2	TM	Cytosolic
434	LG:7670681.1:2001JUN22	1	37	forward 3	TM	Non-Cytosolic
434	LG:7670681.1:2001JUN22	38	60	forward 3	TM	Transmembrane
434	LG:7670681.1:2001JUN22	61	215	forward 3	TM	Cytosolic
435	LG:7687404.1:2001JUN22	1	114	forward 3	TM	Non-Cytosolic
435	LG:7687404.1:2001JUN22	115	137	forward 3	TM	Transmembrane
435	LG:7687404.1:2001JUN22	138	225	forward 3	TM	Cytosolic
435	LG:7687404.1:2001JUN22	226	248	forward 3	TM	Transmembrane
435	LG:7687404.1:2001JUN22	249	370	forward 3	TM	Non-Cytosolic
436	LG:7690030.24:2001JUN22	1	129	forward 1	TM	Cytosolic
436	LG:7690030.24:2001JUN22	1	128	forward 2	TM	Cytosolic
437	LG:7690229.3:2001JUN22	1	20	forward 3	TM	Cytosolic
437	LG:7690229.3:2001JUN22	21	40	forward 3	TM	Transmembrane
437	LG:7690229.3:2001JUN22	41	223	forward 3	TM	Non-Cytosolic
438	LG:7690533.16:2001JUN22	1	9	forward 2	TM	Non-Cytosolic
438	LG:7690533.16:2001JUN22	10	29	forward 2	TM	Transmembrane
438	LG:7690533.16:2001JUN22	30	48	forward 2	TM	Cytosolic
438	LG:7690533.16:2001JUN22	49	71	forward 2	TM	Transmembrane
438	LG:7690533.16:2001JUN22	72	393	forward 2	TM	Non-Cytosolic
439	LG:7691131.2:2001JUN22	1	22	forward 1	TM	Non-Cytosolic
439	LG:7691131.2:2001JUN22	23	45	forward 1	TM	Transmembrane
439	LG:7691131.2:2001JUN22	46	331	forward 1	TM	Cytosolic
439	LG:7691131.2:2001JUN22	1	101	forward 3	TM	Non-Cytosolic
439	LG:7691131.2:2001JUN22	102	124	forward 3	TM	Transmembrane
439	LG:7691131.2:2001JUN22	125	287	forward 3	TM	Cytosolic
439	LG:7691131.2:2001JUN22	288	307	forward 3	TM	Transmembrane
439	LG:7691131.2:2001JUN22	308	330	forward 3	TM	Non-Cytosolic
440	LG:7692559.6:2001JUN22	1	3	forward 1	TM	Non-Cytosolic
440	LG:7692559.6:2001JUN22	4	23	forward 1	TM	Transmembrane
440	LG:7692559.6:2001JUN22	24	35	forward 1	TM	Cytosolic
440	LG:7692559.6:2001JUN22	36	53	forward 1	TM	Transmembrane
440	LG:7692559.6:2001JUN22	54	239	forward 1	TM	Non-Cytosolic
440	LG:7692559.6:2001JUN22	1	48	forward 3	TM	Non-Cytosolic
440	LG:7692559.6:2001JUN22	49	71	forward 3	TM	Transmembrane
440	LG:7692559.6:2001JUN22	72	75	forward 3	TM	Cytosolic
440	LG:7692559.6:2001JUN22	76	98	forward 3	TM	Transmembrane
440	LG:7692559.6:2001JUN22	99	238	forward 3	TM	Non-Cytosolic
441	LG:7684866.10:2001JUN22	1	56	forward 2	TM	Cytosolic
441	LG:7684866.10:2001JUN22	57	79	forward 2	TM	Transmembrane
441	LG:7684866.10:2001JUN22	80	93	forward 2	TM	Non-Cytosolic
441	LG:7684866.10:2001JUN22	94	116	forward 2	TM	Transmembrane
441	LG:7684866.10:2001JUN22	117	170	forward 2	TM	Cytosolic
442	LG:002106.5:2001JUN22	1	344	forward 2	TM	Non-Cytosolic
442	LG:002106.5:2001JUN22	345	367	forward 2	TM	Transmembrane
442	LG:002106.5:2001JUN22	368	387	forward 2	TM	Cytosolic
442	LG:002106.5:2001JUN22	388	410	forward 2	TM	Transmembrane
442	LG:002106.5:2001JUN22	411	419	forward 2	TM	Non-Cytosolic
442	LG:002106.5:2001JUN22	420	439	forward 2	TM	Transmembrane
442	LG:002106.5:2001JUN22	440	548	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
442	LG:002106.5:2001JUN22	1	386	forward 3	TM	Non-Cytosolic
442	LG:002106.5:2001JUN22	387	409	forward 3	TM	Transmembrane
442	LG:002106.5:2001JUN22	410	420	forward 3	TM	Cytosolic
442	LG:002106.5:2001JUN22	421	443	forward 3	TM	Transmembrane
442	LG:002106.5:2001JUN22	444	548	forward 3	TM	Non-Cytosolic
443	LG:004064.1:2001JUN22	1	20	forward 1	TM	Cytosolic
443	LG:004064.1:2001JUN22	21	43	forward 1	TM	Transmembrane
443	LG:004064.1:2001JUN22	44	335	forward 1	TM	Non-Cytosolic
443	LG:004064.1:2001JUN22	1	47	forward 2	TM	Non-Cytosolic
443	LG:004064.1:2001JUN22	48	70	forward 2	TM	Transmembrane
443	LG:004064.1:2001JUN22	71	335	forward 2	TM	Cytosolic
443	LG:004064.1:2001JUN22	1	47	forward 3	TM	Non-Cytosolic
443	LG:004064.1:2001JUN22	48	70	forward 3	TM	Transmembrane
443	LG:004064.1:2001JUN22	71	208	forward 3	TM	Cytosolic
443	LG:004064.1:2001JUN22	209	228	forward 3	TM	Transmembrane
443	LG:004064.1:2001JUN22	229	267	forward 3	TM	Non-Cytosolic
443	LG:004064.1:2001JUN22	268	290	forward 3	TM	Transmembrane
443	LG:004064.1:2001JUN22	291	335	forward 3	TM	Cytosolic
444	LG:007916.8:2001JUN22	1	159	forward 1	TM	Cytosolic
444	LG:007916.8:2001JUN22	160	182	forward 1	TM	Transmembrane
444	LG:007916.8:2001JUN22	183	499	forward 1	TM	Non-Cytosolic
445	LG:014719.14:2001JUN22	1	913	forward 1	TM	Non-Cytosolic
445	LG:014719.14:2001JUN22	914	936	forward 1	TM	Transmembrane
445	LG:014719.14:2001JUN22	937	966	forward 1	TM	Cytosolic
445	LG:014719.14:2001JUN22	1	915	forward 2	TM	Non-Cytosolic
445	LG:014719.14:2001JUN22	916	938	forward 2	TM	Transmembrane
445	LG:014719.14:2001JUN22	939	966	forward 2	TM	Cytosolic
446	LG:021763.31:2001JUN22	81	170	forward 3	SP	
446	LG:021763.31:2001JUN22	1	131	forward 3	TM	Non-Cytosolic
446	LG:021763.31:2001JUN22	132	154	forward 3	TM	Transmembrane
446	LG:021763.31:2001JUN22	155	233	forward 3	TM	Cytosolic
447	LG:025397.1:2001JUN22	1	40	forward 3	TM	Cytosolic
447	LG:025397.1:2001JUN22	41	63	forward 3	TM	Transmembrane
447	LG:025397.1:2001JUN22	64	77	forward 3	TM	Non-Cytosolic
447	LG:025397.1:2001JUN22	78	100	forward 3	TM	Transmembrane
447	LG:025397.1:2001JUN22	101	112	forward 3	TM	Cytosolic
447	LG:025397.1:2001JUN22	113	132	forward 3	TM	Transmembrane
447	LG:025397.1:2001JUN22	133	879	forward 3	TM	Non-Cytosolic
448	LG:029880.20:2001JUN22	1	399	forward 2	TM	Non-Cytosolic
448	LG:029880.20:2001JUN22	400	422	forward 2	TM	Transmembrane
448	LG:029880.20:2001JUN22	423	434	forward 2	TM	Cytosolic
448	LG:029880.20:2001JUN22	435	457	forward 2	TM	Transmembrane
448	LG:029880.20:2001JUN22	458	1076	forward 2	TM	Non-Cytosolic
448	LG:029880.20:2001JUN22	1	316	forward 3	TM	Non-Cytosolic
448	LG:029880.20:2001JUN22	317	339	forward 3	TM	Transmembrane
448	LG:029880.20:2001JUN22	340	565	forward 3	TM	Cytosolic
448	LG:029880.20:2001JUN22	566	588	forward 3	TM	Transmembrane
448	LG:029880.20:2001JUN22	589	1075	forward 3	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	1	344	forward 1	TM	Cytosolic
449	LG:040422.37:2001JUN22	345	367	forward 1	TM	Transmembrane
449	LG:040422.37:2001JUN22	368	386	forward 1	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	387	409	forward 1	TM	Transmembrane
449	LG:040422.37:2001JUN22	410	447	forward 1	TM	Cytosolic
449	LG:040422.37:2001JUN22	448	470	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
449	LG:040422.37:2001JUN22	471	542	forward 1	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	543	565	forward 1	TM	Transmembrane
449	LG:040422.37:2001JUN22	566	639	forward 1	TM	Cytosolic
449	LG:040422.37:2001JUN22	640	662	forward 1	TM	Transmembrane
449	LG:040422.37:2001JUN22	663	671	forward 1	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	672	694	forward 1	TM	Transmembrane
449	LG:040422.37:2001JUN22	695	747	forward 1	TM	Cytosolic
449	LG:040422.37:2001JUN22	748	770	forward 1	TM	Transmembrane
449	LG:040422.37:2001JUN22	771	795	forward 1	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	796	814	forward 1	TM	Transmembrane
449	LG:040422.37:2001JUN22	815	820	forward 1	TM	Cytosolic
449	LG:040422.37:2001JUN22	821	843	forward 1	TM	Transmembrane
449	LG:040422.37:2001JUN22	844	1065	forward 1	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	1	640	forward 2	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	641	663	forward 2	TM	Transmembrane
449	LG:040422.37:2001JUN22	664	674	forward 2	TM	Cytosolic
449	LG:040422.37:2001JUN22	675	696	forward 2	TM	Transmembrane
449	LG:040422.37:2001JUN22	697	742	forward 2	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	743	765	forward 2	TM	Transmembrane
449	LG:040422.37:2001JUN22	766	803	forward 2	TM	Cytosolic
449	LG:040422.37:2001JUN22	804	826	forward 2	TM	Transmembrane
449	LG:040422.37:2001JUN22	827	925	forward 2	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	926	948	forward 2	TM	Transmembrane
449	LG:040422.37:2001JUN22	949	1065	forward 2	TM	Cytosolic
449	LG:040422.37:2001JUN22	1	575	forward 3	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	576	598	forward 3	TM	Transmembrane
449	LG:040422.37:2001JUN22	599	622	forward 3	TM	Cytosolic
449	LG:040422.37:2001JUN22	623	645	forward 3	TM	Transmembrane
449	LG:040422.37:2001JUN22	646	649	forward 3	TM	Non-Cytosolic
449	LG:040422.37:2001JUN22	650	672	forward 3	TM	Transmembrane
449	LG:040422.37:2001JUN22	673	746	forward 3	TM	Cytosolic
449	LG:040422.37:2001JUN22	747	769	forward 3	TM	Transmembrane
449	LG:040422.37:2001JUN22	770	1064	forward 3	TM	Non-Cytosolic
450	LG:065935.11:2001JUN22	1	9	forward 1	TM	Non-Cytosolic
450	LG:065935.11:2001JUN22	10	27	forward 1	TM	Transmembrane
450	LG:065935.11:2001JUN22	28	46	forward 1	TM	Cytosolic
450	LG:065935.11:2001JUN22	47	69	forward 1	TM	Transmembrane
450	LG:065935.11:2001JUN22	70	1451	forward 1	TM	Non-Cytosolic
450	LG:065935.11:2001JUN22	1	33	forward 2	TM	Cytosolic
450	LG:065935.11:2001JUN22	34	56	forward 2	TM	Transmembrane
450	LG:065935.11:2001JUN22	57	65	forward 2	TM	Non-Cytosolic
450	LG:065935.11:2001JUN22	66	88	forward 2	TM	Transmembrane
450	LG:065935.11:2001JUN22	89	312	forward 2	TM	Cytosolic
450	LG:065935.11:2001JUN22	313	335	forward 2	TM	Transmembrane
450	LG:065935.11:2001JUN22	336	370	forward 2	TM	Non-Cytosolic
450	LG:065935.11:2001JUN22	371	393	forward 2	TM	Transmembrane
450	LG:065935.11:2001JUN22	394	449	forward 2	TM	Cytosolic
450	LG:065935.11:2001JUN22	450	472	forward 2	TM	Transmembrane
450	LG:065935.11:2001JUN22	473	498	forward 2	TM	Non-Cytosolic
450	LG:065935.11:2001JUN22	499	518	forward 2	TM	Transmembrane
450	LG:065935.11:2001JUN22	519	538	forward 2	TM	Cytosolic
450	LG:065935.11:2001JUN22	539	561	forward 2	TM	Transmembrane
450	LG:065935.11:2001JUN22	562	1450	forward 2	TM	Non-Cytosolic
450	LG:065935.11:2001JUN22	1	9	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
450	LG:065935.11:2001JUN22	10	27	forward 3	TM	Transmembrane
450	LG:065935.11:2001JUN22	28	39	forward 3	TM	Cytosolic
450	LG:065935.11:2001JUN22	40	62	forward 3	TM	Transmembrane
450	LG:065935.11:2001JUN22	63	71	forward 3	TM	Non-Cytosolic
450	LG:065935.11:2001JUN22	72	94	forward 3	TM	Transmembrane
450	LG:065935.11:2001JUN22	95	370	forward 3	TM	Cytosolic
450	LG:065935.11:2001JUN22	371	393	forward 3	TM	Transmembrane
450	LG:065935.11:2001JUN22	394	1182	forward 3	TM	Non-Cytosolic
450	LG:065935.11:2001JUN22	1183	1202	forward 3	TM	Transmembrane
450	LG:065935.11:2001JUN22	1203	1395	forward 3	TM	Cytosolic
450	LG:065935.11:2001JUN22	1396	1418	forward 3	TM	Transmembrane
450	LG:065935.11:2001JUN22	1419	1450	forward 3	TM	Non-Cytosolic
451	LG:074381.1:2001JUN22	1	318	forward 2	TM	Non-Cytosolic
451	LG:074381.1:2001JUN22	319	341	forward 2	TM	Transmembrane
451	LG:074381.1:2001JUN22	342	361	forward 2	TM	Cytosolic
451	LG:074381.1:2001JUN22	362	384	forward 2	TM	Transmembrane
451	LG:074381.1:2001JUN22	385	421	forward 2	TM	Non-Cytosolic
451	LG:074381.1:2001JUN22	1	229	forward 3	TM	Non-Cytosolic
451	LG:074381.1:2001JUN22	230	252	forward 3	TM	Transmembrane
451	LG:074381.1:2001JUN22	253	256	forward 3	TM	Cytosolic
451	LG:074381.1:2001JUN22	257	279	forward 3	TM	Transmembrane
451	LG:074381.1:2001JUN22	280	317	forward 3	TM	Non-Cytosolic
451	LG:074381.1:2001JUN22	318	340	forward 3	TM	Transmembrane
451	LG:074381.1:2001JUN22	341	352	forward 3	TM	Cytosolic
451	LG:074381.1:2001JUN22	353	375	forward 3	TM	Transmembrane
451	LG:074381.1:2001JUN22	376	394	forward 3	TM	Non-Cytosolic
451	LG:074381.1:2001JUN22	395	417	forward 3	TM	Transmembrane
451	LG:074381.1:2001JUN22	418	421	forward 3	TM	Cytosolic
452	LG:083814.6:2001JUN22	1	736	forward 1	TM	Non-Cytosolic
452	LG:083814.6:2001JUN22	737	756	forward 1	TM	Transmembrane
452	LG:083814.6:2001JUN22	757	790	forward 1	TM	Cytosolic
452	LG:083814.6:2001JUN22	791	809	forward 1	TM	Transmembrane
452	LG:083814.6:2001JUN22	810	817	forward 1	TM	Non-Cytosolic
452	LG:083814.6:2001JUN22	1	757	forward 3	TM	Non-Cytosolic
452	LG:083814.6:2001JUN22	758	777	forward 3	TM	Transmembrane
452	LG:083814.6:2001JUN22	778	788	forward 3	TM	Cytosolic
452	LG:083814.6:2001JUN22	789	806	forward 3	TM	Transmembrane
452	LG:083814.6:2001JUN22	807	816	forward 3	TM	Non-Cytosolic
453	LG:090985.1:2001JUN22	1	11	forward 3	TM	Cytosolic
453	LG:090985.1:2001JUN22	12	34	forward 3	TM	Transmembrane
453	LG:090985.1:2001JUN22	35	37	forward 3	TM	Non-Cytosolic
453	LG:090985.1:2001JUN22	38	60	forward 3	TM	Transmembrane
453	LG:090985.1:2001JUN22	61	206	forward 3	TM	Cytosolic
454	LG:093750.2:2001JUN22	1	392	forward 2	TM	Non-Cytosolic
454	LG:093750.2:2001JUN22	393	410	forward 2	TM	Transmembrane
454	LG:093750.2:2001JUN22	411	411	forward 2	TM	Cytosolic
455	LG:1013708.26:2001JUN22	1	77	forward 1	TM	Cytosolic
455	LG:1013708.26:2001JUN22	78	95	forward 1	TM	Transmembrane
455	LG:1013708.26:2001JUN22	96	109	forward 1	TM	Non-Cytosolic
455	LG:1013708.26:2001JUN22	110	132	forward 1	TM	Transmembrane
455	LG:1013708.26:2001JUN22	133	147	forward 1	TM	Cytosolic
455	LG:1013708.26:2001JUN22	148	170	forward 1	TM	Transmembrane
455	LG:1013708.26:2001JUN22	171	558	forward 1	TM	Non-Cytosolic
455	LG:1013708.26:2001JUN22	1	74	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
455	LG:1013708.26:2001JUN22	75	97	forward 2	TM	Transmembrane
455	LG:1013708.26:2001JUN22	98	100	forward 2	TM	Non-Cytosolic
455	LG:1013708.26:2001JUN22	101	120	forward 2	TM	Transmembrane
455	LG:1013708.26:2001JUN22	121	369	forward 2	TM	Cytosolic
455	LG:1013708.26:2001JUN22	370	392	forward 2	TM	Transmembrane
455	LG:1013708.26:2001JUN22	393	558	forward 2	TM	Non-Cytosolic
455	LG:1013708.26:2001JUN22	1	77	forward 3	TM	Cytosolic
455	LG:1013708.26:2001JUN22	78	100	forward 3	TM	Transmembrane
455	LG:1013708.26:2001JUN22	101	103	forward 3	TM	Non-Cytosolic
455	LG:1013708.26:2001JUN22	104	126	forward 3	TM	Transmembrane
455	LG:1013708.26:2001JUN22	127	146	forward 3	TM	Cytosolic
455	LG:1013708.26:2001JUN22	147	166	forward 3	TM	Transmembrane
455	LG:1013708.26:2001JUN22	167	557	forward 3	TM	Non-Cytosolic
456	LG:1022283.8:2001JUN22	1	1703	forward 1	TM	Non-Cytosolic
456	LG:1022283.8:2001JUN22	1704	1726	forward 1	TM	Transmembrane
456	LG:1022283.8:2001JUN22	1727	1903	forward 1	TM	Cytosolic
456	LG:1022283.8:2001JUN22	1904	1926	forward 1	TM	Transmembrane
456	LG:1022283.8:2001JUN22	1927	2059	forward 1	TM	Non-Cytosolic
456	LG:1022283.8:2001JUN22	2060	2082	forward 1	TM	Transmembrane
456	LG:1022283.8:2001JUN22	2083	2182	forward 1	TM	Cytosolic
456	LG:1022283.8:2001JUN22	2183	2201	forward 1	TM	Transmembrane
456	LG:1022283.8:2001JUN22	2202	2231	forward 1	TM	Non-Cytosolic
456	LG:1022283.8:2001JUN22	2232	2251	forward 1	TM	Transmembrane
456	LG:1022283.8:2001JUN22	2252	2390	forward 1	TM	Cytosolic
456	LG:1022283.8:2001JUN22	1	1894	forward 2	TM	Non-Cytosolic
456	LG:1022283.8:2001JUN22	1895	1917	forward 2	TM	Transmembrane
456	LG:1022283.8:2001JUN22	1918	2060	forward 2	TM	Cytosolic
456	LG:1022283.8:2001JUN22	2061	2083	forward 2	TM	Transmembrane
456	LG:1022283.8:2001JUN22	2084	2173	forward 2	TM	Non-Cytosolic
456	LG:1022283.8:2001JUN22	2174	2196	forward 2	TM	Transmembrane
456	LG:1022283.8:2001JUN22	2197	2207	forward 2	TM	Cytosolic
456	LG:1022283.8:2001JUN22	2208	2225	forward 2	TM	Transmembrane
456	LG:1022283.8:2001JUN22	2226	2229	forward 2	TM	Non-Cytosolic
456	LG:1022283.8:2001JUN22	2230	2252	forward 2	TM	Transmembrane
456	LG:1022283.8:2001JUN22	2253	2264	forward 2	TM	Cytosolic
456	LG:1022283.8:2001JUN22	2265	2284	forward 2	TM	Transmembrane
456	LG:1022283.8:2001JUN22	2285	2390	forward 2	TM	Non-Cytosolic
456	LG:1022283.8:2001JUN22	1	1894	forward 3	TM	Non-Cytosolic
456	LG:1022283.8:2001JUN22	1895	1917	forward 3	TM	Transmembrane
456	LG:1022283.8:2001JUN22	1918	2057	forward 3	TM	Cytosolic
456	LG:1022283.8:2001JUN22	2058	2077	forward 3	TM	Transmembrane
456	LG:1022283.8:2001JUN22	2078	2229	forward 3	TM	Non-Cytosolic
456	LG:1022283.8:2001JUN22	2230	2252	forward 3	TM	Transmembrane
456	LG:1022283.8:2001JUN22	2253	2389	forward 3	TM	Cytosolic
457	LG:1034386.1:2001JUN22	1	37	forward 1	TM	Non-Cytosolic
457	LG:1034386.1:2001JUN22	38	60	forward 1	TM	Transmembrane
457	LG:1034386.1:2001JUN22	61	101	forward 1	TM	Cytosolic
457	LG:1034386.1:2001JUN22	102	124	forward 1	TM	Transmembrane
457	LG:1034386.1:2001JUN22	125	345	forward 1	TM	Non-Cytosolic
457	LG:1034386.1:2001JUN22	1	8	forward 2	TM	Cytosolic
457	LG:1034386.1:2001JUN22	9	31	forward 2	TM	Transmembrane
457	LG:1034386.1:2001JUN22	32	50	forward 2	TM	Non-Cytosolic
457	LG:1034386.1:2001JUN22	51	68	forward 2	TM	Transmembrane
457	LG:1034386.1:2001JUN22	69	112	forward 2	TM	Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
457	LG:1034386.1:2001JUN22	113	135	forward 2	TM	Transmembrane
457	LG:1034386.1:2001JUN22	136	192	forward 2	TM	Non-Cytosolic
457	LG:1034386.1:2001JUN22	193	215	forward 2	TM	Transmembrane
457	LG:1034386.1:2001JUN22	216	226	forward 2	TM	Cytosolic
457	LG:1034386.1:2001JUN22	227	249	forward 2	TM	Transmembrane
457	LG:1034386.1:2001JUN22	250	345	forward 2	TM	Non-Cytosolic
457	LG:1034386.1:2001JUN22	1	102	forward 3	TM	Non-Cytosolic
457	LG:1034386.1:2001JUN22	103	125	forward 3	TM	Transmembrane
457	LG:1034386.1:2001JUN22	126	345	forward 3	TM	Cytosolic
458	LG:1045617.36:2001JUN22	1	334	forward 3	TM	Non-Cytosolic
458	LG:1045617.36:2001JUN22	335	357	forward 3	TM	Transmembrane
458	LG:1045617.36:2001JUN22	358	388	forward 3	TM	Cytosolic
459	LG:1063303.1:2001JUN22	1	22	forward 3	TM	Non-Cytosolic
459	LG:1063303.1:2001JUN22	23	45	forward 3	TM	Transmembrane
459	LG:1063303.1:2001JUN22	46	51	forward 3	TM	Cytosolic
459	LG:1063303.1:2001JUN22	52	74	forward 3	TM	Transmembrane
459	LG:1063303.1:2001JUN22	75	432	forward 3	TM	Non-Cytosolic
459	LG:1063303.1:2001JUN22	433	455	forward 3	TM	Transmembrane
459	LG:1063303.1:2001JUN22	456	575	forward 3	TM	Cytosolic
460	LG:1094200.1:2001JUN22	1	316	forward 1	TM	Non-Cytosolic
460	LG:1094200.1:2001JUN22	317	339	forward 1	TM	Transmembrane
460	LG:1094200.1:2001JUN22	340	372	forward 1	TM	Cytosolic
460	LG:1094200.1:2001JUN22	373	395	forward 1	TM	Transmembrane
460	LG:1094200.1:2001JUN22	396	1061	forward 1	TM	Non-Cytosolic
460	LG:1094200.1:2001JUN22	1	314	forward 2	TM	Non-Cytosolic
460	LG:1094200.1:2001JUN22	315	337	forward 2	TM	Transmembrane
460	LG:1094200.1:2001JUN22	338	366	forward 2	TM	Cytosolic
460	LG:1094200.1:2001JUN22	367	389	forward 2	TM	Transmembrane
460	LG:1094200.1:2001JUN22	390	392	forward 2	TM	Non-Cytosolic
460	LG:1094200.1:2001JUN22	393	412	forward 2	TM	Transmembrane
460	LG:1094200.1:2001JUN22	413	678	forward 2	TM	Cytosolic
460	LG:1094200.1:2001JUN22	679	701	forward 2	TM	Transmembrane
460	LG:1094200.1:2001JUN22	702	1061	forward 2	TM	Non-Cytosolic
460	LG:1094200.1:2001JUN22	1	380	forward 3	TM	Non-Cytosolic
460	LG:1094200.1:2001JUN22	381	403	forward 3	TM	Transmembrane
460	LG:1094200.1:2001JUN22	404	415	forward 3	TM	Cytosolic
460	LG:1094200.1:2001JUN22	416	438	forward 3	TM	Transmembrane
460	LG:1094200.1:2001JUN22	439	1061	forward 3	TM	Non-Cytosolic
461	LG:1099249.19:2001JUN22	1	417	forward 1	TM	Non-Cytosolic
461	LG:1099249.19:2001JUN22	418	437	forward 1	TM	Transmembrane
461	LG:1099249.19:2001JUN22	438	566	forward 1	TM	Cytosolic
461	LG:1099249.19:2001JUN22	567	589	forward 1	TM	Transmembrane
461	LG:1099249.19:2001JUN22	590	615	forward 1	TM	Non-Cytosolic
461	LG:1099249.19:2001JUN22	1	538	forward 2	TM	Non-Cytosolic
461	LG:1099249.19:2001JUN22	539	557	forward 2	TM	Transmembrane
461	LG:1099249.19:2001JUN22	558	569	forward 2	TM	Cytosolic
461	LG:1099249.19:2001JUN22	570	592	forward 2	TM	Transmembrane
461	LG:1099249.19:2001JUN22	593	614	forward 2	TM	Non-Cytosolic
461	LG:1099249.19:2001JUN22	1	490	forward 3	TM	Non-Cytosolic
461	LG:1099249.19:2001JUN22	491	513	forward 3	TM	Transmembrane
461	LG:1099249.19:2001JUN22	514	583	forward 3	TM	Cytosolic
461	LG:1099249.19:2001JUN22	584	606	forward 3	TM	Transmembrane
461	LG:1099249.19:2001JUN22	607	614	forward 3	TM	Non-Cytosolic
462	LG:110667.1:2001JUN22	1	41	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
462	LG:110667.1:2001JUN22	42	64	forward 2	TM	Transmembrane
462	LG:110667.1:2001JUN22	65	70	forward 2	TM	Cytosolic
462	LG:110667.1:2001JUN22	71	93	forward 2	TM	Transmembrane
462	LG:110667.1:2001JUN22	94	857	forward 2	TM	Non-Cytosolic
463	LG:1132386.20:2001JUN22	1	925	forward 1	TM	Non-Cytosolic
463	LG:1132386.20:2001JUN22	926	948	forward 1	TM	Transmembrane
463	LG:1132386.20:2001JUN22	949	1027	forward 1	TM	Cytosolic
463	LG:1132386.20:2001JUN22	1028	1050	forward 1	TM	Transmembrane
463	LG:1132386.20:2001JUN22	1051	1115	forward 1	TM	Non-Cytosolic
463	LG:1132386.20:2001JUN22	1116	1138	forward 1	TM	Transmembrane
463	LG:1132386.20:2001JUN22	1139	1149	forward 1	TM	Cytosolic
463	LG:1132386.20:2001JUN22	1150	1172	forward 1	TM	Transmembrane
463	LG:1132386.20:2001JUN22	1173	1199	forward 1	TM	Non-Cytosolic
463	LG:1132386.20:2001JUN22	1	946	forward 2	TM	Non-Cytosolic
463	LG:1132386.20:2001JUN22	947	969	forward 2	TM	Transmembrane
463	LG:1132386.20:2001JUN22	970	981	forward 2	TM	Cytosolic
463	LG:1132386.20:2001JUN22	982	1004	forward 2	TM	Transmembrane
463	LG:1132386.20:2001JUN22	1005	1023	forward 2	TM	Non-Cytosolic
463	LG:1132386.20:2001JUN22	1024	1046	forward 2	TM	Transmembrane
463	LG:1132386.20:2001JUN22	1047	1199	forward 2	TM	Cytosolic
463	LG:1132386.20:2001JUN22	1	136	forward 3	TM	Cytosolic
463	LG:1132386.20:2001JUN22	137	159	forward 3	TM	Transmembrane
463	LG:1132386.20:2001JUN22	160	775	forward 3	TM	Non-Cytosolic
463	LG:1132386.20:2001JUN22	776	798	forward 3	TM	Transmembrane
463	LG:1132386.20:2001JUN22	799	926	forward 3	TM	Cytosolic
463	LG:1132386.20:2001JUN22	927	949	forward 3	TM	Transmembrane
463	LG:1132386.20:2001JUN22	950	968	forward 3	TM	Non-Cytosolic
463	LG:1132386.20:2001JUN22	969	991	forward 3	TM	Transmembrane
463	LG:1132386.20:2001JUN22	992	997	forward 3	TM	Cytosolic
463	LG:1132386.20:2001JUN22	998	1020	forward 3	TM	Transmembrane
463	LG:1132386.20:2001JUN22	1021	1024	forward 3	TM	Non-Cytosolic
463	LG:1132386.20:2001JUN22	1025	1044	forward 3	TM	Transmembrane
463	LG:1132386.20:2001JUN22	1045	1140	forward 3	TM	Cytosolic
463	LG:1132386.20:2001JUN22	1141	1163	forward 3	TM	Transmembrane
463	LG:1132386.20:2001JUN22	1164	1198	forward 3	TM	Non-Cytosolic
464	LG:116015.2:2001JUN22	1	443	forward 1	TM	Non-Cytosolic
464	LG:116015.2:2001JUN22	444	466	forward 1	TM	Transmembrane
464	LG:116015.2:2001JUN22	467	542	forward 1	TM	Cytosolic
464	LG:116015.2:2001JUN22	543	560	forward 1	TM	Transmembrane
464	LG:116015.2:2001JUN22	561	662	forward 1	TM	Non-Cytosolic
464	LG:116015.2:2001JUN22	663	685	forward 1	TM	Transmembrane
464	LG:116015.2:2001JUN22	686	697	forward 1	TM	Cytosolic
464	LG:116015.2:2001JUN22	698	720	forward 1	TM	Transmembrane
464	LG:116015.2:2001JUN22	721	734	forward 1	TM	Non-Cytosolic
464	LG:116015.2:2001JUN22	735	757	forward 1	TM	Transmembrane
464	LG:116015.2:2001JUN22	758	761	forward 1	TM	Cytosolic
464	LG:116015.2:2001JUN22	762	779	forward 1	TM	Transmembrane
464	LG:116015.2:2001JUN22	780	793	forward 1	TM	Non-Cytosolic
464	LG:116015.2:2001JUN22	794	816	forward 1	TM	Transmembrane
464	LG:116015.2:2001JUN22	817	945	forward 1	TM	Cytosolic
464	LG:116015.2:2001JUN22	946	965	forward 1	TM	Transmembrane
464	LG:116015.2:2001JUN22	966	1062	forward 1	TM	Non-Cytosolic
464	LG:116015.2:2001JUN22	1	446	forward 2	TM	Non-Cytosolic
464	LG:116015.2:2001JUN22	447	469	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
464	LG:116015.2:2001JUN22	470	489	forward 2	TM	Cytosolic
464	LG:116015.2:2001JUN22	490	512	forward 2	TM	Transmembrane
464	LG:116015.2:2001JUN22	513	539	forward 2	TM	Non-Cytosolic
464	LG:116015.2:2001JUN22	540	562	forward 2	TM	Transmembrane
464	LG:116015.2:2001JUN22	563	760	forward 2	TM	Cytosolic
464	LG:116015.2:2001JUN22	761	783	forward 2	TM	Transmembrane
464	LG:116015.2:2001JUN22	784	1062	forward 2	TM	Non-Cytosolic
464	LG:116015.2:2001JUN22	1	442	forward 3	TM	Non-Cytosolic
464	LG:116015.2:2001JUN22	443	465	forward 3	TM	Transmembrane
464	LG:116015.2:2001JUN22	466	543	forward 3	TM	Cytosolic
464	LG:116015.2:2001JUN22	544	561	forward 3	TM	Transmembrane
464	LG:116015.2:2001JUN22	562	1062	forward 3	TM	Non-Cytosolic
465	LG:1173104.15:2001JUN22	1	295	forward 1	TM	Non-Cytosolic
465	LG:1173104.15:2001JUN22	296	318	forward 1	TM	Transmembrane
465	LG:1173104.15:2001JUN22	319	324	forward 1	TM	Cytosolic
465	LG:1173104.15:2001JUN22	325	347	forward 1	TM	Transmembrane
465	LG:1173104.15:2001JUN22	348	516	forward 1	TM	Non-Cytosolic
465	LG:1173104.15:2001JUN22	1	296	forward 2	TM	Cytosolic
465	LG:1173104.15:2001JUN22	297	319	forward 2	TM	Transmembrane
465	LG:1173104.15:2001JUN22	320	328	forward 2	TM	Non-Cytosolic
465	LG:1173104.15:2001JUN22	329	348	forward 2	TM	Transmembrane
465	LG:1173104.15:2001JUN22	349	516	forward 2	TM	Cytosolic
465	LG:1173104.15:2001JUN22	1	209	forward 3	TM	Cytosolic
465	LG:1173104.15:2001JUN22	210	232	forward 3	TM	Transmembrane
465	LG:1173104.15:2001JUN22	233	305	forward 3	TM	Non-Cytosolic
465	LG:1173104.15:2001JUN22	306	323	forward 3	TM	Transmembrane
465	LG:1173104.15:2001JUN22	324	329	forward 3	TM	Cytosolic
465	LG:1173104.15:2001JUN22	330	352	forward 3	TM	Transmembrane
465	LG:1173104.15:2001JUN22	353	516	forward 3	TM	Non-Cytosolic
466	LG:1285109.14:2001JUN22	1	4	forward 1	TM	Cytosolic
466	LG:1285109.14:2001JUN22	5	27	forward 1	TM	Transmembrane
466	LG:1285109.14:2001JUN22	28	483	forward 1	TM	Non-Cytosolic
466	LG:1285109.14:2001JUN22	1	6	forward 3	TM	Cytosolic
466	LG:1285109.14:2001JUN22	7	29	forward 3	TM	Transmembrane
466	LG:1285109.14:2001JUN22	30	61	forward 3	TM	Non-Cytosolic
466	LG:1285109.14:2001JUN22	62	84	forward 3	TM	Transmembrane
466	LG:1285109.14:2001JUN22	85	427	forward 3	TM	Cytosolic
466	LG:1285109.14:2001JUN22	428	450	forward 3	TM	Transmembrane
466	LG:1285109.14:2001JUN22	451	459	forward 3	TM	Non-Cytosolic
466	LG:1285109.14:2001JUN22	460	479	forward 3	TM	Transmembrane
466	LG:1285109.14:2001JUN22	480	483	forward 3	TM	Cytosolic
467	LG:131477.11:2001JUN22	1	1781	forward 1	TM	Non-Cytosolic
467	LG:131477.11:2001JUN22	1782	1804	forward 1	TM	Transmembrane
467	LG:131477.11:2001JUN22	1805	1830	forward 1	TM	Cytosolic
467	LG:131477.11:2001JUN22	1831	1849	forward 1	TM	Transmembrane
467	LG:131477.11:2001JUN22	1850	1858	forward 1	TM	Non-Cytosolic
467	LG:131477.11:2001JUN22	1859	1881	forward 1	TM	Transmembrane
467	LG:131477.11:2001JUN22	1882	1892	forward 1	TM	Cytosolic
467	LG:131477.11:2001JUN22	1893	1915	forward 1	TM	Transmembrane
467	LG:131477.11:2001JUN22	1916	1916	forward 1	TM	Non-Cytosolic
468	LG:1333618.1:2001JUN22	1	15	forward 1	TM	Cytosolic
468	LG:1333618.1:2001JUN22	16	35	forward 1	TM	Transmembrane
468	LG:1333618.1:2001JUN22	36	200	forward 1	TM	Non-Cytosolic
468	LG:1333618.1:2001JUN22	201	223	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
468	LG:1333618.1:2001JUN22	224	338	forward 1	TM	Cytosolic
468	LG:1333618.1:2001JUN22	339	357	forward 1	TM	Transmembrane
468	LG:1333618.1:2001JUN22	358	360	forward 1	TM	Non-Cytosolic
468	LG:1333618.1:2001JUN22	1	19	forward 2	TM	Cytosolic
468	LG:1333618.1:2001JUN22	20	39	forward 2	TM	Transmembrane
468	LG:1333618.1:2001JUN22	40	270	forward 2	TM	Non-Cytosolic
468	LG:1333618.1:2001JUN22	271	293	forward 2	TM	Transmembrane
468	LG:1333618.1:2001JUN22	294	305	forward 2	TM	Cytosolic
468	LG:1333618.1:2001JUN22	306	328	forward 2	TM	Transmembrane
468	LG:1333618.1:2001JUN22	329	337	forward 2	TM	Non-Cytosolic
468	LG:1333618.1:2001JUN22	338	357	forward 2	TM	Transmembrane
468	LG:1333618.1:2001JUN22	358	360	forward 2	TM	Cytosolic
468	LG:1333618.1:2001JUN22	1	19	forward 3	TM	Non-Cytosolic
468	LG:1333618.1:2001JUN22	20	42	forward 3	TM	Transmembrane
468	LG:1333618.1:2001JUN22	43	196	forward 3	TM	Cytosolic
468	LG:1333618.1:2001JUN22	197	216	forward 3	TM	Transmembrane
468	LG:1333618.1:2001JUN22	217	277	forward 3	TM	Non-Cytosolic
468	LG:1333618.1:2001JUN22	278	300	forward 3	TM	Transmembrane
468	LG:1333618.1:2001JUN22	301	359	forward 3	TM	Cytosolic
469	LG:1347760.16:2001JUN22	1	9	forward 2	TM	Non-Cytosolic
469	LG:1347760.16:2001JUN22	10	32	forward 2	TM	Transmembrane
469	LG:1347760.16:2001JUN22	33	44	forward 2	TM	Cytosolic
469	LG:1347760.16:2001JUN22	45	67	forward 2	TM	Transmembrane
469	LG:1347760.16:2001JUN22	68	823	forward 2	TM	Non-Cytosolic
470	LG:1383039.369:2001JUN22	1	165	forward 1	TM	Cytosolic
470	LG:1383039.369:2001JUN22	166	188	forward 1	TM	Transmembrane
470	LG:1383039.369:2001JUN22	189	202	forward 1	TM	Non-Cytosolic
470	LG:1383039.369:2001JUN22	203	225	forward 1	TM	Transmembrane
470	LG:1383039.369:2001JUN22	226	383	forward 1	TM	Cytosolic
471	LG:1383313.3:2001JUN22	1	1068	forward 2	TM	Non-Cytosolic
471	LG:1383313.3:2001JUN22	1069	1091	forward 2	TM	Transmembrane
471	LG:1383313.3:2001JUN22	1092	1116	forward 2	TM	Cytosolic
472	LG:1384075.8:2001JUN22	1	59	forward 2	TM	Non-Cytosolic
472	LG:1384075.8:2001JUN22	60	82	forward 2	TM	Transmembrane
472	LG:1384075.8:2001JUN22	83	101	forward 2	TM	Cytosolic
472	LG:1384075.8:2001JUN22	102	124	forward 2	TM	Transmembrane
472	LG:1384075.8:2001JUN22	125	127	forward 2	TM	Non-Cytosolic
472	LG:1384075.8:2001JUN22	128	150	forward 2	TM	Transmembrane
472	LG:1384075.8:2001JUN22	151	158	forward 2	TM	Cytosolic
472	LG:1384075.8:2001JUN22	159	178	forward 2	TM	Transmembrane
472	LG:1384075.8:2001JUN22	179	192	forward 2	TM	Non-Cytosolic
472	LG:1384075.8:2001JUN22	193	215	forward 2	TM	Transmembrane
472	LG:1384075.8:2001JUN22	216	221	forward 2	TM	Cytosolic
472	LG:1384075.8:2001JUN22	222	244	forward 2	TM	Transmembrane
472	LG:1384075.8:2001JUN22	245	258	forward 2	TM	Non-Cytosolic
472	LG:1384075.8:2001JUN22	259	281	forward 2	TM	Transmembrane
472	LG:1384075.8:2001JUN22	282	293	forward 2	TM	Cytosolic
472	LG:1384075.8:2001JUN22	294	316	forward 2	TM	Transmembrane
472	LG:1384075.8:2001JUN22	317	773	forward 2	TM	Non-Cytosolic
472	LG:1384075.8:2001JUN22	774	796	forward 2	TM	Transmembrane
472	LG:1384075.8:2001JUN22	797	813	forward 2	TM	Cytosolic
472	LG:1384075.8:2001JUN22	1	773	forward 3	TM	Non-Cytosolic
472	LG:1384075.8:2001JUN22	774	796	forward 3	TM	Transmembrane
472	LG:1384075.8:2001JUN22	797	812	forward 3	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
473	LG:1384155.1:2001JUN22	1	12	forward 2	TM	Cytosolic
473	LG:1384155.1:2001JUN22	13	35	forward 2	TM	Transmembrane
473.	LG:1384155.1:2001JUN22	36	461	forward 2	TM	Non-Cytosolic
474	LG:1385280.12:2001JUN22	1	9	forward 3	TM	Non-Cytosolic
474	LG:1385280.12:2001JUN22	10	32	forward 3	TM	Transmembrane
474	LG:1385280.12:2001JUN22	33	278	forward 3	TM	Cytosolic
475	LG:1390535.25:2001JUN22	1	42	forward 3	TM	Cytosolic
475	LG:1390535.25:2001JUN22	43	60	forward 3	TM	Transmembrane
475	LG:1390535.25:2001JUN22	61	89	forward 3	TM	Non-Cytosolic
475	LG:1390535.25:2001JUN22	90	112	forward 3	TM	Transmembrane
475	LG:1390535.25:2001JUN22	113	151	forward 3	TM	Cytosolic
476	LG:1397047.1:2001JUN22	1	75	forward 3	TM	Cytosolic
476	LG:1397047.1:2001JUN22	76	98	forward 3	TM	Transmembrane
476	LG:1397047.1:2001JUN22	99	101	forward 3	TM	Non-Cytosolic
476	LG:1397047.1:2001JUN22	102	124	forward 3	TM	Transmembrane
476	LG:1397047.1:2001JUN22	125	248	forward 3	TM	Cytosolic
476	LG:1397047.1:2001JUN22	249	266	forward 3	TM	Transmembrane
476	LG:1397047.1:2001JUN22	267	507	forward 3	TM	Non-Cytosolic
477	LG:1398646.15:2001JUN22	1	63	forward 1	TM	Non-Cytosolic
477	LG:1398646.15:2001JUN22	64	86	forward 1	TM	Transmembrane
477	LG:1398646.15:2001JUN22	87	287	forward 1	TM	Cytosolic
477	LG:1398646.15:2001JUN22	288	310	forward 1	TM	Transmembrane
477	LG:1398646.15:2001JUN22	311	329	forward 1	TM	Non-Cytosolic
477	LG:1398646.15:2001JUN22	330	352	forward 1	TM	Transmembrane
477	LG:1398646.15:2001JUN22	353	372	forward 1	TM	Cytosolic
477	LG:1398646.15:2001JUN22	373	395	forward 1	TM	Transmembrane
477	LG:1398646.15:2001JUN22	396	748	forward 1	TM	Non-Cytosolic
477	LG:1398646.15:2001JUN22	1	67	forward 2	TM	Cytosolic
477	LG:1398646.15:2001JUN22	68	90	forward 2	TM	Transmembrane
477	LG:1398646.15:2001JUN22	91	334	forward 2	TM	Non-Cytosolic
477	LG:1398646.15:2001JUN22	335	357	forward 2	TM	Transmembrane
477	LG:1398646.15:2001JUN22	358	500	forward 2	TM	Cytosolic
477	LG:1398646.15:2001JUN22	501	520	forward 2	TM	Transmembrane
477	LG:1398646.15:2001JUN22	521	601	forward 2	TM	Non-Cytosolic
477	LG:1398646.15:2001JUN22	602	624	forward 2	TM	Transmembrane
477	LG:1398646.15:2001JUN22	625	748	forward 2	TM	Cytosolic
477	LG:1398646.15:2001JUN22	1	290	forward 3	TM	Non-Cytosolic
477	LG:1398646.15:2001JUN22	291	313	forward 3	TM	Transmembrane
477	LG:1398646.15:2001JUN22	314	333	forward 3	TM	Cytosolic
477	LG:1398646.15:2001JUN22	334	356	forward 3	TM	Transmembrane
477	LG:1398646.15:2001JUN22	357	370	forward 3	TM	Non-Cytosolic
477	LG:1398646.15:2001JUN22	371	393	forward 3	TM	Transmembrane
477	LG:1398646.15:2001JUN22	394	499	forward 3	TM	Cytosolic
477	LG:1398646.15:2001JUN22	500	522	forward 3	TM	Transmembrane
477	LG:1398646.15:2001JUN22	523	536	forward 3	TM	Non-Cytosolic
477	LG:1398646.15:2001JUN22	537	559	forward 3	TM	Transmembrane
477	LG:1398646.15:2001JUN22	560	651	forward 3	TM	Cytosolic
477	LG:1398646.15:2001JUN22	652	674	forward 3	TM	Transmembrane
477	LG:1398646.15:2001JUN22	675	677	forward 3	TM	Non-Cytosolic
477	LG:1398646.15:2001JUN22	678	697	forward 3	TM	Transmembrane
477	LG:1398646.15:2001JUN22	698	748	forward 3	TM	Cytosolic
478	LG:1446193.10:2001JUN22	1	941	forward 1	TM	Non-Cytosolic
478	LG:1446193.10:2001JUN22	942	961	forward 1	TM	Transmembrane
478	LG:1446193.10:2001JUN22	962	1036	forward 1	TM	Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
478	LG:1446193.10:2001JUN22	1037	1059	forward 1	TM	Transmembrane
478	LG:1446193.10:2001JUN22	1060	1073	forward 1	TM	Non-Cytosolic
478	LG:1446193.10:2001JUN22	1074	1096	forward 1	TM	Transmembrane
478	LG:1446193.10:2001JUN22	1097	1171	forward 1	TM	Cytosolic
478	LG:1446193.10:2001JUN22	1172	1194	forward 1	TM	Transmembrane
478	LG:1446193.10:2001JUN22	1195	1371	forward 1	TM	Non-Cytosolic
478	LG:1446193.10:2001JUN22	1	1034	forward 2	TM	Non-Cytosolic
478	LG:1446193.10:2001JUN22	1035	1057	forward 2	TM	Transmembrane
478	LG:1446193.10:2001JUN22	1058	1069	forward 2	TM	Cytosolic
478	LG:1446193.10:2001JUN22	1070	1087	forward 2	TM	Transmembrane
478	LG:1446193.10:2001JUN22	1088	1371	forward 2	TM	Non-Cytosolic
479	LG:1446405.14:2001JUN22	1	3161	forward 1	TM	Non-Cytosolic
479	LG:1446405.14:2001JUN22	3162	3184	forward 1	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3185	3232	forward 1	TM	Cytosolic
479	LG:1446405.14:2001JUN22	3233	3255	forward 1	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3256	3290	forward 1	TM	Non-Cytosolic
479	LG:1446405.14:2001JUN22	3291	3313	forward 1	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3314	3410	forward 1	TM	Cytosolic
479	LG:1446405.14:2001JUN22	3411	3433	forward 1	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3434	3447	forward 1	TM	Non-Cytosolic
479	LG:1446405.14:2001JUN22	1	3409	forward 2	TM	Non-Cytosolic
479	LG:1446405.14:2001JUN22	3410	3432	forward 2	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3433	3447	forward 2	TM	Cytosolic
479	LG:1446405.14:2001JUN22	1	3127	forward 3	TM	Non-Cytosolic
479	LG:1446405.14:2001JUN22	3128	3150	forward 3	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3151	3162	forward 3	TM	Cytosolic
479	LG:1446405.14:2001JUN22	3163	3185	forward 3	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3186	3230	forward 3	TM	Non-Cytosolic
479	LG:1446405.14:2001JUN22	3231	3264	forward 3	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3265	3283	forward 3	TM	Cytosolic
479	LG:1446405.14:2001JUN22	3284	3306	forward 3	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3307	3328	forward 3	TM	Non-Cytosolic
479	LG:1446405.14:2001JUN22	3329	3351	forward 3	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3352	3394	forward 3	TM	Cytosolic
479	LG:1446405.14:2001JUN22	3395	3417	forward 3	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3418	3426	forward 3	TM	Non-Cytosolic
479	LG:1446405.14:2001JUN22	3427	3444	forward 3	TM	Transmembrane
479	LG:1446405.14:2001JUN22	3445	3446	forward 3	TM	Cytosolic
480	LG:1448148.1:2001JUN22	1	139	forward 2	TM	Cytosolic
480	LG:1448148.1:2001JUN22	140	162	forward 2	TM	Transmembrane
480	LG:1448148.1:2001JUN22	163	538	forward 2	TM	Non-Cytosolic
480	LG:1448148.1:2001JUN22	539	561	forward 2	TM	Transmembrane
480	LG:1448148.1:2001JUN22	562	577	forward 2	TM	Cytosolic
481	LG:1452619.13:2001JUN22	1	12	forward 2	TM	Cytosolic
481	LG:1452619.13:2001JUN22	13	35	forward 2	TM	Transmembrane
481	LG:1452619.13:2001JUN22	36	76	forward 2	TM	Non-Cytosolic
481	LG:1452619.13:2001JUN22	77	99	forward 2	TM	Transmembrane
481	LG:1452619.13:2001JUN22	100	105	forward 2	TM	Cytosolic
481	LG:1452619.13:2001JUN22	106	128	forward 2	TM	Transmembrane
481	LG:1452619.13:2001JUN22	129	363	forward 2	TM	Non-Cytosolic
482	LG:1452783.22:2001JUN22	1	85	forward 3	TM	Cytosolic
482	LG:1452783.22:2001JUN22	86	108	forward 3	TM	Transmembrane
482	LG:1452783.22:2001JUN22	109	2326	forward 3	TM	Non-Cytosolic
483	LG:1453417.5:2001JUN22	1	18	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
483	LG:1453417.5:2001JUN22	19	41	forward 1	TM	Transmembrane
483	LG:1453417.5:2001JUN22	42	1206	forward 1	TM	Non-Cytosolic
483	LG:1453417.5:2001JUN22	1	88	forward 3	TM	Non-Cytosolic
483	LG:1453417.5:2001JUN22	89	111	forward 3	TM	Transmembrane
483	LG:1453417.5:2001JUN22	112	117	forward 3	TM	Cytosolic
483	LG:1453417.5:2001JUN22	118	140	forward 3	TM	Transmembrane
483	LG:1453417.5:2001JUN22	141	1206	forward 3	TM	Non-Cytosolic
484	LG:1455222.23:2001JUN22	1	207	forward 2	TM	Cytosolic
484	LG:1455222.23:2001JUN22	208	230	forward 2	TM	Transmembrane
484	LG:1455222.23:2001JUN22	231	596	forward 2	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	1	142	forward 1	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	143	160	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	161	179	forward 1	TM	Cytosolic
485	LG:149121.8:2001JUN22	180	202	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	203	205	forward 1	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	206	228	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	229	240	forward 1	TM	Cytosolic
485	LG:149121.8:2001JUN22	241	263	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	264	293	forward 1	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	294	311	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	312	339	forward 1	TM	Cytosolic
485	LG:149121.8:2001JUN22	340	362	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	363	463	forward 1	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	464	486	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	487	559	forward 1	TM	Cytosolic
485	LG:149121.8:2001JUN22	560	577	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	578	586	forward 1	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	587	609	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	610	831	forward 1	TM	Cytosolic
485	LG:149121.8:2001JUN22	832	854	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	855	868	forward 1	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	869	891	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	892	978	forward 1	TM	Cytosolic
485	LG:149121.8:2001JUN22	979	998	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	999	1129	forward 1	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	1130	1152	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	1153	1300	forward 1	TM	Cytosolic
485	LG:149121.8:2001JUN22	1301	1323	forward 1	TM	Transmembrane
485	LG:149121.8:2001JUN22	1324	1332	forward 1	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	1	142	forward 2	TM	Cytosolic
485	LG:149121.8:2001JUN22	143	165	forward 2	TM	Transmembrane
485	LG:149121.8:2001JUN22	166	197	forward 2	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	198	220	forward 2	TM	Transmembrane
485	LG:149121.8:2001JUN22	221	466	forward 2	TM	Cytosolic
485	LG:149121.8:2001JUN22	467	489	forward 2	TM	Transmembrane
485	LG:149121.8:2001JUN22	490	627	forward 2	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	628	650	forward 2	TM	Transmembrane
485	LG:149121.8:2001JUN22	651	656	forward 2	TM	Cytosolic
485	LG:149121.8:2001JUN22	657	679	forward 2	TM	Transmembrane
485	LG:149121.8:2001JUN22	680	1304	forward 2	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	1305	1327	forward 2	TM	Transmembrane
485	LG:149121.8:2001JUN22	1328	1332	forward 2	TM	Cytosolic
485	LG:149121.8:2001JUN22	1	899	forward 3	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	900	922	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
485	LG:149121.8:2001JUN22	923	973	forward 3	TM	Cytosolic
485	LG:149121.8:2001JUN22	974	996	forward 3	TM	Transmembrane
485	LG:149121.8:2001JUN22	997	1000	forward 3	TM	Non-Cytosolic
485	LG:149121.8:2001JUN22	1001	1023	forward 3	TM	Transmembrane
485	LG:149121.8:2001JUN22	1024	1043	forward 3	TM	Cytosolic
485	LG:149121.8:2001JUN22	1044	1066	forward 3	TM	Transmembrane
485	LG:149121.8:2001JUN22	1067	1331	forward 3	TM	Non-Cytosolic
486	LG:1500175.18:2001JUN22	1	534	forward 1	TM	Non-Cytosolic
486	LG:1500175.18:2001JUN22	535	557	forward 1	TM	Transmembrane
486	LG:1500175.18:2001JUN22	558	576	forward 1	TM	Cytosolic
486	LG:1500175.18:2001JUN22	577	599	forward 1	TM	Transmembrane
486	LG:1500175.18:2001JUN22	600	608	forward 1	TM	Non-Cytosolic
486	LG:1500175.18:2001JUN22	609	631	forward 1	TM	Transmembrane
486	LG:1500175.18:2001JUN22	632	642	forward 1	TM	Cytosolic
486	LG:1500175.18:2001JUN22	1	576	forward 2	TM	Non-Cytosolic
486	LG:1500175.18:2001JUN22	577	599	forward 2	TM	Transmembrane
486	LG:1500175.18:2001JUN22	600	611	forward 2	TM	Cytosolic
486	LG:1500175.18:2001JUN22	612	631	forward 2	TM	Transmembrane
486	LG:1500175.18:2001JUN22	632	642	forward 2	TM	Non-Cytosolic
486	LG:1500175.18:2001JUN22	1	540	forward 3	TM	Non-Cytosolic
486	LG:1500175.18:2001JUN22	541	563	forward 3	TM	Transmembrane
486	LG:1500175.18:2001JUN22	564	569	forward 3	TM	Cytosolic
486	LG:1500175.18:2001JUN22	570	592	forward 3	TM	Transmembrane
486	LG:1500175.18:2001JUN22	593	641	forward 3	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	1	431	forward 1	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	432	454	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	455	515	forward 1	TM	Cytosolic
487	LG:1500434.6:2001JUN22	516	535	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	536	549	forward 1	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	550	572	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	573	576	forward 1	TM	Cytosolic
487	LG:1500434.6:2001JUN22	577	599	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	600	626	forward 1	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	627	649	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	650	693	forward 1	TM	Cytosolic
487	LG:1500434.6:2001JUN22	694	716	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	717	730	forward 1	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	731	753	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	754	759	forward 1	TM	Cytosolic
487	LG:1500434.6:2001JUN22	760	782	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	783	796	forward 1	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	797	819	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	820	984	forward 1	TM	Cytosolic
487	LG:1500434.6:2001JUN22	985	1007	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1008	1035	forward 1	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	1036	1058	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1059	1131	forward 1	TM	Cytosolic
487	LG:1500434.6:2001JUN22	1132	1154	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1155	1168	forward 1	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	1169	1191	forward 1	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1192	1282	forward 1	TM	Cytosolic
487	LG:1500434.6:2001JUN22	1	461	forward 2	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	462	484	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	485	584	forward 2	TM	Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
487	LG:1500434.6:2001JUN22	585	607	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	608	621	forward 2	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	622	644	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	645	729	forward 2	TM	Cytosolic
487	LG:1500434.6:2001JUN22	730	752	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	753	766	forward 2	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	767	786	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	787	867	forward 2	TM	Cytosolic
487	LG:1500434.6:2001JUN22	868	890	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	891	904	forward 2	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	905	927	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	928	1017	forward 2	TM	Cytosolic
487	LG:1500434.6:2001JUN22	1018	1040	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1041	1129	forward 2	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	1130	1152	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1153	1178	forward 2	TM	Cytosolic
487	LG:1500434.6:2001JUN22	1179	1201	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1202	1205	forward 2	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	1206	1228	forward 2	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1229	1282	forward 2	TM	Cytosolic
487	LG:1500434.6:2001JUN22	1	211	forward 3	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	212	234	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	235	515	forward 3	TM	Cytosolic
487	LG:1500434.6:2001JUN22	516	535	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	536	544	forward 3	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	545	564	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	565	584	forward 3	TM	Cytosolic
487	LG:1500434.6:2001JUN22	585	607	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	608	643	forward 3	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	644	666	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	667	688	forward 3	TM	Cytosolic
487	LG:1500434.6:2001JUN22	689	711	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	712	730	forward 3	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	731	753	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	754	765	forward 3	TM	Cytosolic
487	LG:1500434.6:2001JUN22	766	788	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	789	996	forward 3	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	997	1019	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1020	1031	forward 3	TM	Cytosolic
487	LG:1500434.6:2001JUN22	1032	1054	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1055	1093	forward 3	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	1094	1111	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1112	1178	forward 3	TM	Cytosolic
487	LG:1500434.6:2001JUN22	1179	1201	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1202	1204	forward 3	TM	Non-Cytosolic
487	LG:1500434.6:2001JUN22	1205	1222	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1223	1241	forward 3	TM	Cytosolic
487	LG:1500434.6:2001JUN22	1242	1264	forward 3	TM	Transmembrane
487	LG:1500434.6:2001JUN22	1265	1282	forward 3	TM	Non-Cytosolic
488	LG:1501550.19:2001JUN22	1	920	forward 1	TM	Non-Cytosolic
488	LG:1501550.19:2001JUN22	921	943	forward 1	TM	Transmembrane
488	LG:1501550.19:2001JUN22	944	1068	forward 1	TM	Cytosolic
488	LG:1501550.19:2001JUN22	1069	1086	forward 1	TM	Transmembrane
488	LG:1501550.19:2001JUN22	1087	1110	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
488	LG:1501550.19:2001JUN22	1111	1133	forward 1	TM	Transmembrane
488	LG:1501550.19:2001JUN22	1134	1212	forward 1	TM	Cytosolic
488	LG:1501550.19:2001JUN22	1213	1230	forward 1	TM	Transmembrane
488	LG:1501550.19:2001JUN22	1231	1627	forward 1	TM	Non-Cytosolic
488	LG:1501550.19:2001JUN22	1	1083	forward 3	TM	Non-Cytosolic
488	LG:1501550.19:2001JUN22	1084	1106	forward 3	TM	Transmembrane
488	LG:1501550.19:2001JUN22	1107	1211	forward 3	TM	Cytosolic
488	LG:1501550.19:2001JUN22	1212	1234	forward 3	TM	Transmembrane
488	LG:1501550.19:2001JUN22	1235	1238	forward 3	TM	Non-Cytosolic
488	LG:1501550.19:2001JUN22	1239	1261	forward 3	TM	Transmembrane
488	LG:1501550.19:2001JUN22	1262	1281	forward 3	TM	Cytosolic
488	LG:1501550.19:2001JUN22	1282	1304	forward 3	TM	Transmembrane
488	LG:1501550.19:2001JUN22	1305	1357	forward 3	TM	Non-Cytosolic
488	LG:1501550.19:2001JUN22	1358	1375	forward 3	TM	Transmembrane
488	LG:1501550.19:2001JUN22	1376	1626	forward 3	TM	Cytosolic
489	LG:1501923.26:2001JUN22	1	12	forward 1	TM	Non-Cytosolic
489	LG:1501923.26:2001JUN22	13	30	forward 1	TM	Transmembrane
489	LG:1501923.26:2001JUN22	31	204	forward 1	TM	Cytosolic
490	LG:150960.9:2001JUN22	1	215	forward 3	TM	Cytosolic
490	LG:150960.9:2001JUN22	216	238	forward 3	TM	Transmembrane
490	LG:150960.9:2001JUN22	239	257	forward 3	TM	Non-Cytosolic
490	LG:150960.9:2001JUN22	258	277	forward 3	TM	Transmembrane
490	LG:150960.9:2001JUN22	278	297	forward 3	TM	Cytosolic
490	LG:150960.9:2001JUN22	298	320	forward 3	TM	Transmembrane
490	LG:150960.9:2001JUN22	321	323	forward 3	TM	Non-Cytosolic
490	LG:150960.9:2001JUN22	324	346	forward 3	TM	Transmembrane
490	LG:150960.9:2001JUN22	347	474	forward 3	TM	Cytosolic
490	LG:150960.9:2001JUN22	475	497	forward 3	TM	Transmembrane
490	LG:150960.9:2001JUN22	498	521	forward 3	TM	Non-Cytosolic
490	LG:150960.9:2001JUN22	522	544	forward 3	TM	Transmembrane
490	LG:150960.9:2001JUN22	545	550	forward 3	TM	Cytosolic
490	LG:150960.9:2001JUN22	551	573	forward 3	TM	Transmembrane
490	LG:150960.9:2001JUN22	574	763	forward 3	TM	Non-Cytosolic
491	LG:182744.29:2001JUN22	1	193	forward 1	TM	Non-Cytosolic
491	LG:182744.29:2001JUN22	194	216	forward 1	TM	Transmembrane
491	LG:182744.29:2001JUN22	217	389	forward 1	TM	Cytosolic
491	LG:182744.29:2001JUN22	390	409	forward 1	TM	Transmembrane
491	LG:182744.29:2001JUN22	410	719	forward 1	TM	Non-Cytosolic
491	LG:182744.29:2001JUN22	1	151	forward 2	TM	Non-Cytosolic
491	LG:182744.29:2001JUN22	152	174	forward 2	TM	Transmembrane
491	LG:182744.29:2001JUN22	175	193	forward 2	TM	Cytosolic
491	LG:182744.29:2001JUN22	194	216	forward 2	TM	Transmembrane
491	LG:182744.29:2001JUN22	217	719	forward 2	TM	Non-Cytosolic
491	LG:182744.29:2001JUN22	1	65	forward 3	TM	Cytosolic
491	LG:182744.29:2001JUN22	66	85	forward 3	TM	Transmembrane
491	LG:182744.29:2001JUN22	86	718	forward 3	TM	Non-Cytosolic
492	LG:197166.1:2001JUN22	1	14	forward 3	TM	Non-Cytosolic
492	LG:197166.1:2001JUN22	15	37	forward 3	TM	Transmembrane
492	LG:197166.1:2001JUN22	38	84	forward 3	TM	Cytosolic
493	LG:197455.5:2001JUN22	1	202	forward 3	TM	Non-Cytosolic
493	LG:197455.5:2001JUN22	203	225	forward 3	TM	Transmembrane
493	LG:197455.5:2001JUN22	226	237	forward 3	TM	Cytosolic
493	LG:197455.5:2001JUN22	238	260	forward 3	TM	Transmembrane
493	LG:197455.5:2001JUN22	261	316	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
493	LG:197455.5:2001JUN22	317	336	forward 3	TM	Transmembrane
493	LG:197455.5:2001JUN22	337	379	forward 3	TM	Cytosolic
494	LG:198251.8:2001JUN22	1	286	forward 1	TM	Cytosolic
494	LG:198251.8:2001JUN22	287	309	forward 1	TM	Transmembrane
494	LG:198251.8:2001JUN22	310	328	forward 1	TM	Non-Cytosolic
494	LG:198251.8:2001JUN22	329	346	forward 1	TM	Transmembrane
494	LG:198251.8:2001JUN22	347	507	forward 1	TM	Cytosolic
494	LG:198251.8:2001JUN22	508	530	forward 1	TM	Transmembrane
494	LG:198251.8:2001JUN22	531	539	forward 1	TM	Non-Cytosolic
494	LG:198251.8:2001JUN22	540	559	forward 1	TM	Transmembrane
494	LG:198251.8:2001JUN22	560	596	forward 1	TM	Cytosolic
494	LG:198251.8:2001JUN22	1	78	forward 2	TM	Non-Cytosolic
494	LG:198251.8:2001JUN22	79	101	forward 2	TM	Transmembrane
494	LG:198251.8:2001JUN22	102	315	forward 2	TM	Cytosolic
494	LG:198251.8:2001JUN22	316	338	forward 2	TM	Transmembrane
494	LG:198251.8:2001JUN22	339	517	forward 2	TM	Non-Cytosolic
494	LG:198251.8:2001JUN22	518	540	forward 2	TM	Transmembrane
494	LG:198251.8:2001JUN22	541	596	forward 2	TM	Cytosolic
494	LG:198251.8:2001JUN22	1	77	forward 3	TM	Non-Cytosolic
494	LG:198251.8:2001JUN22	78	100	forward 3	TM	Transmembrane
494	LG:198251.8:2001JUN22	101	270	forward 3	TM	Cytosolic
494	LG:198251.8:2001JUN22	271	293	forward 3	TM	Transmembrane
494	LG:198251.8:2001JUN22	294	307	forward 3	TM	Non-Cytosolic
494	LG:198251.8:2001JUN22	308	330	forward 3	TM	Transmembrane
494	LG:198251.8:2001JUN22	331	506	forward 3	TM	Cytosolic
494	LG:198251.8:2001JUN22	507	529	forward 3	TM	Transmembrane
494	LG:198251.8:2001JUN22	530	595	forward 3	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	1	395	forward 1	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	396	418	forward 1	TM	Transmembrane
495	LG:200149.3:2001JUN22	419	605	forward 1	TM	Cytosolic
495	LG:200149.3:2001JUN22	606	628	forward 1	TM	Transmembrane
495	LG:200149.3:2001JUN22	629	642	forward 1	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	643	665	forward 1	TM	Transmembrane
495	LG:200149.3:2001JUN22	666	723	forward 1	TM	Cytosolic
495	LG:200149.3:2001JUN22	724	746	forward 1	TM	Transmembrane
495	LG:200149.3:2001JUN22	747	824	forward 1	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	825	844	forward 1	TM	Transmembrane
495	LG:200149.3:2001JUN22	845	850	forward 1	TM	Cytosolic
495	LG:200149.3:2001JUN22	851	873	forward 1	TM	Transmembrane
495	LG:200149.3:2001JUN22	874	1372	forward 1	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	1	405	forward 2	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	406	428	forward 2	TM	Transmembrane
495	LG:200149.3:2001JUN22	429	605	forward 2	TM	Cytosolic
495	LG:200149.3:2001JUN22	606	628	forward 2	TM	Transmembrane
495	LG:200149.3:2001JUN22	629	647	forward 2	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	648	665	forward 2	TM	Transmembrane
495	LG:200149.3:2001JUN22	666	719	forward 2	TM	Cytosolic
495	LG:200149.3:2001JUN22	720	742	forward 2	TM	Transmembrane
495	LG:200149.3:2001JUN22	743	819	forward 2	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	820	842	forward 2	TM	Transmembrane
495	LG:200149.3:2001JUN22	843	1268	forward 2	TM	Cytosolic
495	LG:200149.3:2001JUN22	1269	1291	forward 2	TM	Transmembrane
495	LG:200149.3:2001JUN22	1292	1305	forward 2	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	1306	1328	forward 2	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
495	LG:200149.3:2001JUN22	1329	1339	forward 2	TM	Cytosolic
495	LG:200149.3:2001JUN22	1340	1362	forward 2	TM	Transmembrane
495	LG:200149.3:2001JUN22	1363	1372	forward 2	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	1	495	forward 3	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	496	515	forward 3	TM	Transmembrane
495	LG:200149.3:2001JUN22	516	575	forward 3	TM	Cytosolic
495	LG:200149.3:2001JUN22	576	595	forward 3	TM	Transmembrane
495	LG:200149.3:2001JUN22	596	604	forward 3	TM	Non-Cytosolic
495	LG:200149.3:2001JUN22	605	627	forward 3	TM	Transmembrane
495	LG:200149.3:2001JUN22	628	643	forward 3	TM	Cytosolic
495	LG:200149.3:2001JUN22	644	666	forward 3	TM	Transmembrane
495	LG:200149.3:2001JUN22	667	1371	forward 3	TM	Non-Cytosolic
496	LG:203483.3:2001JUN22	1	568	forward 2	TM	Non-Cytosolic
496	LG:203483.3:2001JUN22	569	591	forward 2	TM	Transmembrane
496	LG:203483.3:2001JUN22	592	634	forward 2	TM	Cytosolic
497	LG:209701.7:2001JUN22	1	163	forward 1	TM	Non-Cytosolic
497	LG:209701.7:2001JUN22	164	183	forward 1	TM	Transmembrane
497	LG:209701.7:2001JUN22	184	195	forward 1	TM	Cytosolic
497	LG:209701.7:2001JUN22	196	218	forward 1	TM	Transmembrane
497	LG:209701.7:2001JUN22	219	260	forward 1	TM	Non-Cytosolic
497	LG:209701.7:2001JUN22	261	283	forward 1	TM	Transmembrane
497	LG:209701.7:2001JUN22	284	316	forward 1	TM	Cytosolic
497	LG:209701.7:2001JUN22	317	339	forward 1	TM	Transmembrane
497	LG:209701.7:2001JUN22	340	343	forward 1	TM	Non-Cytosolic
497	LG:209701.7:2001JUN22	344	366	forward 1	TM	Transmembrane
497	LG:209701.7:2001JUN22	367	477	forward 1	TM	Cytosolic
497	LG:209701.7:2001JUN22	478	500	forward 1	TM	Transmembrane
497	LG:209701.7:2001JUN22	501	511	forward 1	TM	Non-Cytosolic
497	LG:209701.7:2001JUN22	1	42	forward 2	TM	Cytosolic
497	LG:209701.7:2001JUN22	43	65	forward 2	TM	Transmembrane
497	LG:209701.7:2001JUN22	66	68	forward 2	TM	Non-Cytosolic
497	LG:209701.7:2001JUN22	69	91	forward 2	TM	Transmembrane
497	LG:209701.7:2001JUN22	92	209	forward 2	TM	Cytosolic
497	LG:209701.7:2001JUN22	210	232	forward 2	TM	Transmembrane
497	LG:209701.7:2001JUN22	233	510	forward 2	TM	Non-Cytosolic
497	LG:209701.7:2001JUN22	1	225	forward 3	TM	Non-Cytosolic
497	LG:209701.7:2001JUN22	226	248	forward 3	TM	Transmembrane
497	LG:209701.7:2001JUN22	249	260	forward 3	TM	Cytosolic
497	LG:209701.7:2001JUN22	261	283	forward 3	TM	Transmembrane
497	LG:209701.7:2001JUN22	284	510	forward 3	TM	Non-Cytosolic
498	LG:210614.1:2001JUN22	1	77	forward 1	TM	Non-Cytosolic
498	LG:210614.1:2001JUN22	78	100	forward 1	TM	Transmembrane
498	LG:210614.1:2001JUN22	101	135	forward 1	TM	Cytosolic
498	LG:210614.1:2001JUN22	136	158	forward 1	TM	Transmembrane
498	LG:210614.1:2001JUN22	159	392	forward 1	TM	Non-Cytosolic
498	LG:210614.1:2001JUN22	1	134	forward 2	TM	Cytosolic
498	LG:210614.1:2001JUN22	135	157	forward 2	TM	Transmembrane
498	LG:210614.1:2001JUN22	158	392	forward 2	TM	Non-Cytosolic
499	LG:210672.1:2001JUN22	1	397	forward 1	TM	Cytosolic
499	LG:210672.1:2001JUN22	398	420	forward 1	TM	Transmembrane
499	LG:210672.1:2001JUN22	421	468	forward 1	TM	Non-Cytosolic
499	LG:210672.1:2001JUN22	469	491	forward 1	TM	Transmembrane
499	LG:210672.1:2001JUN22	492	524	forward 1	TM	Cytosolic
499	LG:210672.1:2001JUN22	525	547	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
499	LG:210672.1:2001JUN22	548	794	forward 1	TM	Non-Cytosolic
499	LG:210672.1:2001JUN22	1	76	forward 2	TM	Cytosolic
499	LG:210672.1:2001JUN22	77	99	forward 2	TM	Transmembrane
499	LG:210672.1:2001JUN22	100	102	forward 2	TM	Non-Cytosolic
499	LG:210672.1:2001JUN22	103	125	forward 2	TM	Transmembrane
499	LG:210672.1:2001JUN22	126	402	forward 2	TM	Cytosolic
499	LG:210672.1:2001JUN22	403	425	forward 2	TM	Transmembrane
499	LG:210672.1:2001JUN22	426	794	forward 2.	TM	Non-Cytosolic
500	LG:215051.10:2001JUN22	1	543	forward 2	TM	Non-Cytosolic
500	LG:215051.10:2001JUN22	544	566	forward 2	TM	Transmembrane
500	LG:215051.10:2001JUN22	567	729	forward 2	TM	Cytosolic
501	LG:218989.3:2001JUN22	1	105	forward 2	TM	Cytosolic
501	LG:218989.3:2001JUN22	106	128	forward 2	TM	Transmembrane
501	LG:218989.3:2001JUN22	129	218	forward 2	TM	Non-Cytosolic
501	LG:218989.3:2001JUN22	219	241	forward 2	TM	Transmembrane
501	LG:218989.3:2001JUN22	242	255	forward 2	TM	Cytosolic
502	LG:228107.11:2001JUN22	1	271	forward 1	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	272	294	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	295	341	forward 1	TM	Cytosolic
502	LG:228107.11:2001JUN22	342	364	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	365	378	forward 1	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	379	401	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	402	413	forward 1	TM	Cytosolic
502	LG:228107.11:2001JUN22	414	436	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	437	476	forward 1	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	477	496	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	497	497	forward 1	TM	Cytosolic
502	LG:228107.11:2001JUN22	498	520	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	521	550	forward 1	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	551	570	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	571	702	forward 1	TM	Cytosolic
502	LG:228107.11:2001JUN22	703	725	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	726	781	forward 1	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	782	801	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	802	922	forward 1	TM	Cytosolic
502	LG:228107.11:2001JUN22	923	945	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	946	964	forward 1	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	965	984	forward 1	TM	Transmembrane
502	LG:228107.11:2001JUN22	985	1028	forward 1	TM	Cytosolic
502	LG:228107.11:2001JUN22	1	405	forward 2	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	406	428	forward 2	TM	Transmembrane
502	LG:228107.11:2001JUN22	429	484	forward 2	TM	Cytosolic
502	LG:228107.11:2001JUN22	485	504	forward 2	TM	Transmembrane
502	LG:228107.11:2001JUN22	505	783	forward 2	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	784	801	forward 2	TM	Transmembrane
502	LG:228107.11:2001JUN22	802	906	forward 2	TM	Cytosolic
502	LG:228107.11:2001JUN22	907	929	forward 2	TM	Transmembrane
502	LG:228107.11:2001JUN22	930	938	forward 2	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	939	961	forward 2	TM	Transmembrane
502	LG:228107.11:2001JUN22	962	967	forward 2	TM	Cytosolic
502	LG:228107.11:2001JUN22	968	990	forward 2	TM	Transmembrane
502	LG:228107.11:2001JUN22	991	1004	forward 2	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	1005	1027	forward 2	TM	Transmembrane
502	LG:228107.11:2001JUN22	1028	1028	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
502	LG:228107.11:2001JUN22	1	471	forward 3	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	472	494	forward 3	TM	Transmembrane
502	LG:228107.11:2001JUN22	495	713	forward 3	TM	Cytosolic
502	LG:228107.11:2001JUN22	714	733	forward 3	TM	Transmembrane
502	LG:228107.11:2001JUN22	734	778	forward 3	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	779	801	forward 3	TM	Transmembrane
502	LG:228107.11:2001JUN22	802	900	forward 3	TM	Cytosolic
502	LG:228107.11:2001JUN22	901	923	forward 3	TM	Transmembrane
502	LG:228107.11:2001JUN22	924	932	forward 3	TM	Non-Cytosolic
502	LG:228107.11:2001JUN22	933	955	forward 3	TM	Transmembrane
502	LG:228107.11:2001JUN22	956	1027	forward 3	TM	Cytosolic
503	LG:231016.1:2001JUN22	1	4	forward 2	TM	Non-Cytosolic
503	LG:231016.1:2001JUN22	5	27	forward 2	TM	Transmembrane
503	LG:231016.1:2001JUN22	28	31	forward 2	TM	Cytosolic
503	LG:231016.1:2001JUN22	32	54	forward 2	TM	Transmembrane
503	LG:231016.1:2001JUN22	55	304	forward 2	TM	Non-Cytosolic
504	LG:235943.60:2001JUN22	28	114	forward 1	SP	
504	LG:235943.60:2001JUN22	1	14	forward 1	TM	Non-Cytosolic
504	LG:235943.60:2001JUN22	15	37	forward 1	TM	Transmembrane
504	LG:235943.60:2001JUN22	38	80	forward 1	TM	Cytosolic
504	LG:235943.60:2001JUN22	81	103	forward 1	TM	Transmembrane
504	LG:235943.60:2001JUN22	104	363	forward 1	TM	Non-Cytosolic
505	LG:235970.14:2001JUN22	1	109	forward 1	TM	Cytosolic
505	LG:235970.14:2001JUN22	110	129	forward 1	TM	Transmembrane
505	LG:235970.14:2001JUN22	130	138	forward 1	TM	Non-Cytosolic
505	LG:235970.14:2001JUN22	139	161	forward 1	TM	Transmembrane
505	LG:235970.14:2001JUN22	162	438	forward 1	TM	Cytosolic
505	LG:235970.14:2001JUN22	439	461	forward 1	TM	Transmembrane
505	LG:235970.14:2001JUN22	462	679	forward 1	TM	Non-Cytosolic
506	LG:236697.15:2001JUN22	1	534	forward 1	TM	Non-Cytosolic
506	LG:236697.15:2001JUN22	535	557	forward 1	TM	Transmembrane
506	LG:236697.15:2001JUN22	558	577	forward 1	TM	Cytosolic
506	LG:236697.15:2001JUN22	578	597	forward 1	TM	Transmembrane
506	LG:236697.15:2001JUN22	598	616	forward 1	TM	Non-Cytosolic
506	LG:236697.15:2001JUN22	617	639	forward 1	TM	Transmembrane
506	LG:236697.15:2001JUN22	640	682	forward 1	TM	Cytosolic
506	LG:236697.15:2001JUN22	1	218	forward 2	TM	Non-Cytosolic
506	LG:236697.15:2001JUN22	219	241	forward 2	TM	Transmembrane
506	LG:236697.15:2001JUN22	242	370	forward 2	TM	Cytosolic
506	LG:236697.15:2001JUN22	371	388	forward 2	TM	Transmembrane
506	LG:236697.15:2001JUN22	389	542	forward 2	TM	Non-Cytosolic
506	LG:236697.15:2001JUN22	543	565	forward 2	TM	Transmembrane
506	LG:236697.15:2001JUN22	566	577	forward 2	TM	Cytosolic
506	LG:236697.15:2001JUN22	578	595	forward 2	TM	Transmembrane
506	LG:236697.15:2001JUN22	596	609	forward 2	TM	Non-Cytosolic
506	LG:236697.15:2001JUN22	610	629	forward 2	TM	Transmembrane
506	LG:236697.15:2001JUN22	630	649	forward 2	TM	Cytosolic
506	LG:236697.15:2001JUN22	650	672	forward 2	TM	Transmembrane
506	LG:236697.15:2001JUN22	673	682	forward 2	TM	Non-Cytosolic
506	LG:236697.15:2001JUN22	1	463	forward 3	TM	Non-Cytosolic
506	LG:236697.15:2001JUN22	464	486	forward 3	TM	Transmembrane
506	LG:236697.15:2001JUN22	487	535	forward 3	TM	Cytosolic
506	LG:236697.15:2001JUN22	536	558	forward 3	TM	Transmembrane
506	LG:236697.15:2001JUN22	559	572	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
506	LG:236697.15:2001JUN22	573	592	forward 3	TM	Transmembrane
506	LG:236697.15:2001JUN22	593	614	forward 3	TM	Cytosolic
506	LG:236697.15:2001JUN22	615	637	forward 3	TM	Transmembrane
506	LG:236697.15:2001JUN22	638	681	forward 3	TM	Non-Cytosolic
507	LG:238576.3:2001JUN22	1	36	forward 1	TM	Non-Cytosolic
507	LG:238576.3:2001JUN22	37	59	forward 1	TM	Transmembrane
507	LG:238576.3:2001JUN22	60	150	forward 1	TM	Cytosolic
508	LG:238602.2:2001JUN22	1	139	forward 1	TM	Cytosolic
508	LG:238602.2:2001JUN22	140	162	forward 1	TM	Transmembrane
508	LG:238602.2:2001JUN22	163	183	forward 1	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	184	206	forward 1	TM	Transmembrane
508	LG:238602.2:2001JUN22	207	210	forward 1	TM	Cytosolic
508	LG:238602.2:2001JUN22	211	233	forward 1	TM	Transmembrane
508	LG:238602.2:2001JUN22	234	268	forward 1	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	269	291	forward 1	TM	Transmembrane
508	LG:238602.2:2001JUN22	292	402	forward 1	TM	Cytosolic
508	LG:238602.2:2001JUN22	403	425	forward 1	TM	Transmembrane
508	LG:238602.2:2001JUN22	426	439	forward 1	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	440	462	forward 1	TM	Transmembrane
508	LG:238602.2:2001JUN22	463	487	forward 1	TM	Cytosolic
508	LG:238602.2:2001JUN22	488	507	forward 1	TM	Transmembrane
508	LG:238602.2:2001JUN22	508	892	forward 1	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	1	173	forward 2	TM	Cytosolic
508	LG:238602.2:2001JUN22	174	196	forward 2	TM	Transmembrane
508	LG:238602.2:2001JUN22	197	210	forward 2	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	211	233	forward 2	TM	Transmembrane
508	LG:238602.2:2001JUN22	234	398	forward 2	TM	Cytosolic
508	LG:238602.2:2001JUN22	399	418	forward 2	TM	Transmembrane
508	LG:238602.2:2001JUN22	419	437	forward 2	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	438	460	forward 2	TM	Transmembrane
508	LG:238602.2:2001JUN22	461	480	forward 2	TM	Cytosolic
508	LG:238602.2:2001JUN22	481	503	forward 2	TM	Transmembrane
508	LG:238602.2:2001JUN22	504	892	forward 2	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	1	31	forward 3	TM	Cytosolic
508	LG:238602.2:2001JUN22	32	49	forward 3	TM	Transmembrane
508	LG:238602.2:2001JUN22	50	52	forward 3	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	53	75	forward 3	TM	Transmembrane
508	LG:238602.2:2001JUN22	76	160	forward 3	TM	Cytosolic
508	LG:238602.2:2001JUN22	161	183	forward 3	TM	Transmembrane
508	LG:238602.2:2001JUN22	184	210	forward 3	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	211	233	forward 3	TM	Transmembrane
508	LG:238602.2:2001JUN22	234	303	forward 3	TM	Cytosolic
508	LG:238602.2:2001JUN22	304	326	forward 3	TM	Transmembrane
508	LG:238602.2:2001JUN22	327	356	forward 3	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	357	379	forward 3	TM	Transmembrane
508	LG:238602.2:2001JUN22	380	395	forward 3	TM	Cytosolic
508	LG:238602.2:2001JUN22	396	415	forward 3	TM	Transmembrane
508	LG:238602.2:2001JUN22	416	439	forward 3	TM	Non-Cytosolic
508	LG:238602.2:2001JUN22	440	462	forward 3	TM	Transmembrane
508	LG:238602.2:2001JUN22	463	489	forward 3	TM	Cytosolic
508	LG:238602.2:2001JUN22	490	508	forward 3	TM	Transmembrane
508	LG:238602.2:2001JUN22	509	891	forward 3	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	1	633	forward 1	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	634	656	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
509	LG:241291.46:2001JUN22	657	1032	forward 1	TM	Cytosolic
509	LG:241291.46:2001JUN22	1033	1055	forward 1	TM	Transmembrane
509	LG:241291.46:2001JUN22	1056	1064	forward 1	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	1065	1084	forward 1	TM	Transmembrane
509	LG:241291.46:2001JUN22	1085	1272	forward 1	TM	Cytosolic
509	LG:241291.46:2001JUN22	1273	1295	forward 1	TM	Transmembrane
509	LG:241291.46:2001JUN22	1296	2007	forward 1	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	2008	2025	forward 1	TM	Transmembrane.
509	LG:241291.46:2001JUN22	2026	2037	forward 1	TM	Cytosolic
509	LG:241291.46:2001JUN22	2038	2060	forward 1	TM	Transmembrane
509	LG:241291.46:2001JUN22	2061	2155	forward 1	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	2156	2178	forward 1	TM	Transmembrane
509	LG:241291.46:2001JUN22	2179	2190	forward 1	TM	Cytosolic
509	LG:241291.46:2001JUN22	2191	2213	forward 1	TM	Transmembrane
509	LG:241291.46:2001JUN22	2214	2653	forward 1	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	1	2047	forward 2	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	2048	2070	forward 2	TM	Transmembrane
509	LG:241291.46:2001JUN22	2071	2162	forward 2	TM	Cytosolic
509	LG:241291.46:2001JUN22	2163	2185	forward 2	TM	Transmembrane
509	LG:241291.46:2001JUN22	2186	2199	forward 2	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	2200	2222	forward 2	TM	Transmembrane
509	LG:241291.46:2001JUN22	2223	2228	forward 2	TM	Cytosolic
509	LG:241291.46:2001JUN22	2229	2248	forward 2	TM	Transmembrane
509	LG:241291.46:2001JUN22	2249	2262	forward 2	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	2263	2285	forward 2	TM	Transmembrane
509	LG:241291.46:2001JUN22	2286	2410	forward 2	TM	Cytosolic
509	LG:241291.46:2001JUN22	2411	2433	forward 2	TM	Transmembrane
509	LG:241291.46:2001JUN22	2434	2447	forward 2	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	2448	2470	forward 2	TM	Transmembrane
509	LG:241291.46:2001JUN22	2471	2652	forward 2	TM	Cytosolic
509	LG:241291.46:2001JUN22	1	877	forward 3	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	878	897	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	898	917	forward 3	TM	Cytosolic
509	LG:241291.46:2001JUN22	918	940	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	941	1060	forward 3	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	1061	1083	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	1084	1103	forward 3	TM	Cytosolic
509	LG:241291.46:2001JUN22	1104	1126	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	1127	1964	forward 3	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	1965	1984	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	1985	1996	forward 3	TM	Cytosolic
509	LG:241291.46:2001JUN22	1997	2013	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	2014	2022	forward 3	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	2023	2045	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	2046	2162	forward 3	TM	Cytosolic
509	LG:241291.46:2001JUN22	2163	2185	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	2186	2199	forward 3	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	2200	2222	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	2223	2563	forward 3	TM	Cytosolic
509	LG:241291.46:2001JUN22	2564	2586	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	2587	2610	forward 3	TM	Non-Cytosolic
509	LG:241291.46:2001JUN22	2611	2633	forward 3	TM	Transmembrane
509	LG:241291.46:2001JUN22	2634	2652	forward 3	TM	Cytosolic
510	LG:241742.1:2001JUN22	1	1431	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
510	LG:241742.1:2001JUN22	1432	1454	forward 1	TM	Transmembrane
510	LG:241742.1:2001JUN22	1455	1783	forward 1	TM	Cytosolic
510	LG:241742.1:2001JUN22	1784	1806	forward 1	TM	Transmembrane
510	LG:241742.1:2001JUN22	1807	1847	forward 1	TM	Non-Cytosolic
510	LG:241742.1:2001JUN22	1848	1870	forward 1	TM	Transmembrane
510	LG:241742.1:2001JUN22	1871	1899	forward 1	TM	Cytosolic
510	LG:241742.1:2001JUN22	1	1018	forward 2	TM	Non-Cytosolic
510	LG:241742.1:2001JUN22	1019	1041	forward 2	TM	Transmembrane
510	LG:241742.1:2001JUN22	1042	1133	forward 2	TM	Cytosolic
510	LG:241742.1:2001JUN22	1134	1156	forward 2	TM	Transmembrane
510	LG:241742.1:2001JUN22	1157	1899	forward 2	TM	Non-Cytosolic
510	LG:241742.1:2001JUN22	1	1014	forward 3	TM	Non-Cytosolic
510	LG:241742.1:2001JUN22	1015	1037	forward 3	TM	Transmembrane
510	LG:241742.1:2001JUN22	1038	1136	forward 3	TM	Cytosolic
510	LG:241742.1:2001JUN22	1137	1159	forward 3	TM	Transmembrane
510	LG:241742.1:2001JUN22	1160	1898	forward 3	TM	Non-Cytosolic
511	LG:244520.33:2001JUN22	1	106	forward 3	TM	Non-Cytosolic
511	LG:244520.33:2001JUN22	107	129	forward 3	TM	Transmembrane
511	LG:244520.33:2001JUN22	130	148	forward 3	TM	Cytosolic
511	LG:244520.33:2001JUN22	149	168	forward 3	TM	Transmembrane
511	LG:244520.33:2001JUN22	169	350	forward 3	TM	Non-Cytosolic
512	LG:247556.1:2001JUN22	1	14	forward 1	TM	Non-Cytosolic
512	LG:247556.1:2001JUN22	15	37	forward 1	TM	Transmembrane
512	LG:247556.1:2001JUN22	38	80	forward 1	TM	Cytosolic
512	LG:247556.1:2001JUN22	1	20	forward 2	TM	Cytosolic
512	LG:247556.1:2001JUN22	21	43	forward 2	TM	Transmembrane
512	LG:247556.1:2001JUN22	44	52	forward 2	TM	Non-Cytosolic
512	LG:247556.1:2001JUN22	53	75	forward 2	TM	Transmembrane
512	LG:247556.1:2001JUN22	76	80	forward 2	TM	Cytosolic
513	LG:247792.5:2001JUN22	1	472	forward 3	TM	Non-Cytosolic
513	LG:247792.5:2001JUN22	473	495	forward 3	TM	Transmembrane
513	LG:247792.5:2001JUN22	496	640	forward 3	TM	Cytosolic
514	LG:253580.6:2001JUN22	1	687	forward 1	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	688	710	forward 1	TM	Transmembrane
514	LG:253580.6:2001JUN22	711	729	forward 1	TM	Cytosolic
514	LG:253580.6:2001JUN22	730	752	forward 1	TM	Transmembrane
514	LG:253580.6:2001JUN22	753	766	forward 1	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	767	789	forward 1	TM	Transmembrane
514	LG:253580.6:2001JUN22	790	801	forward 1	TM	Cytosolic
514	LG:253580.6:2001JUN22	802	824	forward 1	TM	Transmembrane
514	LG:253580.6:2001JUN22	825	1245	forward 1	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	1246	1268	forward 1	TM	Transmembrane
514	LG:253580.6:2001JUN22	1269	1390	forward 1	TM	Cytosolic
514	LG:253580.6:2001JUN22	1	213	forward 2	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	214	236	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	237	296	forward 2	TM	Cytosolic
514	LG:253580.6:2001JUN22	297	319	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	320	348	forward 2	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	349	371	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	372	377	forward 2	TM	Cytosolic
514	LG:253580.6:2001JUN22	378	395	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	396	399	forward 2	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	400	422	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	423	444	forward 2	TM	Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
514	LG:253580.6:2001JUN22	445	467	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	468	578	forward 2	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	579	601	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	602	613	forward 2	TM	Cytosolic
514	LG:253580.6:2001JUN22	614	636	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	637	694	forward 2	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	695	717	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	718	729	forward 2	TM	Cytosolic
514	LG:253580.6:2001JUN22	730	749	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	750	763	forward 2	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	764	784	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	785	857	forward 2	TM	Cytosolic
514	LG:253580.6:2001JUN22	858	880	forward 2	TM	Transmembrane
514	LG:253580.6:2001JUN22	881	1390	forward 2	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	1	112	forward 3	TM	Cytosolic
514	LG:253580.6:2001JUN22	113	135	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	136	211	forward 3	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	212	229	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	230	298	forward 3	TM	Cytosolic
514	LG:253580.6:2001JUN22	299	321	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	322	324	forward 3	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	325	342	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	343	348	forward 3	TM	Cytosolic
514	LG:253580.6:2001JUN22	349	371	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	372	380	forward 3	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	381	403	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	404	441	forward 3	TM	Cytosolic
514	LG:253580.6:2001JUN22	442	464	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	465	577	forward 3	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	578	600	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	601	606	forward 3	TM	Cytosolic
514	LG:253580.6:2001JUN22	607	629	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	630	741	forward 3	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	742	764	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	765	815	forward 3	TM	Cytosolic
514	LG:253580.6:2001JUN22	816	838	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	839	857	forward 3	TM	Non-Cytosolic
514	LG:253580.6:2001JUN22	858	880	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	881	1016	forward 3	TM	Cytosolic
514	LG:253580.6:2001JUN22	1017	1039	forward 3	TM	Transmembrane
514	LG:253580.6:2001JUN22	1040	1390	forward 3	TM	Non-Cytosolic
515	LG:291759.5:2001JUN22	1	119	forward 1	TM	Cytosolic
515	LG:291759.5:2001JUN22	120	139	forward 1	TM	Transmembrane
515	LG:291759.5:2001JUN22	140	175	forward 1	TM	Non-Cytosolic
515	LG:291759.5:2001JUN22	176	198	forward 1	TM	Transmembrane
515	LG:291759.5:2001JUN22	199	202	forward 1	TM	Cytosolic
515	LG:291759.5:2001JUN22	203	225	forward 1	TM	Transmembrane
515	LG:291759.5:2001JUN22	226	588	forward 1	TM	Non-Cytosolic
516	LG:298226.1:2001JUN22	1	9	forward 1	TM	Non-Cytosolic
516	LG:298226.1:2001JUN22	10	32	forward 1	TM	Transmembrane
516	LG:298226.1:2001JUN22	33	65	forward 1	TM	Cytosolic
516	LG:298226.1:2001JUN22	66	88	forward 1	TM	Transmembrane
516	LG:298226.1:2001JUN22	89	97	forward 1	TM	Non-Cytosolic
516	LG:298226.1:2001JUN22	98	120	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
516	LG:298226.1:2001JUN22	121	132	forward 1	TM	Cytosolic
516	LG:298226.1:2001JUN22	133	155	forward 1	TM	Transmembrane
516	LG:298226.1:2001JUN22	156	192	forward 1	TM	Non-Cytosolic
516	LG:298226.1:2001JUN22	193	212	forward 1	TM	Transmembrane
516	LG:298226.1:2001JUN22	213	362	forward 1	TM	Cytosolic
516	LG:298226.1:2001JUN22	363	385	forward 1	TM	Transmembrane
516	LG:298226.1:2001JUN22	386	386	forward 1	TM	Non-Cytosolic
516	LG:298226.1:2001JUN22	1	4	forward 2	TM	Non-Cytosolic
516	LG:298226.1:2001JUN22	5	27	forward 2	TM	Transmembrane
516	LG:298226.1:2001JUN22	28	130	forward 2	TM	Cytosolic
516	LG:298226.1:2001JUN22	131	153	forward 2	TM	Transmembrane
516	LG:298226.1:2001JUN22	154	385	forward 2	TM	Non-Cytosolic
516	LG:298226.1:2001JUN22	1	50	forward 3	TM	Non-Cytosolic
516	LG:298226.1:2001JUN22	51	73	forward 3	TM	Transmembrane
516	LG:298226.1:2001JUN22	74	132	forward 3	TM	Cytosolic
516	LG:298226.1:2001JUN22	133	155	forward 3	TM	Transmembrane
516	LG:298226.1:2001JUN22	156	169	forward 3	TM	Non-Cytosolic
516	LG:298226.1:2001JUN22	170	192	forward 3	TM	Transmembrane
516	LG:298226.1:2001JUN22	193	385	forward 3	TM	Cytosolic
517	LG:306342.1:2001JUN22	1	12	forward 2	TM	Cytosolic
517	LG:306342.1:2001JUN22	13	35	forward 2	TM	Transmembrane
517	LG:306342.1:2001JUN22	36	56	forward 2	TM	Non-Cytosolic
517	LG:306342.1:2001JUN22	57	79	forward 2	TM	Transmembrane
517	LG:306342.1:2001JUN22	80	234	forward 2	TM	Cytosolic
517	LG:306342.1:2001JUN22	235	257	forward 2	TM	Transmembrane
517	LG:306342.1:2001JUN22	258	314	forward 2	TM	Non-Cytosolic
518	LG:327144.5:2001JUN22	1	578	forward 1	TM	Non-Cytosolic
518	LG:327144.5:2001JUN22	579	601	forward 1	TM	Transmembrane
518	LG:327144.5:2001JUN22	602	645	forward 1	TM	Cytosolic
518	LG:327144.5:2001JUN22	646	668	forward 1	TM	Transmembrane
518	LG:327144.5:2001JUN22	669	903	forward 1	TM	Non-Cytosolic
518	LG:327144.5:2001JUN22	1	578	forward 3	TM	Non-Cytosolic
518	LG:327144.5:2001JUN22	579	601	forward 3	TM	Transmembrane
518	LG:327144.5:2001JUN22	602	902	forward 3	TM	Cytosolic
519	LG:331499.8:2001JUN22	1	599	forward 1	TM	Non-Cytosolic
519	LG:331499.8:2001JUN22	600	622	forward 1	TM	Transmembrane
519	LG:331499.8:2001JUN22	623	807	forward 1	TM	Cytosolic
520	LG:331582.12:2001JUN22	1	61	forward 1	TM	Cytosolic
520	LG:331582.12:2001JUN22	62	84	forward 1	TM	Transmembrane
520	LG:331582.12:2001JUN22	85	743	forward 1	TM	Non-Cytosolic
520	LG:331582.12:2001JUN22	744	766	forward 1	TM	Transmembrane
520	LG:331582.12:2001JUN22	767	778	forward 1	TM	Cytosolic
520	LG:331582.12:2001JUN22	779	801	forward 1	TM	Transmembrane
520	LG:331582.12:2001JUN22	802	845	forward 1	TM	Non-Cytosolic
520	LG:331582.12:2001JUN22	1	792	forward 2	TM	Non-Cytosolic
520	LG:331582.12:2001JUN22	793	815	forward 2	TM	Transmembrane
520	LG:331582.12:2001JUN22	816	845	forward 2	TM	Cytosolic
521	LG:333017.12:2001JUN22	1	57	forward 3	TM	Cytosolic
521	LG:333017.12:2001JUN22	58	80	forward 3	TM	Transmembrane
521	LG:333017.12:2001JUN22	81	185	forward 3	TM	Non-Cytosolic
522	LG:334438.8:2001JUN22	1	49	forward 1	TM	Non-Cytosolic
522	LG:334438.8:2001JUN22	50	72	forward 1	TM	Transmembrane
522	LG:334438.8:2001JUN22	73	136	forward 1	TM	Cytosolic
522	LG:334438.8:2001JUN22	137	156	forward 1	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
522	LG:334438.8:2001JUN22	157	160	forward 1	TM	Non-Cytosolic
522	LG:334438.8:2001JUN22	161	183	forward 1	TM	Transmembrane
522	LG:334438.8:2001JUN22	184	251	forward 1	TM	Cytosolic
522	LG:334438.8:2001JUN22	252	269	forward 1	TM	Transmembrane
522	LG:334438.8:2001JUN22	270	517	forward 1	TM	Non-Cytosolic
522	LG:334438.8:2001JUN22	518	540	forward 1	TM	Transmembrane
522	LG:334438.8:2001JUN22	541	562	forward 1	TM	Cytosolic
522	LG:334438.8:2001JUN22	1	54	forward 2	TM	Non-Cytosolic
522	LG:334438.8:2001JUN22	55	77	forward 2	TM	Transmembrane
522	LG:334438.8:2001JUN22	78	144	forward 2	TM	Cytosolic
522	LG:334438.8:2001JUN22	145	167	forward 2	TM	Transmembrane
522	LG:334438.8:2001JUN22	168	226	forward 2	TM	Non-Cytosolic
522	LG:334438.8:2001JUN22	227	249	forward 2	TM	Transmembrane
522	LG:334438.8:2001JUN22	250	495	forward 2	TM	Cytosolic
522	LG:334438.8:2001JUN22	496	518	forward 2	TM	Transmembrane
522	LG:334438.8:2001JUN22	519	561	forward 2	TM	Non-Cytosolic
522	LG:334438.8:2001JUN22	1	56	forward 3	TM	Cytosolic
522	LG:334438.8:2001JUN22	57	79	forward 3	TM	Transmembrane
522	LG:334438.8:2001JUN22	80	561	forward 3	TM	Non-Cytosolic
523	LG:337835.7:2001JUN22	1	38	forward 3	TM	Cytosolic
523	LG:337835.7:2001JUN22	39	61	forward 3	TM	Transmembrane
523	LG:337835.7:2001JUN22	62	373	forward 3	TM	Non-Cytosolic
524	LG:346536.12:2001JUN22	1	603	forward 1	TM	Non-Cytosolic
524	LG:346536.12:2001JUN22	604	626	forward 1	TM	Transmembrane
524	LG:346536.12:2001JUN22	627	627.	forward 1	TM	Cytosolic
524	LG:346536.12:2001JUN22	628	647	forward 1	TM	Transmembrane
524	LG:346536.12:2001JUN22	648	1188	forward 1	TM	Non-Cytosolic
524	LG:346536.12:2001JUN22	1	1021	forward 3	TM	Non-Cytosolic
524	LG:346536.12:2001JUN22	1022	1044	forward 3	TM	Transmembrane
524	LG:346536.12:2001JUN22	1045	1188	forward 3	TM	Cytosolic
525	LG:348117.5:2001JUN22	1	135	forward 1	TM	Non-Cytosolic
525	LG:348117.5:2001JUN22	136	155	forward 1	TM	Transmembrane
525	LG:348117.5:2001JUN22	156	274	forward 1	TM	Cytosolic
525	LG:348117.5:2001JUN22	275	297	forward 1	TM	Transmembrane
525	LG:348117.5:2001JUN22	298	654	forward 1	TM	Non-Cytosolic
525	LG:348117.5:2001JUN22	1	251	forward 2	TM	Non-Cytosolic
525	LG:348117.5:2001JUN22	252	274	forward 2	TM	Transmembrane
525	LG:348117.5:2001JUN22	275	285	forward 2	TM	Cytosolic
525	LG:348117.5:2001JUN22	286	308	forward 2	TM	Transmembrane
525	LG:348117.5:2001JUN22	309	653	forward 2	TM	Non-Cytosolic
525	LG:348117.5:2001JUN22	1	37	forward 3	TM	Non-Cytosolic
525	LG:348117.5:2001JUN22	38	60	forward 3	TM	Transmembrane
525	LG:348117.5:2001JUN22	61	296	forward 3	TM	Cytosolic
525	LG:348117.5:2001JUN22	297	319	forward 3	TM	Transmembrane
525	LG:348117.5:2001JUN22	320	653	forward 3	TM	Non-Cytosolic
526	LG:350407.22:2001JUN22	1	70	forward 1	TM	Cytosolic
526	LG:350407.22:2001JUN22	71	93	forward 1	TM	Transmembrane
526	LG:350407.22:2001JUN22	94	102	forward 1	TM	Non-Cytosolic
526	LG:350407.22:2001JUN22	103	125	forward 1	TM	Transmembrane
526	LG:350407.22:2001JUN22	126	144	forward 1	TM	Cytosolic
526	LG:350407.22:2001JUN22	1	85	forward 2	TM	Non-Cytosolic
526	LG:350407.22:2001JUN22	86	108	forward 2	TM	Transmembrane
526	LG:350407.22:2001JUN22	109	144	forward 2	TM	Cytosolic
527	LG:373219.13:2001JUN22	1	23	forward 1	TM	Non-Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
527	LG:373219.13:2001JUN22	24	46	forward 1	TM	Transmembrane
527	LG:373219.13:2001JUN22	47	100	forward 1	TM	Cytosolic
527	LG:373219.13:2001JUN22	101	120	forward 1	TM	Transmembrane
527	LG:373219.13:2001JUN22	121	244	forward 1	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	245	267	forward 1	TM	Transmembrane
527	LG:373219.13:2001JUN22	268	353	forward 1	TM	Cytosolic
527	LG:373219.13:2001JUN22	354	376	forward 1	TM	Transmembrane
527	LG:373219.13:2001JUN22	377	413	forward 1	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	414	436	forward 1	TM	Transmembrane
527	LG:373219.13:2001JUN22	437	461	forward 1	TM	Cytosolic
527	LG:373219.13:2001JUN22	462	484	forward 1	TM	Transmembrane
527	LG:373219.13:2001JUN22	485	986	forward 1	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	1	19	forward 2	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	20	42	forward 2	TM	Transmembrane
527	LG:373219.13:2001JUN22	43	229	forward 2	TM	Cytosolic
527	LG:373219.13:2001JUN22	230	252	forward 2	TM	Transmembrane
527	LG:373219.13:2001JUN22	253	280	forward 2	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	281	303	forward 2	TM	Transmembrane
527	LG:373219.13:2001JUN22	304	440	forward 2	TM	Cytosolic
527	LG:373219.13:2001JUN22	441	460	forward 2	TM	Transmembrane
527	LG:373219.13:2001JUN22	461	464	forward 2	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	465	484	forward 2	TM	Transmembrane
527	LG:373219.13:2001JUN22	485	636	forward 2	TM	Cytosolic
527	LG:373219.13:2001JUN22	637	659	forward 2	TM	Transmembrane
527	LG:373219.13:2001JUN22	660	703	forward 2	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	704	723	forward 2	TM	Transmembrane
527	LG:373219.13:2001JUN22	724	735	forward 2	TM	Cytosolic
527	LG:373219.13:2001JUN22	736	758	forward 2	TM	Transmembrane
527	LG:373219.13:2001JUN22	759	875	forward 2	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	876	898	forward 2	TM	Transmembrane
527	LG:373219.13:2001JUN22	899	910	forward 2	TM	Cytosolic
527	LG:373219.13:2001JUN22	911	933	forward 2	TM	Transmembrane
527	LG:373219.13:2001JUN22	934	986	forward 2	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	1	19	forward 3	TM	Cytosolic
527	LG:373219.13:2001JUN22	20	39	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	40	43	forward 3	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	44	66	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	67	223	forward 3	TM	Cytosolic
527	LG:373219.13:2001JUN22	224	246	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	247	275	forward 3	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	276	298	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	299	327	forward 3	TM	Cytosolic
527	LG:373219.13:2001JUN22	328	347	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	348	361	forward 3	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	362	384	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	385	404	forward 3	TM	Cytosolic
527	LG:373219.13:2001JUN22	405	422	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	423	426	forward 3	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	427	449	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	450	461	forward 3	TM	Cytosolic
527	LG:373219.13:2001JUN22	462	484	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	485	488	forward 3	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	489	511	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	512	515	forward 3	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
527	LG:373219.13:2001JUN22	516	538	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	539	577	forward 3	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	578	600	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	601	709	forward 3	TM	Cytosolic
527	LG:373219.13:2001JUN22	710	732	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	733	741	forward 3	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	742	764	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	765	873	forward 3	TM	Cytosolic
527	LG:373219.13:2001JUN22	874	891	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	892	910	forward 3	TM	Non-Cytosolic
527	LG:373219.13:2001JUN22	911	933	forward 3	TM	Transmembrane
527	LG:373219.13:2001JUN22	934	985	forward 3	TM	Cytosolic
528	LG:375048.15:2001JUN22	1	891	forward 2	TM	Non-Cytosolic
528	LG:375048.15:2001JUN22	892	909	forward 2	TM	Transmembrane
528	LG:375048.15:2001JUN22	910	913	forward 2	TM	Cytosolic
528	LG:375048.15:2001JUN22	914	936	forward 2	TM	Transmembrane
528	LG:375048.15:2001JUN22	937	1309	forward 2	TM	Non-Cytosolic
528	LG:375048.15:2001JUN22	1	117	forward 3	TM	Cytosolic
528	LG:375048.15:2001JUN22	118	135	forward 3	TM	Transmembrane
528	LG:375048.15:2001JUN22	136	175	forward 3	TM	Non-Cytosolic
528	LG:375048.15:2001JUN22	176	198	forward 3	TM	Transmembrane
528	LG:375048.15:2001JUN22	199	292	forward 3	TM	Cytosolic
528	LG:375048.15:2001JUN22	293	315	forward 3	TM	Transmembrane
528	LG:375048.15:2001JUN22	316	334	forward 3	TM	Non-Cytosolic
528	LG:375048.15:2001JUN22	335	357	forward 3	TM	Transmembrane
528	LG:375048.15:2001JUN22	358	403	forward 3	TM	Cytosolic
528	LG:375048.15:2001JUN22	404	423	forward 3	TM	Transmembrane
528	LG:375048.15:2001JUN22	424	1309	forward 3	TM	Non-Cytosolic
529	LG:400114.3:2001JUN22	1	541	forward 1	TM	Cytosolic
529	LG:400114.3:2001JUN22	542	564	forward 1	TM	Transmembrane
529	LG:400114.3:2001JUN22	565	597	forward 1	TM	Non-Cytosolic
529	LG:400114.3:2001JUN22	598	617	forward 1	TM	Transmembrane
529	LG:400114.3:2001JUN22	618	838	forward 1	TM	Cytosolic
529	LG:400114.3:2001JUN22	839	858	forward 1	TM	Transmembrane
529	LG:400114.3:2001JUN22	859	909	forward 1	TM	Non-Cytosolic
529	LG:400114.3:2001JUN22	910	932	forward 1	TM	Transmembrane
529	LG:400114.3:2001JUN22	933	1083	forward 1	TM	Cytosolic
530	LG:400652.1:2001JUN22	1	1115	forward 1	TM	Non-Cytosolic
530	LG:400652.1:2001JUN22	1116	1138	forward 1	TM	Transmembrane
530	LG:400652.1:2001JUN22	1139	1264	forward 1	TM	Cytosolic
530	LG:400652.1:2001JUN22	1265	1287	forward 1	TM	Transmembrane
530	LG:400652.1:2001JUN22	1288	1301	forward 1	TM	Non-Cytosolic
530	LG:400652.1:2001JUN22	1302	1324	forward 1	TM	Transmembrane
530	LG:400652.1:2001JUN22	1325	1351	forward 1	TM	Cytosolic
530	LG:400652.1:2001JUN22	1	494	forward 2	TM	Non-Cytosolic
530	LG:400652.1:2001JUN22	495	517	forward 2	TM	Transmembrane
530	LG:400652.1:2001JUN22	518	613	forward 2	TM	Cytosolic
530	LG:400652.1:2001JUN22	614	636	forward 2	TM	Transmembrane
530	LG:400652.1:2001JUN22	637	1350	forward 2	TM	Non-Cytosolic
530	LG:400652.1:2001JUN22	1	1098	forward 3	TM	Non-Cytosolic
530	LG:400652.1:2001JUN22	1099	1116	forward 3	TM	Transmembrane
530	LG:400652.1:2001JUN22	1117	1120	forward 3	TM	Cytosolic
530	LG:400652.1:2001JUN22	1121	1143	forward 3	TM	Transmembrane
530	LG:400652.1:2001JUN22	1144	1157	forward 3	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
530	LG:400652.1:2001JUN22	1158	1180	forward 3	TM	Transmembrane
530	LG:400652.1:2001JUN22	1181	1192	forward 3	TM	Cytosolic
530	LG:400652.1:2001JUN22	1193	1215	forward 3	TM	Transmembrane
530	LG:400652.1:2001JUN22	1216	1350	forward 3	TM	Non-Cytosolic
531	LG:401313.10:2001JUN22	1	379	forward 3	TM	Non-Cytosolic
531	LG:401313.10:2001JUN22	380	402	forward 3	TM	Transmembrane
531	LG:401313.10:2001JUN22	403	408	forward 3	TM	Cytosolic
531	LG:401313.10:2001JUN22	409	431	forward 3	TM	Transmembrane
531	LG:401313.10:2001JUN22	432	440	forward 3	TM	Non-Cytosolic
531	LG:401313.10:2001JUN22	441	463	forward 3	TM	Transmembrane
531	LG:401313.10:2001JUN22	464	474	forward 3	TM	Cytosolic
532	LG:406389.1:2001JUN22	1	37	forward 2	TM	Cytosolic
532	LG:406389.1:2001JUN22	38	60	forward 2	TM	Transmembrane
532	LG:406389.1:2001JUN22	61	160	forward 2	TM	Non-Cytosolic
532	LG:406389.1:2001JUN22	161	183	forward 2	TM	Transmembrane
532	LG:406389.1:2001JUN22	184	199	forward 2	TM	Cytosolic
532	LG:406389.1:2001JUN22	200	222	forward 2	TM	Transmembrane
532	LG:406389.1:2001JUN22	223	739	forward 2	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	1	4	forward 1	TM	Cytosolic
533	LG:406595.2:2001JUN22	5	27	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	28	41	forward 1	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	42	64	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	65	99	forward 1	TM	Cytosolic
533	LG:406595.2:2001JUN22	100	122	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	123	136	forward 1	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	137	159	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	160	170	forward 1	TM	Cytosolic
533	LG:406595.2:2001JUN22	171	193	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	194	250	forward 1	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	251	273	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	274	443	forward 1	TM	Cytosolic
533	LG:406595.2:2001JUN22	444	466	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	467	485	forward 1	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	486	508	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	509	726	forward 1	TM	Cytosolic
533	LG:406595.2:2001JUN22	727	749	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	750	763	forward 1	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	764	786	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	787	894	forward 1	TM	Cytosolic
533	LG:406595.2:2001JUN22	895	917	forward 1	TM	Transmembrane
533	LG:406595.2:2001JUN22	918	1341	forward 1	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	1	94	forward 2	TM	Cytosolic
533	LG:406595.2:2001JUN22	95	117	forward 2	TM	Transmembrane
533	LG:406595.2:2001JUN22	118	442	forward 2	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	443	465	forward 2	TM	Transmembrane
533	LG:406595.2:2001JUN22	466	633	forward 2	TM	Cytosolic
533	LG:406595.2:2001JUN22	634	653	forward 2	TM	Transmembrane
533	LG:406595.2:2001JUN22	654	1064	forward 2	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	1065	1087	forward 2	TM	Transmembrane
533	LG:406595.2:2001JUN22	1088	1120	forward 2	TM	Cytosolic
533	LG:406595.2:2001JUN22	1121	1143	forward 2	TM	Transmembrane
533	LG:406595.2:2001JUN22	1144	1152	forward 2	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	1153	1172	forward 2	TM	Transmembrane
533	LG:406595.2:2001JUN22	1173	1304	forward 2	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
533	LG:406595.2:2001JUN22	1305	1327	forward 2	TM	Transmembrane
533	LG:406595.2:2001JUN22	1328	1341	forward 2	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	1	336	forward 3	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	337	359	forward 3	TM	Transmembrane
533	LG:406595.2:2001JUN22	360	378	forward 3	TM	Cytosolic
533	LG:406595.2:2001JUN22	379	398	forward 3	TM	Transmembrane
533	LG:406595.2:2001JUN22	399	450	forward 3	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	451	473	forward 3	TM	Transmembrane
533	LG:406595.2:2001JUN22	474	479	forward 3	TM	Cytosolic
533	LG:406595.2:2001JUN22	480	502	forward 3	TM	Transmembrane
533	LG:406595.2:2001JUN22	503	543	forward 3	TM	Non-Cytosolic
533	LG:406595.2:2001JUN22	544	566	forward 3	TM	Transmembrane
533	LG:406595.2:2001JUN22	567	838	forward 3	TM	Cytosolic
533	LG:406595.2:2001JUN22	839	861	forward 3	TM	Transmembrane
533	LG:406595.2:2001JUN22	862	1340	forward 3	TM	Non-Cytosolic
534	LG:410628.21:2001JUN22	1	161	forward 1	TM	Cytosolic
534	LG:410628.21:2001JUN22	162	184	forward 1	TM	Transmembrane
534	LG:410628.21:2001JUN22	185	203	forward 1	TM	Non-Cytosolic
534	LG:410628.21:2001JUN22	1	8	forward 2	TM	Cytosolic
534	LG:410628.21:2001JUN22	9	31	forward 2	TM	Transmembrane
534	LG:410628.21:2001JUN22	32	202	forward 2	TM	Non-Cytosolic
534	LG:410628.21:2001JUN22	1	21	forward 3	TM	Non-Cytosolic
534	LG:410628.21:2001JUN22	22	44	forward 3	TM	Transmembrane
534	LG:410628.21:2001JUN22	45	64	forward 3	TM	Cytosolic
534	LG:410628.21:2001JUN22	65	87	forward 3	TM	Transmembrane
534	LG:410628.21:2001JUN22	88	91	forward 3	TM	Non-Cytosolic
534	LG:410628.21:2001JUN22	92	114	forward 3	TM	Transmembrane
534	LG:410628.21:2001JUN22	115	202	forward 3	TM	Cytosolic
535	LG:413583.15:2001JUN22	1	777	forward 1	TM	Non-Cytosolic
535	LG:413583.15:2001JUN22	778	800	forward 1	TM	Transmembrane
535	LG:413583.15:2001JUN22	801	834	forward 1	TM	Cytosolic
535	LG:413583.15:2001JUN22	835	857	forward 1	TM	Transmembrane
535	LG:413583.15:2001JUN22	858	866	forward 1	TM	Non-Cytosolic
535	LG:413583.15:2001JUN22	867	889	forward 1	TM	Transmembrane
535	LG:413583.15:2001JUN22	890	1120	forward 1	TM	Cytosolic
535	LG:413583.15:2001JUN22	1121	1143	forward 1	TM	Transmembrane
535	LG:413583.15:2001JUN22	1144	1145	forward 1	TM	Non-Cytosolic
535	LG:413583.15:2001JUN22	1	837	forward 2	TM	Non-Cytosolic
535	LG:413583.15:2001JUN22	838	860	forward 2	TM	Transmembrane
535	LG:413583.15:2001JUN22	861	871	forward 2	TM	Cytosolic
535	LG:413583.15:2001JUN22	872	894	forward 2	TM	Transmembrane
535	LG:413583.15:2001JUN22	895	1145	forward 2	TM	Non-Cytosolic
535	LG:413583.15:2001JUN22	1	637	forward 3	TM	Non-Cytosolic
535	LG:413583.15:2001JUN22	638	657	forward 3	TM	Transmembrane
535	LG:413583.15:2001JUN22	658	718	forward 3	TM	Cytosolic
535	LG:413583.15:2001JUN22	719	741	forward 3	TM	Transmembrane
535	LG:413583.15:2001JUN22	742	755	forward 3	TM	Non-Cytosolic
535	LG:413583.15:2001JUN22	756	778	forward 3	TM	Transmembrane
535	LG:413583.15:2001JUN22	779	831	forward 3	TM	Cytosolic
535	LG:413583.15:2001JUN22	832	854	forward 3	TM	Transmembrane
535	LG:413583.15:2001JUN22	855	868	forward 3	TM	Non-Cytosolic
535	LG:413583.15:2001JUN22	869	891	forward 3	TM	Transmembrane
535	LG:413583.15:2001JUN22	892	1145	forward 3	TM	Cytosolic
536	LG:419641.35:2001JUN22	1	530	forward 1	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
536	LG:419641.35:2001JUN22	531	548	forward 1	TM	Transmembrane
536	LG:419641.35:2001JUN22	549	668	forward 1	TM	Cytosolic
536	LG:419641.35:2001JUN22	669	688	forward 1	TM	Transmembrane
536	LG:419641.35:2001JUN22	689	1100	forward 1	TM	Non-Cytosolic
536	LG:419641.35:2001JUN22	1	1002	forward 2	TM	Non-Cytosolic
536	LG:419641.35:2001JUN22	1003	1020	forward 2	TM	Transmembrane
536	LG:419641.35:2001JUN22	1021	1032	forward 2	TM	Cytosolic
536	LG:419641.35:2001JUN22	1033	1055	forward 2	TM	Transmembrane
536	LG:419641.35:2001JUN22	1056	1074	forward 2	TM	Non-Cytosolic
536	LG:419641.35:2001JUN22	1075	1097	forward 2	TM	Transmembrane
536	LG:419641.35:2001JUN22	1098	1100	forward 2	TM	Cytosolic
536	LG:419641.35:2001JUN22	1	93	forward 3	TM	Cytosolic
536	LG:419641.35:2001JUN22	94	116	forward 3	TM	Transmembrane
536	LG:419641.35:2001JUN22	117	996	forward 3	TM	Non-Cytosolic
536	LG:419641.35:2001JUN22	997	1019	forward 3	TM	Transmembrane
536	LG:419641.35:2001JUN22	1020	1099	forward 3	TM	Cytosolic
537	LG:420759.4:2001JUN22	1	100	forward 3	TM	Cytosolic
537	LG:420759.4:2001JUN22	101	123	forward 3	TM	Transmembrane
537	LG:420759.4:2001JUN22	124	125	forward 3	TM	Non-Cytosolic
538	LG:425448.18:2001JUN22	1	355	forward 1	TM	Cytosolic
538	LG:425448.18:2001JUN22	356	378	forward 1	TM	Transmembrane
538	LG:425448.18:2001JUN22	379	1500	forward 1	TM	Non-Cytosolic
539	LG:435717.5:2001JUN22	1	20	forward 1	TM	Cytosolic
539	LG:435717.5:2001JUN22	21	43	forward 1	TM	Transmembrane
539	LG:435717.5:2001JUN22	44	688	forward 1	TM	Non-Cytosolic
539	LG:435717.5:2001JUN22	689	706	forward 1	TM	Transmembrane
539	LG:435717.5:2001JUN22	707	712	forward 1	TM	Cytosolic
539	LG:435717.5:2001JUN22	713	732	forward 1	TM	Transmembrane
539	LG:435717.5:2001JUN22	733	746	forward 1	TM	Non-Cytosolic
539	LG:435717.5:2001JUN22	747	769	forward 1	TM	Transmembrane
539	LG:435717.5:2001JUN22	770	789	forward 1	TM	Cytosolic
539	LG:435717.5:2001JUN22	1	14	forward 2	TM	Non-Cytosolic
539	LG:435717.5:2001JUN22	15	34	forward 2	TM	Transmembrane
539	LG:435717.5:2001JUN22	35	71	forward 2	TM	Cytosolic
539	LG:435717.5:2001JUN22	72	94	forward 2	TM	Transmembrane
539	LG:435717.5:2001JUN22	95	113	forward 2	TM	Non-Cytosolic
539	LG:435717.5:2001JUN22	114	136	forward 2	TM	Transmembrane
539	LG:435717.5:2001JUN22	137	190	forward 2	TM	Cytosolic
539	LG:435717.5:2001JUN22	191	213	forward 2	TM	Transmembrane
539	LG:435717.5:2001JUN22	214	401	forward 2	TM	Non-Cytosolic
539	LG:435717.5:2001JUN22	402	424	forward 2	TM	Transmembrane
539	LG:435717.5:2001JUN22	425	753	forward 2	TM	Cytosolic
539	LG:435717.5:2001JUN22	754	776	forward 2	TM	Transmembrane
539	LG:435717.5:2001JUN22	777	789	forward 2	TM	Non-Cytosolic
539	LG:435717.5:2001JUN22	1	405	forward 3	TM	Non-Cytosolic
539	LG:435717.5:2001JUN22	406	428	forward 3	TM	Transmembrane
539	LG:435717.5:2001JUN22	429	480	forward 3	TM	Cytosolic
539	LG:435717.5:2001JUN22	481	503	forward 3	TM	Transmembrane
539	LG:435717.5:2001JUN22	504	720	forward 3	TM	Non-Cytosolic
539	LG:435717.5:2001JUN22	721	743	forward 3	TM	Transmembrane
539	LG:435717.5:2001JUN22	744	749	forward 3	TM	Cytosolic
539	LG:435717.5:2001JUN22	750	769	forward 3	TM	Transmembrane
539	LG:435717.5:2001JUN22	770	788	forward 3	TM	Non-Cytosolic
540	LG:441159.31:2001JUN22	1	725	forward 1	TM	Non-Cytosolic

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
540	LG:441159.31:2001JUN22	726	748	forward 1	TM	Transmembrane
540	LG:441159.31:2001JUN22	749	767	forward 1	TM	Cytosolic
540	LG:441159.31:2001JUN22	768	787	forward 1	TM	Transmembrane
540	LG:441159.31:2001JUN22	788	810	forward 1	TM	Non-Cytosolic
540	LG:441159.31:2001JUN22	811	833	forward 1	TM	Transmembrane
540	LG:441159.31:2001JUN22	834	835	forward 1	TM	Cytosolic
540	LG:441159.31:2001JUN22	1	242	forward 2	TM	Non-Cytosolic
540	LG:441159.31:2001JUN22	243	265	forward 2	TM	Transmembrane
540	LG:441159.31:2001JUN22	266	618	forward 2	TM	Cytosolic
540	LG:441159.31:2001JUN22	619	641	forward 2	TM	Transmembrane
540	LG:441159.31:2001JUN22	642	725	forward 2	TM	Non-Cytosolic
540	LG:441159.31:2001JUN22	726	748	forward 2	TM	Transmembrane
540	LG:441159.31:2001JUN22	749	768	forward 2	TM	Cytosolic
540	LG:441159.31:2001JUN22	769	788	forward 2	TM	Transmembrane
540	LG:441159.31:2001JUN22	789	834	forward 2	TM	Non-Cytosolic
540	LG:441159.31:2001JUN22	1	459	forward 3	TM	Non-Cytosolic
540	LG:441159.31:2001JUN22	460	482	forward 3	TM	Transmembrane
540	LG:441159.31:2001JUN22	483	486	forward 3	TM	Cytosolic
540	LG:441159.31:2001JUN22	487	509	forward 3	TM	Transmembrane
540	LG:441159.31:2001JUN22	510	722	forward 3	TM	Non-Cytosolic
540	LG:441159.31:2001JUN22	723	745	forward 3	TM	Transmembrane
540	LG:441159.31:2001JUN22	746	765	forward 3	TM	Cytosolic
540	LG:441159.31:2001JUN22	766	788	forward 3	TM	Transmembrane
540	LG:441159.31:2001JUN22	789	834	forward 3	TM	Non-Cytosolic
541	LG:461375.2:2001JUN22	1	1414	forward 1	TM	Non-Cytosolic
541	LG:461375.2:2001JUN22	1415	1437	forward 1	TM	Transmembrane
541	LG:461375.2:2001JUN22	1438	1438	forward 1	TM	Cytosolic
541	LG:461375.2:2001JUN22	1439	1461	forward 1	TM	Transmembrane
541	LG:461375.2:2001JUN22	1462	1613	forward 1	TM	Non-Cytosolic
541	LG:461375.2:2001JUN22	1	260	forward 2	TM	Non-Cytosolic
541	LG:461375.2:2001JUN22	261	283	forward 2	TM	Transmembrane
541	LG:461375.2:2001JUN22	284	303	forward 2	TM	Cytosolic
541	LG:461375.2:2001JUN22	304	326	forward 2	TM	Transmembrane
541	LG:461375.2:2001JUN22	327	335	forward 2	TM	Non-Cytosolic
541	LG:461375.2:2001JUN22	336	358	forward 2	TM	Transmembrane
541	LG:461375.2:2001JUN22	359	423	forward 2	TM	Cytosolic
541	LG:461375.2:2001JUN22	424	446	forward 2	TM	Transmembrane
541	LG:461375.2:2001JUN22	447	1357	forward 2	TM	Non-Cytosolic
541	LG:461375.2:2001JUN22	1358	1380	forward 2	TM	Transmembrane
541	LG:461375.2:2001JUN22	1381	1434	forward 2	TM	Cytosolic
541	LG:461375.2:2001JUN22	1435	1457	forward 2	TM	Transmembrane
541	LG:461375.2:2001JUN22	1458	1547	forward 2	TM	Non-Cytosolic
541	LG:461375.2:2001JUN22	1548	1570	forward 2	TM	Transmembrane
541	LG:461375.2:2001JUN22	1571	1582	forward 2	TM	Cytosolic
541	LG:461375.2:2001JUN22	1583	1605	forward 2	TM	Transmembrane
541	LG:461375.2:2001JUN22	1606	1613	forward 2	TM	Non-Cytosolic
541	LG:461375.2:2001JUN22	1	1318	forward 3	TM	Non-Cytosolic
541	LG:461375.2:2001JUN22	1319	1341	forward 3	TM	Transmembrane
541	LG:461375.2:2001JUN22	1342	1440	forward 3	TM	Cytosolic
541	LG:461375.2:2001JUN22	1441	1463	forward 3	TM	Transmembrane
541	LG:461375.2:2001JUN22	1464	1477	forward 3	TM	Non-Cytosolic
541	LG:461375.2:2001JUN22	1478	1500	forward 3	TM	Transmembrane
541	LG:461375.2:2001JUN22	1501	1578	forward 3	TM	Cytosolic
541	LG:461375.2:2001JUN22	1579	1598	forward 3	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
541	LG:461375.2:2001JUN22	1599	1613	forward 3	TM	Non-Cytosolic
542	LG:474674.34:2001JUN22	1	4	forward 1	TM	Non-Cytosolic
542	LG:474674.34:2001JUN22	5	27	forward 1	TM	Transmembrane
542	LG:474674.34:2001JUN22	28	125	forward 1	TM	Cytosolic
542	LG:474674.34:2001JUN22	126	148	forward 1	TM	Transmembrane
542	LG:474674.34:2001JUN22	149	284	forward 1	TM	Non-Cytosolic
542	LG:474674.34:2001JUN22	1	14	forward 3	TM	Non-Cytosolic
542	LG:474674.34:2001JUN22	15	33	forward 3	TM	Transmembrane
542	LG:474674.34:2001JUN22	34	283	forward 3	TM	Cytosolic
543	LG:481414.8:2001JUN22	1	857	forward 1	TM	Non-Cytosolic
543	LG:481414.8:2001JUN22	858	880	forward 1	TM	Transmembrane
543	LG:481414.8:2001JUN22	881	886	forward 1	TM	Cytosolic
543	LG:481414.8:2001JUN22	887	906	forward 1	TM	Transmembrane
543	LG:481414.8:2001JUN22	907	982	forward 1	TM	Non-Cytosolic
543	LG:481414.8:2001JUN22	1	480	forward 2	TM	Non-Cytosolic
543	LG:481414.8:2001JUN22	481	503	forward 2	TM	Transmembrane
543	LG:481414.8:2001JUN22	504	635	forward 2	TM	Cytosolic
543	LG:481414.8:2001JUN22	636	658	forward 2	TM	Transmembrane
543	LG:481414.8:2001JUN22	659	981	forward 2	TM	Non-Cytosolic
544	LG:7669276.1:2001JUN22	1	174	forward 2	TM	Non-Cytosolic
544	LG:7669276.1:2001JUN22	175	197	forward 2	TM	Transmembrane
544	LG:7669276.1:2001JUN22	198	202	forward 2	TM	Cytosolic
545	LG:7677848.1:2001JUN22	1	9	forward 1	TM	Non-Cytosolic
545	LG:7677848.1:2001JUN22	10	32	forward 1	TM	Transmembrane
545	LG:7677848.1:2001JUN22	33	62	forward 1	TM	Cytosolic
545	LG:7677848.1:2001JUN22	63	85	forward 1	TM	Transmembrane
545	LG:7677848.1:2001JUN22	86	109	forward 1	TM	Non-Cytosolic
546	LG:7684981.3:2001JUN22	1	25	forward 1	TM	Cytosolic
546	LG:7684981.3:2001JUN22	26	48	forward 1	TM	Transmembrane
546	LG:7684981.3:2001JUN22	49	128	forward 1	TM	Non-Cytosolic
546	LG:7684981.3:2001JUN22	129	151	forward 1	TM	Transmembrane
546	LG:7684981.3:2001JUN22	152	471	forward 1	TM	Cytosolic
546	LG:7684981.3:2001JUN22	472	494	forward 1	TM	Transmembrane
546	LG:7684981.3:2001JUN22	495	718	forward 1	TM	Non-Cytosolic
546	LG:7684981.3:2001JUN22	1	128	forward 2	TM	Non-Cytosolic
546	LG:7684981.3:2001JUN22	129	151	forward 2	TM	Transmembrane
546	LG:7684981.3:2001JUN22	152	484	forward 2	TM	Cytosolic
546	LG:7684981.3:2001JUN22	485	507	forward 2	TM	Transmembrane
546	LG:7684981.3:2001JUN22	508	718	forward 2	TM'	Non-Cytosolic
546	LG:7684981.3:2001JUN22	1	20	forward 3	TM	Cytosolic
546	LG:7684981.3:2001JUN22	21	43	forward 3	TM	Transmembrane
546	LG:7684981.3:2001JUN22	44	128	forward 3	TM	Non-Cytosolic
546	LG:7684981.3:2001JUN22	129	151	forward 3	TM	Transmembrane
546	LG:7684981.3:2001JUN22	152	171	forward 3	TM	Cytosolic
546	LG:7684981.3:2001JUN22	172	191	forward 3	TM	Transmembrane
546	LG:7684981.3:2001JUN22	192	717	forward 3	TM	Non-Cytosolic
547	LG:7685048.6:2001JUN22	1	20	forward 1	TM	Cytosolic
547	LG:7685048.6:2001JUN22	21	43	forward 1	TM	Transmembrane
547	LG:7685048.6:2001JUN22	44	180	forward 1	TM	Non-Cytosolic
547	LG:7685048.6:2001JUN22	1	20	forward 3	TM	Cytosolic
547	LG:7685048.6:2001JUN22	21	43	forward 3	TM	Transmembrane
547	LG:7685048.6:2001JUN22	44	179	forward 3	TM	Non-Cytosolic
548	LG:7688302.1:2001JUN22	1	245	forward 1	TM	Cytosolic
548	LG:7688302.1:2001JUN22	246	268	forward 1	TM	Transmembrane

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
548	LG:7688302.1:2001JUN22	269	282	forward 1	TM	Non-Cytosolic
548	LG:7688302.1:2001JUN22	283	305	forward 1	TM	Transmembrane
548	LG:7688302.1:2001JUN22	306	309	forward 1	TM	Cytosolic
548	LG:7688302.1:2001JUN22	1	244	forward 3	TM	Non-Cytosolic
548	LG:7688302.1:2001JUN22	245	267	forward 3	TM	Transmembrane
548	LG:7688302.1:2001JUN22	268	273	forward 3	TM	Cytosolic
548	LG:7688302.1:2001JUN22	274	296	forward 3	TM	Transmembrane
548	LG:7688302.1:2001JUN22	297	308	forward 3	TM	Non-Cytosolic
549	LG:7690463.3:2001JUN22	1	337	forward 1	TM	Non-Cytosolic
549	LG:7690463.3:2001JUN22	338	360	forward 1	TM	Transmembrane
549	LG:7690463.3:2001JUN22	361	401	forward 1	TM	Cytosolic
549	LG:7690463.3:2001JUN22	1	338	forward 3	TM	Non-Cytosolic
549	LG:7690463.3:2001JUN22	339	361	forward 3	TM	Transmembrane
549	LG:7690463.3:2001JUN22	362	400	forward 3	TM	Cytosolic
550	LG:7691479.5:2001JUN22	1	19	forward 1	TM	Non-Cytosolic
550	LG:7691479.5:2001JUN22	20	42	forward 1	TM	Transmembrane
550	LG:7691479.5:2001JUN22	43	94	forward 1	TM	Cytosolic
550	LG:7691479.5:2001JUN22	95	117	forward 1	TM	Transmembrane
550	LG:7691479.5:2001JUN22	118	199	forward 1	TM	Non-Cytosolic
551	LG:7691527.4:2001JUN22	1	38	forward 1	TM	Cytosolic
551	LG:7691527.4:2001JUN22	39	56	forward 1	TM	Transmembrane
551	LG:7691527.4:2001JUN22	57	95	forward 1	TM	Non-Cytosolic
551	LG:7691527.4:2001JUN22	96	115	forward 1	TM	Transmembrane
551	LG:7691527.4:2001JUN22	116	192	forward 1	TM	Cytosolic
551	LG:7691527.4:2001JUN22	1	79	forward 3	TM	Cytosolic
551	LG:7691527.4:2001JUN22	80	102	forward 3	TM	Transmembrane
551	LG:7691527.4:2001JUN22	103	191	forward 3	TM	Non-Cytosolic
552	LG:7691663.1:2001JUN22	1	213	forward 1	TM	Non-Cytosolic
552	LG:7691663.1:2001JUN22	214	236	forward 1	TM	Transmembrane
552	LG:7691663.1:2001JUN22	237	265	forward 1	TM	Cytosolic
552	LG:7691663.1:2001JUN22	1	207	forward 3	TM	Cytosolic
552	LG:7691663.1:2001JUN22	208	230	forward 3	TM	Transmembrane
552	LG:7691663.1:2001JUN22	231	264	forward 3	TM	Non-Cytosolic
553	LG:7691854.1:2001JUN22	1	258	forward 1	TM	Cytosolic
553	LG:7691854.1:2001JUN22	259	281	forward 1	TM	Transmembrane
553	LG:7691854.1:2001JUN22	282	298	forward 1	TM	Non-Cytosolic
553	LG:7691854.1:2001JUN22	1	269	forward 2	TM	Non-Cytosolic
553	LG:7691854.1:2001JUN22	270	292	forward 2	TM	Transmembrane
553	LG:7691854.1:2001JUN22	293	298	forward 2	TM	Cytosolic
553	LG:7691854.1:2001JUN22	1	269	forward 3	TM	Non-Cytosolic
553	LG:7691854.1:2001JUN22	270	292	forward 3	TM	Transmembrane
553	LG:7691854.1:2001JUN22	293	298	forward 3	TM	Cytosolic
554	LG:7692235.2:2001JUN22	1	134	forward 2	TM	Cytosolic
554	LG:7692235.2:2001JUN22	135	154	forward 2	TM	Transmembrane
554	LG:7692235.2:2001JUN22	155	163	forward 2	TM	Non-Cytosolic
554	LG:7692235.2:2001JUN22	164	186	forward 2	TM	Transmembrane
554	LG:7692235.2:2001JUN22	187	190	forward 2	TM	Cytosolic
554	LG:7692235.2:2001JUN22	191	213	forward 2	TM	Transmembrane
554	LG:7692235.2:2001JUN22	214	232	forward 2	TM	Non-Cytosolic
554	LG:7692235.2:2001JUN22	233	252	forward 2	TM	Transmembrane
554	LG:7692235.2:2001JUN22	253	259	forward 2	TM	Cytosolic
555	LG:7692239.1:2001JUN22	1	431	forward 1	TM	Non-Cytosolic
555	LG:7692239.1:2001JUN22	432	454	forward 1	TM	Transmembrane
555	LG:7692239.1:2001JUN22	455	474	forward 1	TM	Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
555	LG:7692239.1:2001JUN22	475	497	forward 1	TM	Transmembrane
555	LG:7692239.1:2001JUN22	498	519	forward 1	TM	Non-Cytosolic
555	LG:7692239.1:2001JUN22	520	542	forward 1	TM	Transmembrane
555	LG:7692239.1:2001JUN22	543	553	forward 1	TM	Cytosolic
555	LG:7692239.1:2001JUN22	1	381	forward 3	TM	Cytosolic
555	LG:7692239.1:2001JUN22	382	404	forward 3	TM	Transmembrane
555	LG:7692239.1:2001JUN22	405	485	forward 3	TM	Non-Cytosolic
555	LG:7692239.1:2001JUN22	486	508	forward 3	TM	Transmembrane
555	LG:7692239.1:2001JUN22	509	520	forward 3	TM	Cytosolic
555	LG:7692239.1:2001JUN22	521	543	forward 3	TM	Transmembrane
555	LG:7692239.1:2001JUN22	544	553	forward 3	TM	Non-Cytosolic
556	LG:7692575.1:2001JUN22	1	154	forward 1	TM	Cytosolic
556	LG:7692575.1:2001JUN22	155	177	forward 1	TM	Transmembrane
556	LG:7692575.1:2001JUN22	178	207	forward 1	TM	Non-Cytosolic
556	LG:7692575.1:2001JUN22	208	230	forward 1	TM	Transmembrane
556	LG:7692575.1:2001JUN22	231	375	forward 1	TM	Cytosolic
556	LG:7692575.1:2001JUN22	376	395	forward 1	TM	Transmembrane
556	LG:7692575.1:2001JUN22	396	443	forward 1	TM	Non-Cytosolic
556	LG:7692575.1:2001JUN22	444	466	forward 1	TM	Transmembrane
556	LG:7692575.1:2001JUN22	467	472	forward 1	TM	Cytosolic
556	LG:7692575.1:2001JUN22	473	495	forward 1	TM	Transmembrane
556	LG:7692575.1:2001JUN22	496	498	forward 1	TM	Non-Cytosolic
556	LG:7692575.1:2001JUN22	499	521	forward 1	TM	Transmembrane
556	LG:7692575.1:2001JUN22	522	658	forward 1	TM	Cytosolic
556	LG:7692575.1:2001JUN22	1	522	forward 2	TM	Non-Cytosolic
556	LG:7692575.1:2001JUN22	523	545	forward 2	TM	Transmembrane
556	LG:7692575.1:2001JUN22	546	658	forward 2	TM	Cytosolic
556	LG:7692575.1:2001JUN22	1	20	forward 3	TM	Cytosolic
556	LG:7692575.1:2001JUN22	21	43	forward 3	TM	Transmembrane
556	LG:7692575.1:2001JUN22	44	196	forward 3	TM	Non-Cytosolic
556	LG:7692575.1:2001JUN22	197	219	forward 3	TM	Transmembrane
556	LG:7692575.1:2001JUN22	220	319	forward 3	TM	Cytosolic
556	LG:7692575.1:2001JUN22	320	342	forward 3	TM	Transmembrane
556	LG:7692575.1:2001JUN22	343	425	forward 3	TM	Non-Cytosolic
556	LG:7692575.1:2001JUN22	426	448	forward 3	TM	Transmembrane
556	LG:7692575.1:2001JUN22	449	482	forward 3	TM	Cytosolic
556	LG:7692575.1:2001JUN22	483	505	forward 3	TM	Transmembrane
556	LG:7692575.1:2001JUN22	506	657	forward 3	TM	Non-Cytosolic
557	LG:7692742.1:2001JUN22	1	25	forward 1	TM	Non-Cytosolic
557	LG:7692742.1:2001JUN22	26	45	forward 1	TM	Transmembrane
557	LG:7692742.1:2001JUN22	46	56	forward 1	TM	Cytosolic
557	LG:7692742.1:2001JUN22	57	79	forward 1	TM	Transmembrane
557	LG:7692742.1:2001JUN22	80	227	forward 1	TM	Non-Cytosolic
557	LG:7692742.1:2001JUN22	1	30	forward 3	TM	Cytosolic
557	LG:7692742.1:2001JUN22	31	53	forward 3	TM	Transmembrane
557	LG:7692742.1:2001JUN22	54	226	forward 3	TM	Non-Cytosolic
558	LG:7693942.1:2001JUN22	1	6	forward 1	TM	Cytosolic
558	LG:7693942.1:2001JUN22	7	26	forward 1	TM	Transmembrane
558	LG:7693942.1:2001JUN22	27	787	forward 1	TM	Non-Cytosolic
558	LG:7693942.1:2001JUN22	1	19	forward 2	TM	Non-Cytosolic
558	LG:7693942.1:2001JUN22	20	42	forward 2	TM	Transmembrane
558	LG:7693942.1:2001JUN22	43	372	forward 2	TM	Cytosolic
558	LG:7693942.1:2001JUN22	373	395	forward 2	TM	Transmembrane
558	LG:7693942.1:2001JUN22	396	473	forward 2	TM	Non-Cytosolic

TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
558	LG:7693942.1:2001JUN22	474	496	forward 2	TM	Transmembrane
558	LG:7693942.1:2001JUN22	497	507	forward 2	TM	Cytosolic
558	LG:7693942.1:2001JUN22	508	530	forward 2	TM	Transmembrane
558	LG:7693942.1:2001JUN22	531	556	forward 2	TM	Non-Cytosolic
558	LG:7693942.1:2001JUN22	557	579	forward 2	TM	Transmembrane
558	LG:7693942.1:2001JUN22	580	787	forward 2	TM	Cytosolic
559	LG:899248.22:2001JUN22	1	72	forward 1	TM	Cytosolic
559	LG:899248.22:2001JUN22	73	95	forward 1	TM	Transmembrane
559	LG:899248.22:2001JUN22	96	986	forward 1	TM	Non-Cytosolic
560	LG:979051.25:2001JUN22	1	867	forward 1	TM	Non-Cytosolic
560	LG:979051.25:2001JUN22	868	890	forward 1	TM	Transmembrane
560	LG:979051.25:2001JUN22	891	1143	forward 1	TM	Cytosolic
560	LG:979051.25:2001JUN22	1144	1166	forward 1	TM	Transmembrane
560	LG:979051.25:2001JUN22	1167	1703	forward 1	TM	Non-Cytosolic
560	LG:979051.25:2001JUN22	1	40	forward 2	TM	Cytosolic
560	LG:979051.25:2001JUN22	41	63	forward 2	TM	Transmembrane
560	LG:979051.25:2001JUN22	64	77	forward 2	TM	Non-Cytosolic
560	LG:979051.25:2001JUN22	78	100	forward 2	TM	Transmembrane
560	LG:979051.25:2001JUN22	101	120	forward 2	TM	Cytosolic
560	LG:979051.25:2001JUN22	121	143	forward 2	TM	Transmembrane
560	LG:979051.25:2001JUN22	144	911	forward 2	TM	Non-Cytosolic
560	LG:979051.25:2001JUN22	912	931	forward 2	TM	Transmembrane
560	LG:979051.25:2001JUN22	932	1143	forward 2	TM	Cytosolic
560	LG:979051.25:2001JUN22	1144	1166	forward 2	TM	Transmembrane
560	LG:979051.25:2001JUN22	1167	1703	forward 2	TM	Non-Cytosolic
561	LG:979054.18:2001JUN22	1	388	forward 1	TM	Non-Cytosolic
561	LG:979054.18:2001JUN22	389	411	forward 1	TM	Transmembrane
561	LG:979054.18:2001JUN22	412	412	forward 1	TM	Cytosolic
561	LG:979054.18:2001JUN22	413	435	forward 1	TM	Transmembrane
561	LG:979054.18:2001JUN22	436	1047	forward 1	TM	Non-Cytosolic
561	LG:979054.18:2001JUN22	1	388	forward 2	TM	Non-Cytosolic
561	LG:979054.18:2001JUN22	389	411	forward 2	TM	Transmembrane
561	LG:979054.18:2001JUN22	412	417	forward 2	TM	Cytosolic
561	LG:979054.18:2001JUN22	418	440	forward 2	TM	Transmembrane
561	LG:979054.18:2001JUN22	441	1047	forward 2	TM	Non-Cytosolic
562	LG:979415.1:2001JUN22	1	63	forward 1	TM	Cytosolic
562	LG:979415.1:2001JUN22	64	86	forward 1	TM	Transmembrane
562	LG:979415.1:2001JUN22	87	95	forward 1	TM	Non-Cytosolic
562	LG:979415.1:2001JUN22	96	118	forward 1	TM	Transmembrane
562	LG:979415.1:2001JUN22	119	278	forward 1	TM	Cytosolic
562	LG:979415.1:2001JUN22	279	301	forward 1	TM	Transmembrane
562	LG:979415.1:2001JUN22	302	371	forward 1	TM	Non-Cytosolic
562	LG:979415.1:2001JUN22	372	394	forward 1	TM	Transmembrane
562	LG:979415.1:2001JUN22	395	406	forward 1	TM	Cytosolic
562	LG:979415.1:2001JUN22	407	429	forward 1	TM	Transmembrane
562	LG:979415.1:2001JUN22	430	452	forward 1	TM	Non-Cytosolic
562	LG:979415.1:2001JUN22	453	472	forward 1	TM	Transmembrane
562	LG:979415.1:2001JUN22	473	569	forward 1	TM	Cytosolic
562	LG:979415.1:2001JUN22	570	592	forward 1	TM	Transmembrane
562	LG:979415.1:2001JUN22	593	1665	forward 1	TM	Non-Cytosolic
562	LG:979415.1:2001JUN22	1	20	forward 2	TM	Cytosolic
562	LG:979415.1:2001JUN22	21	43	forward 2	TM	Transmembrane
562	LG:979415.1:2001JUN22	44	108	forward 2	TM	Non-Cytosolic
562	LG:979415.1:2001JUN22	109	128	forward 2	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
562	LG:979415.1:2001JUN22	129	453	forward 2	TM	Cytosolic
562	LG:979415.1:2001JUN22	454	476	forward 2	TM	Transmembrane
562	LG:979415.1:2001JUN22	477	1665	forward 2	TM	Non-Cytosolic
562	LG:979415.1:2001JUN22	1	20	forward 3	TM	Cytosolic
562	LG:979415.1:2001JUN22	21	43	forward 3	TM	Transmembrane
562	LG:979415.1:2001JUN22	44	71	forward 3	TM	Non-Cytosolic
562	LG:979415.1:2001JUN22	72	91	forward 3	TM	Transmembrane
562	LG:979415.1:2001JUN22	92	157	forward 3	TM	Cytosolic
562	LG:979415.1:2001JUN22	158	177	forward 3	TM	Transmembrane
562	LG:979415.1:2001JUN22	178	1665	forward 3	TM	Non-Cytosolic
563	LG:980685.1:2001JUN22	1	1193	forward 2	TM	Non-Cytosolic
563	LG:980685.1:2001JUN22	1194	1216	forward 2	TM	Transmembrane
563	LG:980685.1:2001JUN22	1217	1228	forward 2	TM	Cytosolic
563	LG:980685.1:2001JUN22	1229	1251	forward 2	TM	Transmembrane
563	LG:980685.1:2001JUN22	1252	1286	forward 2	TM	Non-Cytosolic
563	LG:980685.1:2001JUN22	1287	1309	forward 2	TM	Transmembrane
563	LG:980685.1:2001JUN22	1310	1390	forward 2	TM	Cytosolic
563	LG:980685.1:2001JUN22	1	587	forward 3	TM	Non-Cytosolic
563	LG:980685.1:2001JUN22	588	610	forward 3	TM	Transmembrane
563	LG:980685.1:2001JUN22	611	616	forward 3	TM	Cytosolic
563	LG:980685.1:2001JUN22	617	639	forward 3	TM	Transmembrane
563	LG:980685.1:2001JUN22	640	1389	forward 3	TM	Non-Cytosolic
564	LG:981272.6:2001JUN22	1	25	forward 1	TM	Cytosolic
564	LG:981272.6:2001JUN22	26	48	forward 1	TM	Transmembrane
564	LG:981272.6:2001JUN22	49	115	forward 1	TM	Non-Cytosolic
564	LG:981272.6:2001JUN22	116	138	forward 1	TM	Transmembrane
564	LG:981272.6:2001JUN22	139	157	forward 1	TM	Cytosolic
564	LG:981272.6:2001JUN22	158	177	forward 1	TM	Transmembrane
564	LG:981272.6:2001JUN22	178	448	forward 1	TM	Non-Cytosolic
564	LG:981272.6:2001JUN22	449	471	forward 1	TM	Transmembrane
564	LG:981272.6:2001JUN22	472	504	forward 1	TM	Cytosolic
564	LG:981272.6:2001JUN22	1	36	forward 2	TM	Non-Cytosolic
564	LG:981272.6:2001JUN22	37	59	forward 2	TM	Transmembrane
564	LG:981272.6:2001JUN22	60	133	forward 2	TM	Cytosolic
564	LG:981272.6:2001JUN22	134	156	forward 2	TM	Transmembrane
564	LG:981272.6:2001JUN22	157	504	forward 2	TM	Non-Cytosolic
564	LG:981272.6:2001JUN22	1	40	forward 3	TM	Non-Cytosolic
564	LG:981272.6:2001JUN22	41	63	forward 3	TM	Transmembrane
564	LG:981272.6:2001JUN22	64	114	forward 3	TM	Cytosolic
564	LG:981272.6:2001JUN22	115	137	forward 3	TM	Transmembrane
564	LG:981272.6:2001JUN22	138	182	forward 3	TM	Non-Cytosolic
564	LG:981272.6:2001JUN22	183	205	forward 3	TM	Transmembrane
564	LG:981272.6:2001JUN22	206	442	forward 3	TM	Cytosolic
564	LG:981272.6:2001JUN22	443	465	forward 3	TM	Transmembrane
564	LG:981272.6:2001JUN22	466	504	forward 3	TM	Non-Cytosolic
565	LG:982723.4:2001JUN22	1	118	forward 1	TM	Cytosolic
565	LG:982723.4:2001JUN22	119	141	forward 1	TM	Transmembrane
565	LG:982723.4:2001JUN22	142	185	forward 1	TM	Non-Cytosolic
565	LG:982723.4:2001JUN22	186	208	forward 1	TM	Transmembrane
565	LG:982723.4:2001JUN22	209	363	forward 1	TM	Cytosolic
565	LG:982723.4:2001JUN22	364	386	forward 1	TM	Transmembrane
565	LG:982723.4:2001JUN22	387	769	forward 1	TM	Non-Cytosolic
565	LG:982723.4:2001JUN22	1	116	forward 2	TM	Cytosolic
565	LG:982723.4:2001JUN22	117	139	forward 2	TM	Transmembrane

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TABLE 2

SEQ D NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
565	LG:982723.4:2001JUN22	140	186	forward 2	TM	Non-Cytosolic
565	LG:982723.4:2001JUN22	187	209	forward 2	TM	Transmembrane
565	LG:982723.4:2001JUN22	210	304	forward 2	TM	Cytosolic
565	LG:982723.4:2001JUN22	305	327	forward 2	TM	Transmembrane
565	LG:982723.4:2001JUN22	328	362	forward 2	TM	Non-Cytosolic
565	LG:982723.4:2001JUN22	363	385	forward 2	TM	Transmembrane
565	LG:982723.4:2001JUN22	386	477	forward 2	TM	Cytosolic
565	LG:982723.4:2001JUN22	478	497	forward 2	TM	Transmembrane
565	LG:982723.4:2001JUN22	498	769	forward 2	TM	Non-Cytosolic
565	LG:982723.4:2001JUN22	1	184	forward 3	TM	Cytosolic
565	LG:982723.4:2001JUN22	185	207	forward 3	TM	Transmembrane
565	LG:982723.4:2001JUN22	208	769	forward 3	TM	Non-Cytosolic
566	LG:982915.8:2001JUN22	1	2391	forward 2	TM	Non-Cytosolic
566	LG:982915.8:2001JUN22	2392	2414	forward 2	TM	Transmembrane
566	LG:982915.8:2001JUN22	2415	2420	forward 2	TM	Cytosolic
566	LG:982915.8:2001JUN22	2421	2443	forward 2	TM	Transmembrane
566	LG:982915.8:2001JUN22	2444	2462	forward 2	TM	Non-Cytosolic
566	LG:982915.8:2001JUN22	2463	2485	forward 2	TM	Transmembrane
566	LG:982915.8:2001JUN22	2486	2493	forward 2	TM	Cytosolic
566	LG:982915.8:2001JUN22	2494	2516	forward 2	TM	Transmembrane
566	LG:982915.8:2001JUN22	2517	2527	forward 2	TM	Non-Cytosolic
567	LG:987785.10:2001JUN22	407	499	forward 2	SP	
567	LG:987785.10:2001JUN22	407	499	forward 2	SP	
567	LG:987785.10:2001JUN22	1	466	forward 1	TM	Non-Cytosolic
567	LG:987785.10:2001JUN22	467	489	forward 1	TM	Transmembrane
567	LG:987785.10:2001JUN22	490	687	forward 1	TM	Cytosolic
567	LG:987785.10:2001JUN22	688	710	forward 1	TM	Transmembrane
567	LG:987785.10:2001JUN22	711	911	forward 1	TM	Non-Cytosolic
567	LG:987785.10:2001JUN22	1	338	forward 2	TM	Non-Cytosolic
567	LG:987785.10:2001JUN22	339	361	forward 2	TM	Transmembrane
567	LG:987785.10:2001JUN22	362	476	forward 2	TM	Cytosolic
567	LG:987785.10:2001JUN22	477	499	forward 2	TM	Transmembrane
567	LG:987785.10:2001JUN22	500	911	forward 2	TM	Non-Cytosolic
567	LG:987785.10:2001JUN22	1	466	forward 3	TM	Non-Cytosolic
567	LG:987785.10:2001JUN22	467	489	forward 3	TM	Transmembrane
567	LG:987785.10:2001JUN22	490	603	forward 3	TM	Cytosolic
567	LG:987785.10:2001JUN22	604	626	forward 3	TM	Transmembrane
567	LG:987785.10:2001JUN22	627	687	forward 3	TM	Non-Cytosolic
567	LG:987785.10:2001JUN22	688	710	forward 3	TM	Transmembrane
567	LG:987785.10:2001JUN22	711	769	forward 3	TM	Cytosolic
567	LG:987785.10:2001JUN22	770	792	forward 3	TM	Transmembrane
567	LG:987785.10:2001JUN22	793	910	forward 3	TM	Non-Cytosolic

Table 3

1/LG:1041015.22:2001MAR30 || 394-871; 341-519; 1-520; 204-497; 325-377; 253-374

2/LG:106877.10:2001MAR30 || 1-326; 1-240; 11-536; 11-449; 17-379; 18-590; 70-207; 70-214; 185-764; 225-499; 285-490; 319-788; 319-565; 319-948; 375-628; 379-908; 475-948; 505-1066; 519-635; 587-1038; 587-727; 620-840; 620-841; 637-884; 638-1252; 688-1146; 706-1206; 772-1216; 776-1037; 778-910; 797-1089; 797-1229; 803-1090; 834-1459; 847-1139; 847-1107; 855-1057; 943-1150; 951-1245; 959-1153; 988-1214; 1003-1354; 1008-1263; 1036-1309; 1042-1305; 1045-1293; 1077-1339; 1084-1279; 1099-1744; 1127-1401; 1133-1698; 1133-1381; 1172-1402; 1196-1445; 1204-1742; 1207-1365; 1212-1525; 1247-1775; 1232-1451; 1275-1381; 1305-1534; 1306-1917; 1309-1694; 1331-1582; 1356-1599; 1370-1640; 1433-1761; 1446-1930; 1456-1797; 1446-1669; 1468-1777; 1516-2044; 1552-1766; 1555-1713; 1590-1933; 1618-2115; 1598-1732; 1624-2097; 1616-1901; 1681-1929; 1683-2221; 1683-1862; 1760-2250; 1790-2069; 1797-2047; 1807-2060; 1831-2112; 1843-2112; 1848-2071; 1856-2108; 1884-2139; 1912-2208; 1916-2210; 1930-2169; 1938-2209; 1938-2204; 1944-2063; 1945-2215; 1948-2157; 1957-2269; 1957-2170; 1973-2534; 1986-2235; 1997-2497; 1997-2406; 1997-2229; 1997-2221; 2003-2185; 2012-2284; 2012-2186; 2031-2274; 2031-2258; 2033-2342; 2044-2258; 2048-2325; 2048-2289; 2050-2331; 2062-2296; 2063-2470; 2073-2627; 2073-2318; 2072-2315; 2073-2317; 2075-2434; 2075-2280; 2075-2274; 2097-2635; 2098-2650; 2101-2716; 2112-2722; 2116-2350; 2137-2649; 2130-2702; 2145-2715; 2145-2381; 2159-2385; 2172-2409; 2189-2442; 2190-2364; 2195-2807; 2215-2693; 2215-2707; 2215-2614; 2215-2432; 2215-2402; 2217-2466; 2220-2467; 2235-2660; 2225-2708; 2227-2709; 2232-2712; 2243-2713; 2245-2548; 2254-2704; 2254-2574; 2261-2711; 2263-2520; 2275-2760; 2280-2722; 2283-2529; 2288-2751; 2288-2755; 2293-2516; 2295-2756; 2294-2751; 2301-2540; 2302-2558; 2301-2550; 2305-2760; 2306-2750; 2322-2754; 2323-2765; 2323-2571; 2324-2751; 2331-2743; 2332-2750; 2334-2562; 2338-2750; 2341-2753; 2341-2750; 2342-2750; 2344-2747; 2346-2753; 2347-2752; 2346-2748; 2351-2751; 2352-2750; 2356-2750; 2366-2753; 2367-2666; 2374-2743; 2379-2750; 2386-2749; 2389-2628; 2392-2750; 2394-2751; 2397-2750; 2401-2743; 2405-2657; 2429-2742; 2430-2858; 2432-2575; 2437-2750; 2437-2818; 2452-2750; 2456-2743; 2459-2754; 2485-2750; 2485-2703; 2491-2708; 2495-2798; 2496-2747; 2502-2748; 2528-2750; 2536-2742; 2556-2750; 2567-2743; 2570-2754; 2589-2750; 2634-2755; 2637-2750; 2646-2743; 2663-2750; 2662-2776; 2673-2753; 2679-2765; 2701-2761

3/LG:1138554.16:2001MAR30 || 1-263; 37-270; 90-515; 95-524; 96-307; 95-526; 101-567; 107-591; 112-582; 113-296; 136-385; 144-515; 152-412; 159-513; 167-517; 183-499; 185-518; 218-486; 218-824; 220-470; 242-859; 253-653; 269-457; 321-511; 320-568; 343-899; 359-515; 390-654; 441-960; 478-732; 501-746; 541-999; 560-1003; 667-998; 423-862

4/LG:1383277.7:2001MAR30 || 1-94; 10-252; 22-639; 35-636; 85-657; 169-433; 174-632; 190-463; 266-604; 266-555; 269-567; 336-664; 570-771

5/LG:1397614.15:2001MAR30 || 1-469; 25-475; 65-327; 142-380; 146-432; 152-721; 234-464; 241-461; 268-646; 271-558; 295-549; 331-456; 335-604; 348-652; 367-771; 376-654; 393-625; 394-654; 423-490; 430-681; 443-707; 454-728; 488-694; 498-771; 504-772; 532-803; 575-825; 578-749; 617-833; 632-877; 632-946; 639-892; 639-1074; 644-1157; 647-916; 651-902; 660-925; 660-1214; 660-948; 683-913; 683-992; 702-917; 702-939; 714-1114; 714-1060; 734-1191; 736-1013; 752-1270; 752-954; 754-874; 769-981; 774-907; 793-1256; 810-1176; 824-1078; 833-1130; 836-1073; 843-1109; 867-1031; 874-1380; 886-1142; 890-1173; 892-1158; 901-1133; 906-1117; 917-1173; 920-1520; 920-1060; 938-1157; 946-1218; 951-1218; 988-1248; 988-1256; 990-1551; 993-1263; 997-1233; 996-1521; 996-1510; 996-1236; 1000-1211; 1014-1299; 1020-1473; 1031-1538; 1043-1289; 1046-1199; 1047-1317; 1051-1237; 1058-1304; 1064-1312; 1064-1304; 1068-1266; 1088-1351; 1103-1602; 1103-1366; 1131-1368; 1139-1405; 1173-1389; 1182-1504; 1193-1814; 1195-1408; 1198-1431; 1198-1429; 1218-1750; 1221-1425; 1228-1488; 1240-1745; 1240-1407; 1242-1744; 1249-1581; 1250-1513; 1252-1491; 1268-1878; 1270-1540; 1271-1546; 1315-1578; 1323-1898; 1325-1590; 1326-1571; 1328-1882; 1332-1896; 1335-1594; 1338-

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Table 4

SEQ ID NO:	Template ID	Tissue Distribution
1	LG:1041015.22:2001MAR30	Endocrine System - 31%, Exocrine Glands - 31%, Hemic and Immune System - 23%
2	LG:106877.10:2001MAR30	Unclassified/Mixed - 19%, Exocrine Glands - 13%, Male Genitalia - 12%
3	LG:1138554.16:2001MAR30	Sense Organs - 23%, Germ Cells - 13%, Embryonic Structures - 11%
4	LG:1383277.7:2001MAR30	Urinary Tract - 33%, Unclassified/Mixed - 23%, Digestive System - 13%, Endocrine System - 13%
5	LG:1397614.15:2001MAR30	Urinary Tract - 18%, Nervous System - 15%, Exocrine Glands - 11%
6	LG:1399315.8:2001MAR30	Unclassified/Mixed - 30%, Respiratory System - 11%, Connective Tissue - 10%
7	LG:198782.1:2001MAR30	Embryonic Structures - 10%
8	LG:236046.1:2001MAR30	Connective Tissue - 15%, Germ Cells - 12%, Endocrine System - 11%
9	LG:332122.6:2001MAR30	Musculoskeletal System - 15%, Cardiovascular System - 13%, Respiratory System - 13%
10	LG:345320.16:2001MAR30	Hemic and Immune System - 24%, Liver - 19%, Unclassified/Mixed - 14%
11	LG:350827.10:2001MAR30	Germ Cells - 17%
12	LG:399901.5:2001MAR30	Germ Cells - 16%, Unclassified/Mixed - 15%, Embryonic Structures - 14%
13	LG:404563.1:2001MAR30	Liver - 29%, Unclassified/Mixed - 15%
14	LG:977812.15:2001MAR30	Nervous System - 47%, Respiratory System - 17%, Embryonic Structures - 15%, Endocrine System - 15%
15	LG:983810.1:2001MAR30	Sense Organs - 33%, Nervous System - 31%
16	LG:984488.1:2001MAR30	Sense Organs - 39%, Unclassified/Mixed - 27%
17	LG:011606.1:2001MAR30	Exocrine Glands - 24%, Pancreas - 18%, Male Genitalia - 14%
18	LG:025465.5:2001MAR30	Embryonic Structures - 16%, Cardiovascular System - 13%, Germ Cells - 13%
19	LG:025724.10:2001MAR30	Skin - 23%, Pancreas - 11%
20	LG:1095426.1:2001MAR30	Germ Cells - 31%, Unclassified/Mixed - 13%, Respiratory System - 12%
21	LG:1132418.1:2001MAR30	Liver - 90%, Nervous System - 10%
22	LG:1377900.14:2001MAR30	Hemic and Immune System - 15%, Embryonic Structures - 11%, Endocrine System - 11%, Pancreas - 11%
23	LG:1383812.1:2001MAR30	Nervous System - 35%, Unclassified/Mixed - 33%, Male Genitalia - 23%
24	LG:1468687.1:2001MAR30	Pancreas - 100%
25	LG:1505513.1:2001MAR30	Digestive System - 29%, Respiratory System - 29%, Nervous System - 29%
26	LG:178823.9:2001MAR30	Connective Tissue - 14%, Exocrine Glands - 10%
27	LG:198342.3:2001MAR30	widely distributed
28	LG:210672.1:2001MAR30	Female Genitalia - 26%, Nervous System - 24%, Connective Tissue - 21%
29	LG:212823.8:2001MAR30	Unclassified/Mixed - 29%, Urinary Tract - 29%, Digestive System - 17%, Nervous System - 17%
30	LG:220495.9:2001MAR30	Unclassified/Mixed - 17%, Skin - 12%
31	LG:238262.1:2001MAR30	Embryonic Structures - 18%, Liver - 15%, Sense Organs - 11%
32	LG:239410.21:2001MAR30	Digestive System - 31%, Male Genitalia - 23%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
33	LG:245854.7:2001MAR30	Male Genitalia - 13%
34	LG:294697.1:2001MAR30	Unclassified/Mixed - 70%, Digestive System - 20%, Hemic and Immune System - 10%
35	LG:345884.1:2001MAR30	Respiratory System - 63%, Hemic and Immune System - 38%
36	LG:400095.15:2001MAR30	Nervous System - 35%, Germ Cells - 16%, Respiratory System - 14%
37	LG:402180.1:2001MAR30	Liver - 31%, Cardiovascular System - 24%, Nervous System - 21%
38	LG:403401.1:2001MAR30	Urinary Tract - 37%, Respiratory System - 15%, Unclassified/Mixed - 13%
39	LG:411327.29:2001MAR30	Germ Cells - 24%
40	LG:417464.10:2001MAR30	Skin - 23%, Female Genitalia - 22%, Embryonic Structures - 15%
41	LG:481997.1:2001MAR30	Connective Tissue - 27%, Embryonic Structures - 17%, Urinary Tract - 13%, Respiratory System - 13%, Unclassified/Mixed - 13%
42	LG:979304.7:2001MAR30	Unclassified/Mixed - 20%, Exocrine Glands - 12%, Respiratory System - 10%
43	LG:997964.1:2001MAR30	Germ Cells - 14%, Stomatognathic System - 11%
44	LG:998845.1:2001MAR30	Germ Cells - 61%, Musculoskeletal System - 17%, Endocrine System - 11%, Nervous System - 11%
45	LG:000014.1:2001MAR30	Connective Tissue - 70%, Male Genitalia - 20%, Hemic and Immune System - 10%
46	LG:000290.9:2001MAR30	Sense Organs - 39%, Female Genitalia - 13%
47	LG:001923.1:2001MAR30	Sense Organs - 61%
48	LG:008606.21:2001MAR30	Skin - 18%
49	LG:009699.32:2001MAR30	Unclassified/Mixed - 17%, Germ Cells - 16%, Connective Tissue - 10%
50	LG:016723.6:2001MAR30	Hemic and Immune System - 28%, Endocrine System - 18%, Pancreas - 15%
51	LG:017126.5:2001MAR30	Germ Cells - 37%, Cardiovascular System - 13%, Hemic and Immune System - 11%, Unclassified/Mixed - 11%
52	LG:019362.10:2001MAR30	Connective Tissue - 14%, Embryonic Structures - 12%
53	LG:022183.1:2001MAR30	Skin - 58%, Liver - 25%
54	LG:028493.1:2001MAR30	Liver - 16%, Nervous System - 13%, Male Genitalia - 13%
55	LG:034197.1:2001MAR30	Endocrine System - 55%, Nervous System - 39%
56	LG:054096.31:2001MAR30	Germ Cells - 26%
57	LG:054807.3:2001MAR30	Liver - 16%, Pancreas - 16%, Exocrine Glands - 14%
58	LG:065873.12:2001MAR30	Stomatognathic System - 16%, Germ Cells - 15%
59	LG:083814.6:2001MAR30	Embryonic Structures - 16%
60	LG:093477.1:2001MAR30	Unclassified/Mixed - 65%, Exocrine Glands - 20%, Respiratory System - 10%
61	LG:099572.12:2001MAR30	Hemic and Immune System - 26%
62	LG:100396.31:2001MAR30	Germ Cells - 28%, Respiratory System - 24%
63	LG:1026903.5:2001MAR30	Unclassified/Mixed - 39%, Cardiovascular System - 21%, Musculoskeletal System - 18%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
64	LG:1060168.6:2001MAR30	Hemic and Immune System - 50%, Male Genitalia - 33%, Nervous System - 17%
65	LG:1086906.41:2001MAR30	Exocrine Glands - 16%, Connective Tissue - 14%, Respiratory System - 10%
66	LG:1089326.18:2001MAR30	Unclassified/Mixed - 33%, Digestive System - 17%, Nervous System - 14%
67	LG:1090862.32:2001MAR30	Unclassified/Mixed - 25%, Female Genitalia - 21%, Respiratory System - 13%
68	LG:1091941.41:2001MAR30	Connective Tissue - 37%, Liver - 17%, Embryonic Structures - 17%
69	LG:1093386.8:2001MAR30	Embryonic Structures - 16%
70	LG:1094187.33:2001MAR30	Hemic and Immune System - 18%
71	LG:1098692.18:2001MAR30	Digestive System - 31%, Liver - 19%, Skin - 11%
72	LG:1173104.22:2001MAR30	Sense Organs - 18%, Liver - 13%, Germ Cells - 10%
73	LG:1215335.7:2001MAR30	Embryonic Structures - 11%
74	LG:1256753.1:2001MAR30	Embryonic Structures - 13%, Female Genitalia - 10%
75	LG:1326702.10:2001MAR30	Connective Tissue - 15%, Cardiovascular System - 11%, Embryonic Structures - 10%
76	LG:1327239.15:2001MAR30	Sense Organs - 19%, Respiratory System - 13%
77	LG:1327867.15:2001MAR30	Embryonic Structures - 13%, Nervous System - 10%
78	LG:1383232.1:2001MAR30	Sense Organs - 21%, Skin - 18%, Exocrine Glands - 12%
79	LG:1383368.40:2001MAR30	Respiratory System - 11%
80	LG:1384477.1:2001MAR30	Endocrine System - 31%, Liver - 17%, Urinary Tract - 13%
81	LG:1390822.1:2001MAR30	widely distributed
82	LG:1398274.13:2001MAR30	Skin - 15%
83	LG:1398646.1:2001MAR30	Unclassified/Mixed - 18%
84	LG:1398905.1:2001MAR30	Unclassified/Mixed - 22%, Nervous System - 13%, Musculoskeletal System - 10%, Digestive System - 10%
85	LG:1399785.1:2001MAR30	Embryonic Structures - 11%
86	LG:1446193.10:2001MAR30	Sense Organs - 34%
87	LG:1446210.8:2001MAR30	Skin - 16%, Pancreas - 11%
88	LG:1450054.6:2001MAR30	Sense Organs - 14%, Unclassified/Mixed - 12%
89	LG:1452516.4:2001MAR30	Unclassified/Mixed - 23%, Skin - 12%, Connective Tissue - 12%
90	LG:1455293.7:2001MAR30	Endocrine System - 19%, Respiratory System - 16%, Urinary Tract - 14%
91	LG:1498113.1:2001MAR30	Liver - 100%
92	LG:1500042.1:2001MAR30	Female Genitalia - 44%, Exocrine Glands - 19%, Respiratory System - 14%
93	LG:1500434.4:2001MAR30	Stomatognathic System - 22%, Sense Organs - 18%
94	LG:1501102.4:2001MAR30	Embryonic Structures - 45%, Liver - 21%, Musculoskeletal System - 14%
95	LG:1501768.2:2001MAR30	Digestive System - 50%, Respiratory System - 50%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
96	LG:1502155.6:2001MAR30	Liver - 24%, Female Genitalia - 24%, Embryonic Structures - 12%
97	LG:1512304.2:2001MAR30	Unclassified/Mixed - 27%, Connective Tissue - 27%, Cardiovascular System - 15%, Endocrine System - 15%
98	LG:1512931.11:2001MAR30	Unclassified/Mixed - 38%, Embryonic Structures - 13%, Urinary Tract - 11%
99	LG:155076.18:2001MAR30	Respiratory System - 13%, Endocrine System - 12%
100	LG:159111.41:2001MAR30	Germ Cells - 15%, Connective Tissue - 10%
101	LG:170604.1:2001MAR30	Respiratory System - 50%, Urinary Tract - 30%, Female Genitalia - 20%
102	LG:190477.4:2001MAR30	Sense Organs - 28%, Unclassified/Mixed - 14%
103	LG:198087.8:2001MAR30	Embryonic Structures - 12%, Unclassified/Mixed - 10%, Nervous System - 10%
104	LG:198743.2:2001MAR30	Unclassified/Mixed - 12%, Nervous System - 11%
105	LG:199194.1:2001MAR30	Sense Organs - 16%, Embryonic Structures - 13%
106	LG:200727.6:2001MAR30	Unclassified/Mixed - 22%, Germ Cells - 12%
107	LG:201572.20:2001MAR30	widely distributed
108	LG:201669.25:2001MAR30	Digestive System - 10%, Pancreas - 10%
109	LG:208588.4:2001MAR30	Digestive System - 100%
110	LG:210412.29:2001MAR30	Respiratory System - 30%, Embryonic Structures - 27%, Musculoskeletal System - 18%
111	LG:215051.15:2001MAR30	Nervous System - 11%, Skin - 10%, Urinary Tract - 10%
112	LG:215475.21:2001MAR30	Embryonic Structures - 20%
113	LG:224523.1:2001MAR30	Respiratory System - 67%, Nervous System - 33%
114	LG:228186.1:2001MAR30	Germ Cells - 17%, Urinary Tract - 11%
115	LG:233138.2:2001MAR30	Cardiovascular System - 15%
116	LG:234811.10:2001MAR30	Liver - 38%
117	LG:236092.1:2001MAR30	Urinary Tract - 14%, Embryonic Structures - 14%, Germ Cells - 13%
118	LG:236098.12:2001MAR30	Unclassified/Mixed - 11%
119	LG:236697.15:2001MAR30	Sense Organs - 15%
120	LG:237503.21:2001MAR30	Sense Organs - 42%
121	LG:238023.7:2001MAR30	Exocrine Glands - 22%, Unclassified/Mixed - 18%, Nervous System - 15%
122	LG:238209.1:2001MAR30	Skin - 16%
123	LG:238456.10:2001MAR30	Germ Cells - 14%, Endocrine System - 12%, Urinary Tract - 10%
124	LG:239245.1:2001MAR30	Musculoskeletal System - 11%, Sense Organs - 11%
125	LG:239579.8:2001MAR30	Embryonic Structures - 12%, Cardiovascular System - 10%
126	LG:239601.22:2001MAR30	Embryonic Structures - 13%, Unclassified/Mixed - 12%
127	LG:240121.1:2001MAR30	Unclassified/Mixed - 21%, Skin - 16%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
128	LG:241110.2:2001MAR30	Stomatognathic System - 16%, Urinary Tract - 13%, Respiratory System - 11%
129	LG:244948.4:2001MAR30	Skin - 18%
130	LG:245378.6:2001MAR30	Exocrine Glands - 10%
131	LG:248203.9:2001MAR30	Unclassified/Mixed - 13%
132	LG:249247.1:2001MAR30	Cardiovascular System - 18%, Nervous System - 18%
133	LG:267153.16:2001MAR30	Germ Cells - 16%
134	LG:291759.5:2001MAR30	Connective Tissue - 17%, Germ Cells - 11%, Digestive System - 10%, Endocrine System - 10%
135	LG:298102.1:2001MAR30	Male Genitalia - 67%, Nervous System - 33%
136	LG:308891.1:2001MAR30	Endocrine System - 80%, Nervous System - 20%
137	LG:312668.4:2001MAR30	Unclassified/Mixed - 21%, Female Genitalia - 11%
138	LG:331642.6:2001MAR30	Connective Tissue - 60%
139	LG:331851.12:2001MAR30	Unclassified/Mixed - 15%, Sense Organs - 11%
140	LG:332414.5:2001MAR30	Germ Cells - 35%, Hemic and Immune System - 13%, Unclassified/Mixed - 11%
141	LG:332730.12:2001MAR30	Unclassified/Mixed - 12%
142	LG:333062.22:2001MAR30	Hemic and Immune System - 83%, Exocrine Glands - 13%
143	LG:335705.2:2001MAR30	widely distributed
144	LG:337930.16:2001MAR30	Skin - 58%, Stomatognathic System - 31%
145	LG:346481.15:2001MAR30	Female Genitalia - 50%, Digestive System - 50%
146	LG:349164.1:2001MAR30	Stomatognathic System - 27%, Cardiovascular System - 22%, Musculoskeletal System - 11%
147	LG:350957.5:2001MAR30	Germ Cells - 49%, Female Genitalia - 20%
148	LG:383512.8:2001MAR30	Nervous System - 11%, Liver - 11%
149	LG:401163.10:2001MAR30	Liver - 23%, Hemic and Immune System - 13%
150	LG:402133.1:2001MAR30	Unclassified/Mixed - 23%, Nervous System - 23%, Respiratory System - 16%
151	LG:405820.1:2001MAR30	Unclassified/Mixed - 26%, Liver - 18%, Connective Tissue - 14%
152	LG:405846.1:2001MAR30	Male Genitalia - 58%, Female Genitalia - 17%, Nervous System - 17%
153	LG:407401.2:2001MAR30	Germ Cells - 36%
154	LG:408448.10:2001MAR30	Unclassified/Mixed - 28%, Germ Cells - 19%, Skin - 12%
155	LG:408854.13:2001MAR30	Musculoskeletal System - 21%, Cardiovascular System - 14%, Digestive System - 14%, Endocrine System - 14%
156	LG:411150.14:2001MAR30	Urinary Tract - 13%
157	LG:411466.1:2001MAR30	Unclassified/Mixed - 25%, Germ Cells - 14%, Female Genitalia - 10%
158	LG:413969.68:2001MAR30	Respiratory System - 20%, Embryonic Structures - 19%, Digestive System - 14%
159	LG:419641.35:2001MAR30	Unclassified/Mixed - 14%, Respiratory System - 10%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
160	LG:428206.7:2001MAR30	Urinary Tract - 28%, Germ Cells - 20%, Unclassified/Mixed - 12%
161	LG:430059.1:2001MAR30	Exocrine Glands - 16%
162	LG:448040.3:2001MAR30	Exocrine Glands - 25%, Urinary Tract - 18%, Endocrine System - 11%, Embryonic Structures - 11%
163	LG:451274.1:2001MAR30	Exocrine Glands - 47%, Embryonic Structures - 26%
164	LG:456110.1:2001MAR30	Nervous System - 100%
165	LG:456954.1:2001MAR30	Nervous System - 100%
166	LG:474942.12:2001MAR30	Cardiovascular System - 31%, Nervous System - 27%, Musculoskeletal System - 21%
167	LG:475119.14:2001MAR30	Germ Cells - 27%, Unclassified/Mixed - 17%, Endocrine System - 16%
168	LG:479908.77:2001MAR30	Exocrine Glands - 50%, Digestive System - 25%, Nervous System - 25%
169	LG:480127.47:2001MAR30	Germ Cells - 21%, Skin - 13%, Urinary Tract - 13%, Connective Tissue - 13%
170	LG:481154.12:2001MAR30	Unclassified/Mixed - 36%, Urinary Tract - 13%
171	LG:481414.6:2001MAR30	Unclassified/Mixed - 20%
172	LG:481941.1:2001MAR30	Nervous System - 61%, Sense Organs - 19%
173	LG:887216.4:2001MAR30	Germ Cells - 84%
174	LG:899402.3:2001MAR30	widely distributed
175	LG:899894.2:2001MAR30	Unclassified/Mixed - 11%, Embryonic Structures - 11%
176	LG:977908.1:2001MAR30	Stomatognathic System - 11%
177	LG:977929.1:2001MAR30	Sense Organs - 39%, Male Genitalia - 11%
178	LG:978008.14:2001MAR30	Germ Cells - 17%, Unclassified/Mixed - 13%, Embryonic Structures - 11%
179	LG:979054.18:2001MAR30	Nervous System - 14%, Sense Organs - 12%, Digestive System - 11%, Embryonic Structures - 11%
180	LG:979185.10:2001MAR30	Sense Organs - 38%, Nervous System - 21%
181	LG:983654.1:2001MAR30	Urinary Tract - 32%, Unclassified/Mixed - 20%, Digestive System - 12%
182	LG:985092.12:2001MAR30	Exocrine Glands - 21%, Cardiovascular System - 18%, Unclassified/Mixed - 18%
183	LG:987396.8:2001MAR30	Germ Cells - 30%
184	LG:987418.10:2001MAR30	Germ Cells - 12%, Embryonic Structures - 10%
185	LG:997203.25:2001MAR30	Germ Cells - 20%
186	LG:997477.8:2001MAR30	Male Genitalia - 100%
187	LG:998855.4:2001MAR30	Embryonic Structures - 37%, Exocrine Glands - 16%, Unclassified/Mixed - 14%
188	LG:999093.1:2001MAR30	Germ Cells - 12%
189	LG:999183.1:2001MAR30	Embryonic Structures - 10%
190	LI:1032972.1:2001MAY17	Liver - 15%, Male Genitalia - 11%, Respiratory System - 11%
191	LI:170666.6:2001MAY17	Sense Organs - 97%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
192	LI:197048.10:2001MAY17	Skin - 16%, Endocrine System - 11%
193	LI:228655.5:2001MAY17	Unclassified/Mixed - 48%, Pancreas - 23%, Exocrine Glands - 20%
194	LI:229789.6:2001MAY17	Female Genitalia - 42%, Digestive System - 33%, Hemic and Immune System - 17%
195	LI:231500.8:2001MAY17	Endocrine System - 26%, Hemic and Immune System - 23%, Digestive System - 23%
196	LI:253851.26:2001MAY17	Endocrine System - 38%, Male Genitalia - 13%, Female Genitalia - 11%
197	LI:373302.1:2001MAY17	Exocrine Glands - 56%, Female Genitalia - 22%, Nervous System - 22%
198	LI:405707.12:2001MAY17	Nervous System - 28%, Connective Tissue - 24%, Endocrine System - 17%
199	LI:41141.8:2001MAY17	Nervous System - 61%, Skin - 17%, Pancreas - 11%
200	LI:758193.3:2001MAY17	Urinary Tract - 18%, Nervous System - 15%, Exocrine Glands - 11%
201	LI:1028562.3:2001MAY17	Unclassified/Mixed - 100%
202	LI:1046507.7:2001MAY17	Nervous System - 63%, Urinary Tract - 25%, Female Genitalia - 13%
204	LI:1144528.4:2001MAY17	Respiratory System - 35%, Unclassified/Mixed - 27%, Hemic and Immune System - 16%
205	LI:1172210.7:2001MAY17	Endocrine System - 26%, Musculoskeletal System - 21%, Connective Tissue - 21%
206	LI:1178659.14:2001MAY17	Germ Cells - 30%, Urinary Tract - 14%, Nervous System - 12%
207	LI:1983726.3:2001MAY17	Unclassified/Mixed - 97%
208	LI:2051495.3:2001MAY17	Sense Organs - 41%, Embryonic Structures - 26%
209	LI:2117629.1:2001MAY17	Urinary Tract - 33%, Nervous System - 33%, Hemic and Immune System - 17%, Male Genitalia - 17%
210	LI:2118007.3:2001MAY17	Nervous System - 100%
211	LI:2118292.9:2001MAY17	Connective Tissue - 26%, Male Genitalia - 19%, Exocrine Glands - 19%
212	LI:2118733.7:2001MAY17	Connective Tissue - 100%
213	LI:212702.3:2001MAY17	Germ Cells - 13%, Nervous System - 11%, Unclassified/Mixed - 11%
214	LI:2207871.10:2001MAY17	Germ Cells - 34%, Endocrine System - 15%, Male Genitalia - 14%
215	LI:2207876.5:2001MAY17	Nervous System - 100%
216	LI:2208743.1:2001MAY17	Sense Organs - 67%, Urinary Tract - 17%, Endocrine System - 11%
217	LI:2208744.1:2001MAY17	Female Genitalia - 43%, Connective Tissue - 32%, Endocrine System - 11%
218	LI:230905.3:2001MAY17	Skin - 13%, Cardiovascular System - 12%, Embryonic Structures - 11%
219	LI:235233.95:2001MAY17	Embryonic Structures - 56%, Cardiovascular System - 22%, Hemic and Immune System - 11%, Male Genitalia - 11%
220	LI:235359.24:2001MAY17	Male Genitalia - 16%, Endocrine System - 13%, Liver - 12%
221	LI:238365.6:2001MAY17	Nervous System - 57%, Hemic and Immune System - 43%
223	LI:321069.2:2001MAY17	Urinary Tract - 14%, Unclassified/Mixed - 11%
224	LI:331499.8:2001MAY17	Respiratory System - 13%, Male Genitalia - 13%, Exocrine Glands - 12%
225	LI:332176.8:2001MAY17	Germ Cells - 27%, Unclassified/Mixed - 18%, Exocrine Glands - 11%, Endocrine System - 11%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
226	LI:333952.7:2001MAY17	Respiratory System - 69%, Hemic and Immune System - 31%
228	LI:343869.2:2001MAY17	widely distributed
229	LI:363532.1:2001MAY17	Digestive System - 67%, Nervous System - 33%
231	LI:416650.1:2001MAY17	Cardiovascular System - 47%, Connective Tissue - 41%, Digestive System - 12%
232	LI:444767.32:2001MAY17	Musculoskeletal System - 19%, Hemic and Immune System - 11%
233	LI:759073.1:2001MAY17	Exocrine Glands - 45%, Respiratory System - 15%, Hemic and Immune System - 15%
234	LI:759902.4:2001MAY17	Skin - 100%
235	LI:762268.1:2001MAY17	Pancreas - 84%
236	LI:813699.1:2001MAY17	Endocrine System - 40%, Liver - 26%, Respiratory System - 14%, Female Genitalia - 14%
237	LI:024142.16:2001MAY17	Sense Organs - 40%, Pancreas - 13%
238	LI:1018424.4:2001MAY17	Connective Tissue - 12%, Nervous System - 11%
239	LI:1085250.6:2001MAY17	Cardiovascular System - 25%, Embryonic Structures - 22%, Respiratory System - 12%
241	LI:2207125.3:2001MAY17	Male Genitalia - 100%
242	LI:235153.44:2001MAY17	Connective Tissue - 18%, Embryonic Structures - 11%
243	LI:007101.10:2001MAY17	Germ Cells - 25%, Connective Tissue - 23%
244	LI:008541.2:2001MAY17	Unclassified/Mixed - 39%, Exocrine Glands - 24%, Female Genitalia - 18%
245	LI:009658.13:2001MAY17	Embryonic Structures - 70%
246	LI:020012.14:2001MAY17	Germ Cells - 33%
247	LI:020691.1:2001MAY17	Female Genitalia - 78%, Digestive System - 22%
248	LI:021188.12:2001MAY17	Respiratory System - 18%, Female Genitalia - 12%
249	LI:021324.4:2001MAY17	Endocrine System - 37%, Liver - 18%, Nervous System - 15%
250	LI:021834.15:2001MAY17	Liver - 15%, Nervous System - 11%
251	LI:024841.1:2001MAY17	Hemic and Immune System - 17%, Connective Tissue - 14%, Pancreas - 10%
252	LI:025724.12:2001MAY17	Skin - 17%, Pancreas - 11%
253	LI:029328.2:2001MAY17	Germ Cells - 13%
254	LI:032171.5:2001MAY17	Skin - 15%, Urinary Tract - 11%, Hemic and Immune System - 11%
255	LI:035055.1:2001MAY17	Musculoskeletal System - 30%, Respiratory System - 28%, Endocrine System - 20%
256	LI:036747.17:2001MAY17	Skin - 13%, Hemic and Immune System - 12%
257	LI:044301.2:2001MAY17	Urinary Tract - 28%, Unclassified/Mixed - 17%, Nervous System - 12%
258	LI:061585.10:2001MAY17	Embryonic Structures - 27%, Respiratory System - 18%
259	LI:066742.21:2001MAY17	widely distributed
260	LI:075492.206:2001MAY17	Liver - 15%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
261	LI:090782.3:2001MAY17	Musculoskeletal System - 39%, Exocrine Glands - 28%, Cardiovascular System - 22%
262	LI:1031308.1:2001MAY17	Germ Cells - 52%, Endocrine System - 23%
263	LI:1054377.1:2001MAY17	Exocrine Glands - 29%, Digestive System - 24%, Urinary Tract - 24%
264	LI:1072074.10:2001MAY17	Endocrine System - 10%
265	LI:1072889.15:2001MAY17	Embryonic Structures - 13%
266	LI:1077480.1:2001MAY17	Urinary Tract - 86%, Digestive System - 14%
267	LI:1079555.1:2001MAY17	Pancreas - 37%, Unclassified/Mixed - 12%
268	LI:1084992.28:2001MAY17	Digestive System - 75%, Female Genitalia - 25%
269	LI:1085472.5:2001MAY17	Urinary Tract - 18%, Exocrine Glands - 14%, Female Genitalia - 11%
270	LI:1086800.7:2001MAY17	Urinary Tract - 12%, Embryonic Structures - 10%
271	LI:1089871.9:2001MAY17	Cardiovascular System - 12%
272	LI:110297.6:2001MAY17	Endocrine System - 14%, Unclassified/Mixed - 11%, Embryonic Structures - 10%
273	LI:1143463.8:2001MAY17	Germ Cells - 18%, Skin - 16%
274	LI:1144466.1:2001MAY17	Embryonic Structures - 41%
275	LI:1170624.2:2001MAY17	Endocrine System - 45%, Digestive System - 18%, Hemic and Immune System - 18%, Nervous System - 18%
276	LI:1171602.39:2001MAY17	Liver - 90%, Nervous System - 10%
277	LI:1182361.3:2001MAY17	Connective Tissue - 100%
278	LI:1188194.15:2001MAY17	Embryonic Structures - 38%, Musculoskeletal System - 36%
279	LI:1189195.7:2001MAY17	Germ Cells - 46%, Respiratory System - 12%
280	LI:1190092.13:2001MAY17	Hemic and Immune System - 100%
281	LI:1190318.4:2001MAY17	Germ Cells - 61%
282	LI:144233.1:2001MAY17	Unclassified/Mixed - 42%, Urinary Tract - 33%, Hemic and Immune System - 17%
283	LI:154608.1:2001MAY17	Urinary Tract - 33%, Hemic and Immune System - 25%, Nervous System - 25%
284	LI:170101.1:2001MAY17	Urinary Tract - 33%, Respiratory System - 33%, Exocrine Glands - 21%
285	LI:180043.1:2001MAY17	Pancreas - 45%, Endocrine System - 41%, Hemic and Immune System - 14%
286	LI:193050.1:2001MAY17	Urinary Tract - 28%, Nervous System - 21%, Exocrine Glands - 15%
287	LI:197477.31:2001MAY17	Embryonic Structures - 18%, Sense Organs - 14%, Hemic and Immune System - 12%
288	LI:199639.12:2001MAY17	Skin - 15%, Sense Organs - 11%
289	LI:200058.6:2001MAY17	Urinary Tract - 35%, Unclassified/Mixed - 22%, Hemic and Immune System - 22%, Male Genitalia - 22%
290	LI:201374.23:2001MAY17	Unclassified/Mixed - 71%, Digestive System - 29%
291	LI:201824.1:2001MAY17	Musculoskeletal System - 13%, Cardiovascular System - 12%, Exocrine Glands - 11%
292	LI:201989.11:2001MAY17	Germ Cells - 23%, Unclassified/Mixed - 22%, Digestive System - 10%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
293	LI:2035159.1:2001MAY17	Pancreas - 71%, Female Genitalia - 14%, Male Genitalia - 14%
294	LI:204818.10:2001MAY17	Skin - 29%, Endocrine System - 16%, Urinary Tract - 15%
295	LI:2048337.1:2001MAY17	Stomatognathic System - 30%, Endocrine System - 13%, Sense Organs - 13%
296	LI:2049697.4:2001MAY17	Embryonic Structures - 25%, Germ Cells - 19%
297	LI:2050808.19:2001MAY17	Liver - 24%, Embryonic Structures - 13%, Respiratory System - 12%
298	LI:209773.25:2001MAY17	Male Genitalia - 100%
299	LI:2117881.32:2001MAY17	Sense Organs - 82%
300	LI:2118140.9:2001MAY17	Liver - 47%, Digestive System - 21%, Respiratory System - 16%
301	LI:2118151.15:2001MAY17	Unclassified/Mixed - 15%, Germ Cells - 15%
302	LI:2118324.9:2001MAY17	Germ Cells - 15%, Female Genitalia - 12%
303	LI:2118368.12:2001MAY17	Musculoskeletal System - 20%, Pancreas - 14%, Liver - 13%
304	LI:2119448.5:2001MAY17	Stomatognathic System - 58%, Embryonic Structures - 16%
305	LI:212023.7:2001MAY17	Germ Cells - 51%, Pancreas - 12%
306	LI:2120556.1:2001MAY17	Sense Organs - 36%, Unclassified/Mixed - 12%, Pancreas - 12%
307	LI:2121577.3:2001MAY17	Skin - 76%, Endocrine System - 24%
308	LI:2123395.11:2001MAY17	Unclassified/Mixed - 13%, Female Genitalia - 11%, Embryonic Structures - 11%
309	LI:2123452.9:2001MAY17	Exocrine Glands - 14%, Musculoskeletal System - 11%
310	LI:2164109.1:2001MAY17	Hemic and Immune System - 100%
311	LI:2168320.1:2001MAY17	Digestive System - 100%
312	LI:2173577.1:2001MAY17	Male Genitalia - 100%
313	LI:2179256.1:2001MAY17	Unclassified/Mixed - 100%
314	LI:2180388.1:2001MAY17	Male Genitalia - 100%
315	LI:2199713.8:2001MAY17	Urinary Tract - 28%, Endocrine System - 11%, Male Genitalia - 10%
316	LI:2200587.2:2001MAY17	Female Genitalia - 49%, Respiratory System - 18%, Exocrine Glands - 12%
317	LI:2200761.12:2001MAY17	Nervous System - 100%
318	LI:2203624.1:2001MAY17	Respiratory System - 19%, Endocrine System - 19%, Exocrine Glands - 19%
319	LI:220495.9:2001MAY17	Embryonic Structures - 12%, Liver - 11%
320	LI:2205532.1:2001MAY17	Liver - 64%, Respiratory System - 21%, Hemic and Immune System - 14%
321	LI:2206277.1:2001MAY17	Embryonic Structures - 29%, Skin - 24%, Musculoskeletal System - 15%
323	LI:2208404.4:2001MAY17	Nervous System - 100%
325	LI:2208766.2:2001MAY17	Stomatognathic System - 21%, Embryonic Structures - 11%
326	LI:2209636.3:2001MAY17	Exocrine Glands - 23%, Urinary Tract - 20%, Nervous System - 20%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
328	LI:229267.1:2001MAY17	Hemic and Immune System - 100%
329	LI:229648.2:2001MAY17	Nervous System - 77%, Endocrine System - 19%
330	LI:231016.1:2001MAY17	Digestive System - 36%, Respiratory System - 27%, Hemic and Immune System - 18%, Male Genitalia - 18%
331	LI:231140.5:2001MAY17	Embryonic Structures - 30%, Hemic and Immune System - 16%, Urinary Tract - 12%, Cardiovascular System - 12%
333	LI:232846.24:2001MAY17	widely distributed
334	LI:233411.11:2001MAY17	Nervous System - 10%
335	LI:233545.13:2001MAY17	Liver - 17%, Endocrine System - 11%, Musculoskeletal System - 10%
336	LI:234671.101:2001MAY17	Sense Organs - 29%
337	LI:236098.14:2001MAY17	Unclassified/Mixed - 14%
338	LI:236196.15:2001MAY17	Endocrine System - 15%, Musculoskeletal System - 15%, Exocrine Glands - 11%
339	LI:237086.1:2001MAY17	Exocrine Glands - 33%, Urinary Tract - 27%, Hemic and Immune System - 20%, Nervous System - 20%
340	LI:238585.30:2001MAY17	Female Genitalia - 50%, Hemic and Immune System - 50%
341	LI:238672.6:2001MAY17	Germ Cells - 21%, Urinary Tract - 19%, Exocrine Glands - 14%
342	LI:239579.9:2001MAY17	Sense Organs - 11%, Connective Tissue - 11%, Cardiovascular System - 10%
343	LI:239720.1:2001MAY17	Unclassified/Mixed - 16%, Nervous System - 16%, Endocrine System - 12%
344	LI:240037.6:2001MAY17	Urinary Tract - 33%, Exocrine Glands - 17%, Liver - 11%
345	LI:243900.7:2001MAY17	Stomatognathic System - 34%, Male Genitalia - 16%, Skin - 15%
346	LI:244378.1:2001MAY17	Skin - 12%, Sense Organs - 12%
347	LI:245500.3:2001MAY17	Cardiovascular System - 13%
348	LI:245982.24:2001MAY17	widely distributed
349	LI:246054.1:2001MAY17	Stomatognathic System - 13%, Urinary Tract - 11%
350	LI:256051.229:2001MAY17	Exocrine Glands - 22%, Cardiovascular System - 17%, Digestive System - 17%
351	LI:260629.7:2001MAY17	Unclassified/Mixed - 100%
352	LI:272723.1:2001MAY17	Cardiovascular System - 67%, Hemic and Immune System - 33%
353	LI:272766.1:2001MAY17	Digestive System - 50%, Hemic and Immune System - 50%
354	LI:275726.1:2001MAY17	Cardiovascular System - 67%, Nervous System - 33%
355	LI:276815.1:2001MAY17	Endocrine System - 71%, Female Genitalia - 29%
356	LI:283562.5:2001MAY17	Sense Organs - 27%, Germ Cells - 13%, Unclassified/Mixed - 12%
357	LI:289066.15:2001MAY17	Sense Organs - 14%
358	LI:331040.17:2001MAY17	Unclassified/Mixed - 12%, Sense Organs - 12%
359	LI:332414.5:2001MAY17	Germ Cells - 35%, Hemic and Immune System - 12%, Unclassified/Mixed - 12%
360	LI:332730.16:2001MAY17	widely distributed

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
362	LI:337038.15:2001MAY17	Germ Cells - 19%
363	LI:337606.6:2001MAY17	Germ Cells - 77%
364	LI:338032.10:2001MAY17	Nervous System - 100%
365	LI:339265.16:2001MAY17	Germ Cells - 29%, Nervous System - 17%, Urinary Tract - 13%
366	LI:344646.4:2001MAY17	Sense Organs - 23%, Connective Tissue - 12%, Respiratory System - 11%, Unclassified/Mixed - 11%
367	LI:347393.7:2001MAY17	Embryonic Structures - 24%, Cardiovascular System - 20%, Connective Tissue - 17%
369	LI:351120.6:2001MAY17	widely distributed
370	LI:358762.41:2001MAY17	Cardiovascular System - 40%, Endocrine System - 19%, Embryonic Structures - 13%
371	LI:363003.48:2001MAY17	Male Genitalia - 15%
372	LI:370899.6:2001MAY17	Embryonic Structures - 14%, Skin - 13%, Unclassified/Mixed - 12%
373	LI:376470.1:2001MAY17	Hemic and Immune System - 100%
374	LI:400961.18:2001MAY17	Skin - 16%, Embryonic Structures - 13%
375	LI:404482.20:2001MAY17	Hemic and Immune System - 13%, Connective Tissue - 11%, Exocrine Glands - 11%
376	LI:405985.1:2001MAY17	Nervous System - 69%, Female Genitalia - 31%
377	LI:406389.1:2001MAY17	Embryonic Structures - 44%, Nervous System - 24%, Respiratory System - 11%, Male Genitalia - 11%
378	LI:406833.1:2001MAY17	Musculoskeletal System - 16%, Unclassified/Mixed - 15%, Urinary Tract - 10%
379	LI:407921.3:2001MAY17	Germ Cells - 29%
380	LI:409078.54:2001MAY17	Male Genitalia - 24%, Skin - 20%, Liver - 11%
381	LI:423601.6:2001MAY17	Hemic and Immune System - 21%, Musculoskeletal System - 13%, Connective Tissue - 13%
382	LI:425024.5:2001MAY17	Skin - 31%, Pancreas - 19%, Exocrine Glands - 17%
383	LI:427909.29:2001MAY17	Stomatognathic System - 10%
384	LI:428198.20:2001MAY17	Digestive System - 17%, Male Genitalia - 15%, Urinary Tract - 14%
385	LI:429738.6:2001MAY17	Nervous System - 45%, Respiratory System - 27%, Hemic and Immune System - 27%
386	LI:449437.1:2001MAY17	Female Genitalia - 50%, Hemic and Immune System - 50%
387	LI:459269.25:2001MAY17	Sense Organs - 16%, Digestive System - 11%, Nervous System - 11%, Connective Tissue - 11%
388	LI:464206.1:2001MAY17	Germ Cells - 20%, Connective Tissue - 13%, Endocrine System - 13%
389	LI:465821.2:2001MAY17.	Liver - 16%, Musculoskeletal System - 12%
390	LI:474414.28:2001MAY17	Embryonic Structures - 12%
391	LI:474435.14:2001MAY17	Germ Cells - 10%
392	LI:474458.11:2001MAY17	widely distributed
393	LI:477127.18:2001MAY17	Hemic and Immune System - 13%
394	LI:480375.55:2001MAY17	Germ Cells - 14%, Digestive System - 12%

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Table 4

SEQ ID NO:	Template ID	Tissue Distribution
395	LI:480467.24:2001MAY17	Skin - 34%, Connective Tissue - 16%, Nervous System - 11%
396	LI:480587.1:2001MAY17	widely distributed
397	LI:480798.13:2001MAY17	Sense Organs - 16%
398	LI:481203.14:2001MAY17	Exocrine Glands - 16%
399	LI:481237.11:2001MAY17	Embryonic Structures - 14%, Unclassified/Mixed - 12%
400	LI:481368.12:2001MAY17	Pancreas - 14%, Hemic and Immune System - 11%, Urinary Tract - 10%
401	LI:482301.8:2001MAY17	Germ Cells - 13%
402	LI:482482.29:2001MAY17	Musculoskeletal System - 30%, Endocrine System - 20%, Connective Tissue - 15%
403	LI:758877.26:2001MAY17	Pancreas - 26%, Respiratory System - 13%, Unclassified/Mixed - 13%, Exocrine Glands - 13%
404	LI:791042.1:2001MAY17	Embryonic Structures - 28%, Male Genitalia - 28%, Urinary Tract - 22%
405	LI:808999.26:2001MAY17	widely distributed
406	LI:815715.10:2001MAY17	Hemic and Immune System - 13%, Unclassified/Mixed - 12%
407	LI:902980.16:2001MAY17	Sense Organs - 15%, Connective Tissue - 13%
408	LI:903196.25:2001MAY17	Sense Organs - 15%, Exocrine Glands - 11%
409	LI:903914.10:2001MAY17	Unclassified/Mixed - 15%, Nervous System - 12%, Connective Tissue - 12%
410	LG:006764.2:2001JUN22	Unclassified/Mixed - 24%, Respiratory System - 18%, Embryonic Structures - 16%, Male Genitalia - 16%
411	LG:014704.8:2001JUN22	Germ Cells - 13%, Female Genitalia - 11%, Liver - 10%
412	LG:1447607.7:2001JUN22	Stomatognathic System - 16%, Germ Cells - 14%, Female Genitalia - 10%
413	LG:1455032.3:2001JUN22	Skin - 10%
414	LG:1501898.18:2001JUN22	Germ Cells - 23%, Urinary Tract - 12%, Connective Tissue - 11%
415	LG:1502692.5:2001JUN22	Sense Organs - 15%, Embryonic Structures - 11%
416	LG:208949.8:2001JUN22	Unclassified/Mixed - 60%, Exocrine Glands - 19%, Urinary Tract - 17%
417	LG:240501.10:2001JUN22	Embryonic Structures - 43%, Hemic and Immune System - 14%, Nervous System - 14%
418	LG:329228.27:2001JUN22	Musculoskeletal System - 27%, Liver - 20%, Exocrine Glands - 18%
419	LG:337056.11:2001JUN22	Liver - 100%
420	LG:346663.9:2001JUN22	Endocrine System - 33%, Unclassified/Mixed - 22%, Female Genitalia - 15%, Cardiovascular System - 15%
421	LG:7685586.2:2001JUN22	Unclassified/Mixed - 76%, Cardiovascular System - 24%
422	LG:407730.13:2001JUN22	Sense Organs - 100%
423	LG:025465.5:2001JUN22	Embryonic Structures - 15%, Urinary Tract - 15%, Cardiovascular System - 12%
424	LG:054509.14:2001JUN22	Germ Cells - 13%
425	LG:1067876.1:2001JUN22	Unclassified/Mixed - 55%, Female Genitalia - 36%
426	LG:1327699.55:2001JUN22	Exocrine Glands - 100%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
427	LG:1482904.10:2001JUN22	Embryonic Structures - 13%, Female Genitalia - 11%
428	LG:222317.4:2001JUN22	Female Genitalia - 50%, Digestive System - 50%
429	LG:332701.3:2001JUN22	Unclassified/Mixed - 14%
430	LG:369881.5:2001JUN22	Skin - 51%, Unclassified/Mixed - 23%
431	LG:404381.2:2001JUN22	Endocrine System - 24%, Pancreas - 24%, Nervous System - 21%
432	LG:405709.2:2001JUN22	Endocrine System - 39%, Connective Tissue - 30%, Hemic and Immune System - 17%
433	LG:406664.17:2001JUN22	Hemic and Immune System - 100%
434	LG:7670681.1:2001JUN22	Musculoskeletal System - 100%
435	LG:7687404.1:2001JUN22	Female Genitalia - 40%, Endocrine System - 40%, Digestive System - 20%
436	LG:7690030.24:2001JUN22	Hemic and Immune System - 100%
437	LG:7690229.3:2001JUN22	Unclassified/Mixed - 86%, Nervous System - 14%
438	LG:7690533.16:2001JUN22	Pancreas - 30%, Musculoskeletal System - 20%, Male Genitalia - 20%
439	LG:7691131.2:2001JUN22	Unclassified/Mixed - 53%, Pancreas - 19%
440	LG:7692559.6:2001JUN22	Musculoskeletal System - 55%, Endocrine System - 36%
441	LG:7684866.10:2001JUN22	Female Genitalia - 100%
442	LG:002106.5:2001JUN22	Musculoskeletal System - 28%, Liver - 21%, Respiratory System - 16%
443	LG:004064.1:2001JUN22	Urinary Tract - 70%, Male Genitalia - 20%, Hemic and Immune System - 10%
444	LG:007916.8:2001JUN22	Female Genitalia - 32%, Liver - 26%, Digestive System - 12%, Endocrine System - 12%
445	LG:014719.14:2001JUN22	Skin - 16%, Nervous System - 14%, Female Genitalia - 12%
446	LG:021763.31:2001JUN22	Urinary Tract - 17%, Male Genitalia - 14%, Cardiovascular System - 13%
447	LG:025397.1:2001JUN22	Musculoskeletal System - 31%, Sense Organs - 14%, Endocrine System - 12%
448	LG:029880.20:2001JUN22	Sense Organs - 24%, Digestive System - 14%, Nervous System - 13%
449	LG:040422.37:2001JUN22	Germ Cells - 18%, Unclassified/Mixed - 13%
450	LG:065935.11:2001JUN22	Unclassified/Mixed - 13%, Germ Cells - 13%, Sense Organs - 12%
451	LG:074381.1:2001JUN22	Unclassified/Mixed - 21%, Female Genitalia - 12%, Germ Cells - 11%, Endocrine System - 11%
452	LG:083814.6:2001JUN22	Embryonic Structures - 15%
453	LG:090985.1:2001JUN22	Digestive System - 100%
454	LG:093750.2:2001JUN22	Connective Tissue - 33%, Female Genitalia - 19%, Urinary Tract - 14%
455	LG:1013708.26:2001JUN22	Skin - 27%, Unclassified/Mixed - 16%, Embryonic Structures - 12%
456	LG:1022283.8:2001JUN22	Skin - 11%
457	LG:1034386.1:2001JUN22	Urinary Tract - 83%, Digestive System - 17%
458	LG:1045617.36:2001JUN22	Liver - 47%, Cardiovascular System - 21%, Endocrine System - 21%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
459	LG:1063303.1:2001JUN22	Embryonic Structures - 21%, Connective Tissue - 15%, Nervous System - 11%
460	LG:1094200.1:2001JUN22	Germ Cells - 23%, Unclassified/Mixed - 11%
461	LG:1099249.19:2001JUN22	Connective Tissue - 22%, Unclassified/Mixed - 21%, Urinary Tract - 15%
462	LG:110667.1:2001JUN22	Liver - 38%, Nervous System - 29%, Respiratory System - 21%
463	LG:1132386.20:2001JUN22	Nervous System - 13%, Embryonic Structures - 11%, Sense Organs - 11%
464	LG:116015.2:2001JUN22	Sense Organs - 21%, Germ Cells - 15%
465	LG:1173104.15:2001JUN22	Liver - 15%, Female Genitalia - 12%, Embryonic Structures - 11%
466	LG:1285109.14:2001JUN22	Germ Cells - 16%, Cardiovascular System - 14%, Connective Tissue - 12%
467	LG:131477.11:2001JUN22	Sense Organs - 21%, Germ Cells - 11%
468	LG:1333618.1:2001JUN22	Female Genitalia - 50%, Respiratory System - 50%
469	LG:1347760.16:2001JUN22	Connective Tissue - 14%, Embryonic Structures - 13%, Nervous System - 12%
470	LG:1383039.369:2001JUN22	Embryonic Structures - 64%, Hemic and Immune System - 21%, Digestive System - 14%
471	LG:1383313.3:2001JUN22	Germ Cells - 18%, Nervous System - 16%
472	LG:1384075.8:2001JUN22	Unclassified/Mixed - 25%
473	LG:1384155.1:2001JUN22	Embryonic Structures - 13%
474	LG:1385280.12:2001JUN22	Unclassified/Mixed - 30%, Embryonic Structures - 13%
475	LG:1390535.25:2001JUN22	Female Genitalia - 17%, Connective Tissue - 15%, Musculoskeletal System - 14%
476	LG:1397047.1:2001JUN22	Unclassified/Mixed - 50%, Female Genitalia - 33%, Male Genitalia - 17%
477	LG:1398646.15:2001JUN22	Skin - 15%, Female Genitalia - 14%, Unclassified/Mixed - 10%
478	LG:1446193.10:2001JUN22	Sense Organs - 29%
479	LG:1446405.14:2001JUN22	Unclassified/Mixed - 10%
480	LG:1448148.1:2001JUN22	Unclassified/Mixed - 22%, Male Genitalia - 18%, Urinary Tract - 17%
481	LG:1452619.13:2001JUN22	Exocrine Glands - 67%, Female Genitalia - 17%
482	LG:1452783.22:2001JUN22	Respiratory System - 14%, Embryonic Structures - 12%, Female Genitalia - 10%
483	LG:1453417.5:2001JUN22	Nervous System - 32%, Skin - 19%, Endocrine System - 18%
484	LG:1455222.23:2001JUN22	Embryonic Structures - 37%, Pancreas - 18%, Exocrine Glands - 16%
485	LG:149121.8:2001JUN22	widely distributed
486	LG:1500175.18:2001JUN22	Sense Organs - 27%
487	LG:1500434.6:2001JUN22	Stomatognathic System - 21%, Sense Organs - 18%
488	LG:1501550.19:2001JUN22	Urinary Tract - 34%, Sense Organs - 14%
489	LG:1501923.26:2001JUN22	Liver - 64%, Nervous System - 36%
490	LG:150960.9:2001JUN22	Skin - 14%, Unclassified/Mixed - 10%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
491	LG:182744.29:2001JUN22	Respiratory System - 20%, Pancreas - 18%, Nervous System - 16%
492	LG:197166.1:2001JUN22	Nervous System - 100%
493	LG:197455.5:2001JUN22	Exocrine Glands - 50%, Nervous System - 21%, Endocrine System - 17%
494	LG:198251.8:2001JUN22	Sense Organs - 19%, Nervous System - 14%
495	LG:200149.3:2001JUN22	Germ Cells - 16%, Skin - 15%, Connective Tissue - 12%
496	LG:203483.3:2001JUN22	Unclassified/Mixed - 23%, Exocrine Glands - 14%, Digestive System - 14%
497	LG:209701.7:2001JUN22	Nervous System - 34%, Connective Tissue - 24%, Respiratory System - 17%
498	LG:210614.1:2001JUN22	Hemic and Immune System - 50%, Digestive System - 33%, Nervous System - 17%
499	LG:210672.1:2001JUN22	Female Genitalia - 22%, Nervous System - 22%, Connective Tissue - 17%
500	LG:215051.10:2001JUN22	Unclassified/Mixed - 21%, Nervous System - 14%
501	LG:218989.3:2001JUN22	Embryonic Structures - 21%, Skin - 16%, Female Genitalia - 11%, Pancreas - 11%
502	LG:228107.11:2001JUN22	Nervous System - 13%, Pancreas - 13%, Male Genitalia - 13%
503	LG:231016.1:2001JUN22	Digestive System - 57%, Male Genitalia - 29%, Hemic and Immune System - 14%
504	LG:235943.60:2001JUN22	Pancreas - 28%, Female Genitalia - 14%, Respiratory System - 12%
505	LG:235970.14:2001JUN22	Stomatognathic System - 15%
506	LG:236697.15:2001JUN22	Sense Organs - 14%
507	LG:238576.3:2001JUN22	Embryonic Structures - 90%, Nervous System - 10%
508	LG:238602.2:2001JUN22	widely distributed
509	LG:241291.46:2001JUN22	widely distributed
510	LG:241742.1:2001JUN22	widely distributed
511	LG:244520.33:2001JUN22	Pancreas - 36%, Cardiovascular System - 28%, Hemic and Immune System - 16%
512	LG:247556.1:2001JUN22	Exocrine Glands - 100%
513	LG:247792.5:2001JUN22	Germ Cells - 47%
514	LG:253580.6:2001JUN22	widely distributed
515	LG:291759.5:2001JUN22	Embryonic Structures - 14%, Connective Tissue - 12%, Digestive System - 12%
516	LG:298226.1:2001JUN22	Musculoskeletal System - 52%, Embryonic Structures - 39%
517	LG:306342.1:2001JUN22	Endocrine System - 44%, Hemic and Immune System - 33%, Male Genitalia - 22%
518	LG:327144.5:2001JUN22	Germ Cells - 16%, Unclassified/Mixed - 14%, Hemic and Immune System - 11%
519	LG:331499.8:2001JUN22	Skin - 13%, Unclassified/Mixed - 12%, Exocrine Glands - 11%
520	LG:331582.12:2001JUN22	Embryonic Structures - 50%
521	LG:333017.12:2001JUN22	Germ Cells - 49%, Unclassified/Mixed - 15%
522	LG:334438.8:2001JUN22	Urinary Tract - 19%, Connective Tissue - 15%, Cardiovascular System - 12%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
523	LG:337835.7:2001JUN22.	Germ Cells - 32%, Skin - 21%
524	LG:346536.12:2001JUN22	Nervous System - 10%
525	LG:348117.5:2001JUN22	Urinary Tract - 19%, Musculoskeletal System - 12%, Female Genitalia - 11%
526	LG:350407.22:2001JUN22	Urinary Tract - 17%, Female Genitalia - 16%, Digestive System - 12%
527	LG:373219.13:2001JUN22	Respiratory System - 17%, Exocrine Glands - 11%
528	LG:375048.15:2001JUN22	Sense Organs - 18%, Male Genitalia - 18%, Urinary Tract - 13%
529	LG:400114.3:2001JUN22	Skin - 24%, Digestive System - 19%, Respiratory System - 17%
530	LG:400652.1:2001JUN22	Skin - 19%, Cardiovascular System - 12%, Digestive System - 10%
531	LG:401313.10:2001JUN22	Nervous System - 35%, Embryonic Structures - 29%, Unclassified/Mixed - 19%
532	LG:406389.1:2001JUN22	Embryonic Structures - 38%, Nervous System - 35%, Respiratory System - 10%
533	LG:406595.2:2001JUN22	Sense Organs - 15%, Urinary Tract - 13%, Embryonic Structures - 11%
534	LG:410628.21:2001JUN22	Digestive System - 33%, Male Genitalia - 33%, Hemic and Immune System - 25%
535	LG:413583.15:2001JUN22	Stomatognathic System - 23%, Sense Organs - 13%
536	LG:419641.35:2001JUN22	Unclassified/Mixed - 13%
537	LG:420759.4:2001JUN22	Urinary Tract - 100%
538	LG:425448.18:2001JUN22	Sense Organs - 15%, Embryonic Structures - 10%
539	LG:435717.5:2001JUN22	Skin - 13%, Sense Organs - 12%, Endocrine System - 11%
540	LG:441159.31:2001JUN22	Unclassified/Mixed - 18%, Urinary Tract - 15%
541	LG:461375.2:2001JUN22	Embryonic Structures - 16%, Connective Tissue - 13%
542	LG:474674.34:2001JUN22	Liver - 23%, Endocrine System - 17%, Germ Cells - 14%
543	LG:481414.8:2001JUN22	Unclassified/Mixed - 16%
544	LG:7669276.1:2001JUN22	Nervous System - 100%
545	LG:7677848.1:2001JUN22	Cardiovascular System - 100%
546	LG:7684981.3:2001JUN22	Nervous System - 19%, Liver - 12%, Male Genitalia - 12%
547	LG:7685048.6:2001JUN22	Hemic and Immune System - 50%, Nervous System - 50%
548	LG:7688302.1:2001JUN22	Skin - 30%, Embryonic Structures - 20%, Musculoskeletal System - 13%
549	LG:7690463.3:2001JUN22	Liver - 17%, Urinary Tract - 17%, Exocrine Glands - 12%
550	LG:7691479.5:2001JUN22	Hemic and Immune System - 100%
551	LG:7691527.4:2001JUN22	Nervous System - 26%, Respiratory System - 20%, Musculoskeletal System - 17%
552	LG:7691663.1:2001JUN22	Embryonic Structures - 20%, Pancreas - 20%, Liver - 19%, Male Genitalia - 19%
553	LG:7691854.1:2001JUN22	Liver - 32%, Unclassified/Mixed - 21%, Musculoskeletal System - 21%
554	LG:7692235.2:2001JUN22	Hemic and Immune System - 100%

Table 4

SEQ ID NO:	Template ID	Tissue Distribution
555	LG:7692239.1:2001JUN22	Exocrine Glands - 20%, Digestive System - 17%, Nervous System - 14%
556	LG:7692575.1:2001JUN22	Sense Organs - 69%
557	LG:7692742.1:2001JUN22	Nervous System - 50%, Female Genitalia - 33%, Hemic and Immune System - 17%
558	LG:7693942.1:2001JUN22	Musculoskeletal System - 19%, Exocrine Glands - 15%, Embryonic Structures - 14%
559	LG:899248.22:2001JUN22	Musculoskeletal System - 34%, Embryonic Structures - 14%, Connective Tissue - 10%
560	LG:979051.25:2001JUN22	Liver - 11%
561	LG:979054.18:2001JUN22	Nervous System - 14%, Sense Organs - 12%, Embryonic Structures - 11%
562	LG:979415.1:2001JUN22	Skin - 37%, Sense Organs - 27%
563	LG:980685.1:2001JUN22	Digestive System - 12%, Female Genitalia - 11%, Hemic and Immune System - 11%
564	LG:981272.6:2001JUN22	Unclassified/Mixed - 29%, Female Genitalia - 16%, Connective Tissue - 16%
565	LG:982723.4:2001JUN22	Embryonic Structures - 21%, Hemic and Immune System - 17%, Digestive System - 15%
566	LG:982915.8:2001JUN22	Digestive System - 14%
567	LG:987785.10:2001JUN22	Sense Organs - 14%, Pancreas - 12%, Unclassified/Mixed - 12%

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
587	1	335	112	1116	g16550386	1.00E-154	unnamed protein product
587	1	335	112	1116	g12836009	1.00E-120	evidence:NAS~hypothetical protein~putative
587	1	335	112	1116	g296164	3.00E-09	156 kDa Protein
591	3	180	3	542	g13325269	4.00E-77	Similar to RIKEN cDNA 2400006N03 gene
591	3	180	3	542	g12845621	3.00E-62	data source:SPTR, source key:Q9W704, evidence:ISS~putative~related to XENOPUS RPA INTERACTING PROTEIN ALPHA
591	3	180	3	542	g5262751	2.00E-31	Xenopus RPA interacting protein alpha
592	2	263	2	790	g12847529	1.00E-101	data source:SPTR, source key:Q15546, evidence:ISS~homolog to MONOCYTE TO MACROPHAGE DIFFERENTIATION PROTEIN~putative
592	2	263	2	790	g12836289	1.00E-101	data source:SPTR, source key:Q15546, evidence:ISS~homolog to MONOCYTE TO MACROPHAGE DIFFERENTIATION PROTEIN~putative
592	2	263	2	790	g18314462	1.00E-101	monocyte to macrophage differentiation-associated
594	1	162	547	1032	g12846755	7.00E-70	data source:SPTR, source key:Q9H5H0, evidence:ISS~homolog to CDNA: FLJ23445 FIS, CLONE HSI01721~putative
594	1	162	547	1032	g12840994	7.00E-70	data source:SPTR, source key:Q9H5H0, evidence:ISS~homolog to CDNA: FLJ23445 FIS, CLONE HSI01721~putative
594	1	162	547	1032	g12837553	7.00E-70	data source:SPTR, source key:Q9H5H0, evidence:ISS~homolog to CDNA: FLJ23445 FIS, CLONE HSI01721~putative
595	2	127	143	523	g7689013	1.00E-56	uncharacterized hematopoietic stem/progenitor cells protein MDS033
595	2	127	143	523	g16307000	1.00E-56	uncharacterized hematopoietic stem/progenitor cells protein MDS033
595	2	127	143	523	g12841276	5.00E-55	data source:SPTR, source key:Q9NZ42, evidence:ISS~homolog to UNCHARACTERIZED HEMATOPOIETIC STEM/PROGENITOR CELLS PROTEIN MDS033~putative
596	3	392	99	1274	g12018147	2.00E-07	vegetative cell wall protein gp1
596	3	392	99	1274	g14571744	8.00E-07	probable protease 1 like protein
596	3	392	99	1274	g15213204	4.00E-06	unknown
599	2	239	392	1108	g12845540	1.00E-79	data source:SPTR, source key:Q9HA82, evidence:ISS~homolog to CDNA FLJ12089 FIS, CLONE HEMBB1002550, WEAKLY SIMILAR TO HYPOTHETICAL UOG-1
599	2	239	392	1108	g13936285	1.00E-79	TRH4
599	2	239	392	1108	g14715021	4.00E-62	Similar to RIKEN cDNA 2310081H14 gene
601	2	584	2	1753	g14042044	0	unnamed protein product
601	2	584	2	1753	g15779199	0	NG22 protein
601	2	584	2	1753	g4529890	0	NG22

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
602	3	454	3	1364	g14272810	0	unnamed protein product
602	3	454	3	1364	g12804631	0	golgi membrane protein GP73
602	3	454	3	1364	g7271867	0	golgi membrane protein GP73
603	3	88	408	671	g10944516	2.00E-34	dJ408B20.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein (hs6M1-32))
603	3	88	408	671	g18480408	1.00E-26	olfactory receptor MOR256-11
603	3	88	408	671	g18480406	3.00E-26	olfactory receptor MOR256-10
604	1	167	76	576	g14278719	2.00E-88	B cell crosslinked IgM-activating sequence protein
604	1	167	76	576	g13591714	2.00E-88	immunoglobulin superfamily receptor translocation associated protein 2c
604	1	167	76	576	g13591712	2.00E-88	immunoglobulin superfamily receptor translocation associated protein 2b
605	1	156	1	468	g16041100	8.00E-89	hypothetical protein
605	1	156	1	468	g4454851	8.00E-89	protein phosphatase 2A BR gamma subunit
605	1	156	1	468	g619215	2.00E-88	protein phosphatase 2A1 B gamma subunit
608	1	178	130	663	g15523799	2.00E-79	unnamed protein product
608	1	178	130	663	g16551407	2.00E-44	unnamed protein product
608	1	178	130	663	g2992628	4.00E-15	putative seven pass transmembrane protein
611	3	110	3	332	g14043139	2.00E-61	RIKEN cDNA 2610511F20 gene
611	3	110	3	332	g12848653	1.00E-59	data source:SPTR, source key:Q9UK27, evidence:ISS~homolog to LEUCINE-RICH REPEATS CONTAINING F-BOX PROTEIN FBL3~putative
611	3	110	3	332	g7022695	3.00E-45	unnamed protein product
612	3	429	3	1289	g15930223	0	poliovirus receptor
612	3	429	3	1289	g7798736	0	poliovirus receptor
612	3	429	3	1289	g190205	0	poliovirus receptor
613	2	176	2	529	g7259234	1.00E-17	contains transmembrane (TM) region
613	2	176	2	529	g12837694	1.00E-17	MRNA, COMPLETE CDS, CLONE:1-107~data source:SPTR, source key:Q9JMG4, evidence:ISS~putative
613	2	176	2	529	g12861877	1.00E-17	MRNA, COMPLETE CDS, CLONE:1-107~data source:SPTR, source key:Q9JMG4, evidence:ISS~putative
614	1	80	514	753	g3002527	2.00E-10	neuronal thread protein AD7c-NTP
614	1	80	514	753	g18490197	4.00E-10	Unknown (protein for MGC:23782)
614	1	80	514	753	g6650810	6.00E-10	PRO1902
615	1	280	1	840	g7242977	1.00E-142	KIAA1311 protein

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
615	1	280	1	840	g14042145	1.00E-45	unnamed protein product
615	1	280	1	840	g14041949	2.00E-45	unnamed protein product
624	3	133	390	788	g14189960	3.00E-25	PRO0764
624	3	133	390	788	g15214765	8.00E-23	Similar to hypothetical protein
624	3	133	390	788	g9280152	2.00E-20	unnamed portein product
626	1	372	214	1329	g13543940	0	Similar to RIKEN cDNA 2610017G09 gene
626	1	372	214	1329	g14035978	0	unnamed protein product
626	1	372	214	1329	g14272784	0	unnamed protein product
627	2	167	1559	2059	g11493483	1.00E-20	PRO2550
627	2	167	1559	2059	g7020440	1.00E-19	unnamed protein product
627	2	167	1559	2059	g1872200	2.00E-18	alternatively spliced product using exon 13A
628	2	272	1262	2077	g12654109	1.00E-100	PRO0659 protein
628	2	272	1262	2077	g6690250	1.00E-100	PRO0659
629	1	207	604	1224	g14717079	1.00E-110	dJ469A13.2 (Novel protein)
629	1	207	604	1224	g12857138	1.00E-71	data source:SPTR, source key:Q9H8P4, evidence:ISS~homolog to CDNA FLJ13346 FIS, CLONE OVARC1002107~putative
629	1	207	604	1224	g12839239	1.00E-71	data source:SPTR, source key:Q9H8P4, evidence:ISS~homolog to CDNA FLJ13346 FIS, CLONE OVARC1002107~putative
630	2	207	2	622	g14717079	2.00E-82	dJ469A13.2 (Novel protein)
630	2	207	2	622	g12839239	3.00E-47	data source:SPTR, source key:Q9H8P4, evidence:ISS~homolog to CDNA FLJ13346 FIS, CLONE OVARC1002107~putative
630	2	207	2	622	g12857255	3.00E-47	data source:SPTR, source key:Q9H8P4, evidence:ISS~homolog to CDNA FLJ13346 FIS, CLONE OVARC1002107~putative
631	3	81	234	476	g10437569	2.00E-18	unnamed protein product
631	3	81	234	476	g10437485	4.00E-17	unnamed protein product
631	3	81	234	476	g14189960	6.00E-17	PRO0764
632	1	792	73	2448	g2232150	0	FYN binding protein
632	1	792	73	2448	g2078273	0	SLP-76 associated protein
632	1	792	73	2448	g7416993	0	EVH1 domain binding protein
638	2	134	515	916	g12851779	3.00E-24	evidence:NAS~hypothetical protein~putative
638	2	134	515	916	g12836995	1.00E-23	evidence:NAS~hypothetical protein~putative
640	3	110	3	332	g13937933	6.00E-08	Unknown (protein for IMAGE:3838856)

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
643	2	307	2	922	g16740557	1.00E-165	Similar to hypothetical protein FLJ10134
643	2	307	2	922	g14035908	1.00E-165	unnamed protein product
643	2	307	2	922	g17390505	1.00E-131	Similar to hypothetical protein FLJ10134
644	3	138	405	818	g12805623	9.00E-06	Unknown (protein for MGC:8183)
645	1	584	181	1932	g14549207	0	URAX1
645	1	584	181	1932	g17907795	0	TGF-beta induced apotosis protein 3
645	1	584	181	1932	g17049034	0	unnamed protein product
646	2	123	125	493	g13276669	2.00E-53	hypothetical protein
647	2	917	2	2752	g14041780	0	AKAP-2 protein
647	2	917	2	2752	g4589472	0	KIAA0920 protein
647	2	917	2	2752	g17384432	0	bA151F5.1 (A kinase (PRKA) anchor protein 2)
649	2	181	92	634	g10433669	1.00E-49	unnamed protein product
649	2	181	92	634	g14133229	1.00E-49	KIAA0999 protein
650	1	124	562	933	g12698182	1.00E-29	hypothetical protein
650	1	124	562	933	g7020440	7.00E-24	unnamed protein product
650	1	124	562	933	g11493483	3.00E-23	PRO2550
651	2	331	65	1057	g14290590	0	Similar to CGI-62 protein
651	2	331	65	1057	g4929593	0	CGI-62 protein.
651	2	331	65	1057	g12854328	5.00E-43	data source:SPTR, source key:Q9Y372, evidence:ISS~homolog to CGI-62 PROTEIN~putative
652	2	120	1394	1753	g16041152	2.00E-10	hypothetical protein
652	2	120	1394	1753	g10435380	3.00E-07	unnamed protein product
653	1	212	25	660	g2665836	1.00E-103	dynein light intermediate chain 2
653	1	212	25	660	g2618478	1.00E-100	dynein light intermediate chain 53/55
653	1	212	25	660	g2618484	1.00E-100	dynein light intermediate chain 53/55
655	2	184	668	1219	g10436645	1.00E-93	unnamed protein product
655	2	184	668	1219	g13905156	6.00E-61	Unknown (protein for MGC:11798)
655	2	184	668	1219	g7243155	3.00E-60	KIAA1387 protein
657	2	115	890	1234	g6691806	7.00E-16	alternatively spliced form
657	2	115	890	1234	g12007315	1.00E-09	unknown.
658	1	207	136	756	g14248997	1.00E-89	lung seven transmembrane receptor 1
658	1	207	136	756	g10047325	1.00E-82	KIAA1624 protein
658	1	207	136	756	g14248999	2.00E-62	lung seven transmembrane receptor 2

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Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
660	1	166	175	672	g14272514	1.00E-76	unnamed protein product
660	1	166	175	672	g12845046	7.00E-76	data source:SPTR, source key:O77262, evidence:ISS~putative~related to EG:22E5.9 PROTEIN
660	1	166	175	672	g12848539	7.00E-76	data source:SPTR, source key:O77262, evidence:ISS~putative~related to EG:22E5.9 PROTEIN
661	2	1435	2	4306	g4432953	0	annexin V-binding protein (ABP-10)
661	2	1435	2	4306	g10438646	1.00E-140	unnamed protein product
661	2	1435	2	4306	g11994784	2.00E-50	gene_id:T19N8.6~unknown protein
662	3	398	3	1196	g14017883	0	KIAA1833 protein
662	3	398	3	1196	g15617725	7.00E-31	Hypothetical protein C34G6.1
662	3	398	3	1196	g7105685	7.00E-31	Hypothetical protein C34G6.1
663	2	162	122	607	g16554238	3.00E-72	unnamed protein product
663	2	162	122	607	g15620835	3.00E-72	KIAA1888 protein
663	2	162	122	607	g17223620	3.00E-72	ATP-binding cassette A5
664	1	130	115	504	g203072	6.00E-70	0-44 protein
664	1	130	115	504	g12848292	1.00E-69	data source:SPTR, source key:P38718, evidence:ISS~homolog to 0-44 PROTEIN~putative
664	1	130	115	504	g17390760	1.00E-69	RIKEN cDNA 2610205H19 gene
666	3	241	3	725	g14198207	2.00E-83	Similar to CG4452 gene product
666	3	241	3	725	g4200234	4.00E-77	hypothetical protein
666	3	241	3	725	g4200238	3.00E-72	hypothetical protein
668	1	85	1	255	g18027778	1.00E-29	unknown
668	1	85	1	255	g15485600	1.00E-29	putative alpha mannosyltransferase
668	1	85	1	255	g12804615	1.00E-29	Unknown (protein for MGC:3136)
669	1	240	1	720	g9857700	5.00E-93	myeloid cell leukemia protein 1
669	1	240	1	720	g8388943	5.00E-93	myeloid cell differentiation protein
669	1	240	1	720	g7582272	5.00E-93	Mcl-1 delta S/TM
670	3	61	63	245	g8248885	3.00E-30	metallothionein-I gene transcription activator
670	3	61	63	245	g717187	8.00E-30	RNA polymerase II
670	3	61	63	245	g17390349	8.00E-30	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)
671	3	129	3	389	g12848031	4.00E-48	evidence:NAS~hypothetical protein~putative
671	3	129	3	389	g12718388	1.00E-13	conserved hypothetical protein
671	3	129	3	389	g9758240	2.00E-08	emblCAB61034.1~gene_id:K3K7.8~similar to unknown protein
672	3	383	438	1586	g6808038	0	hypothetical protein
672	3	383	438	1586	g5081610	1.00E-179	huntington yeast partner C

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
672	3	383	438	1586	g10440161	1.00E-179	unnamed protein product
673	3	417	2553	3803	g7243185	0	KIAA1402 protein
673	3	417	2553	3803	g18043971	0	Unknown (protein for IMAGE:3987018)
673	3	417	2553	3803	g15426519	1.00E-130	hypothetical protein FLJ22678
674	3	89	396	662	g7022185	5.00E-11	unnamed protein product
674	3	89	396	662	g16549259	3.00E-09	unnamed protein product
674	3	89	396	662	g18203809	3.00E-09	Unknown (protein for MGC:19764)
675	3	466	1080	2477	g17046100	0	ATP-binding cassette protein
675	3	466	1080	2477	g17223620	0	ATP-binding cassette A5
675	3	466	1080	2477	g4240130	2.00E-66	KIAA0822 protein
676	2	290	2	871	g4160666	1.00E-161	NG,NG-dimethylarginine dimethylaminohydrolase
676	2	290	2	871	g10279810	1.00E-160	unnamed protein product
676	2	290	2	871	g12845868	1.00E-152	data source:MGD, source key:MGI:1916469, evidence:ISS-dimethylarginine dimethylaminohydrolase 1~putative
679	2	303	80	988	g13544020	1.00E-162	Similar to RIKEN cDNA 6030457N17 gene
679	2	303	80	988	g12833947	1.00E-112	data source:Pfam, source key:PF01754, evidence:ISS-hypothetical A20-like zinc finger containing protein~putative
679	2	303	80	988	g7299642	3.00E-15	CG5333 gene product
680	1	233	667	1365	g16877144	1.00E-121	Unknown (protein for MGC:10135)
680	1	233	667	1365	g14041999	1.00E-121	unnamed protein product
680	1	233	667	1365	g14042471	1.00E-121	unnamed protein product
681	3	495	363	1847	g7959331	0	KIAA1532 protein
681	3	495	363	1847	g2959559	0	fos39554_1
681	3	495	363	1847	g18314468	1.00E-113	Unknown (protein for IMAGE:4825062)
682	1	54	118	279	g18044412	7.00E-06	Similar to KIAA0475 gene product
682	1	54	118	279	g3413912	7.00E-06	KIAA0475 protein
684	1	441	28	1350	g13936285	1.00E-168	TRH4
684	1	441	28	1350	g12845540	1.00E-168	data source:SPTR, source key:Q9HA82, evidence:ISS-homolog to CDNA FLJ12089 FIS, CLONE HEMBB1002550, WEAKLY SIMILAR TO HYPOTHETICAL UOG-1
684	1	441	28	1350	g15077841	5.00E-86	Trh1
688	2	467	92	1492	g6330019	0	KIAA1145 protein
688	2	467	92	1492	g13874437	1.00E-133	cerebral protein-11

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
688	2	467	92	1492	g6634047	1.00E-133	KIAA0481 protein
691	1	205	25	639	g12539946	1.00E-108	unnamed protein product
691	1	205	25	639	g12001948	1.00E-108	My004 protein
691	1	205	25	639	g12539948	1.00E-102	unnamed protein product
692	1	238	484	1197	g13543615	1.00E-131	Unknown:(protein for MGC:14607)
692	1	238	484	1197	g13111774	1.00E-131	Similar to steroidogenic acute regulatory protein related
692	1	238	484	1197	g4309949	1.00E-131	similar to MLN 64; similar to I38027 (PID:g2135214)
693	3	313	3	941	g6808093	1.00E-130	hypothetical protein
693	3	313	3	941	g4263043	1.0E-14	putative calcium channel
693	3	313	3	941	g4206210	1.0E-14	putative calcium channel
694	2	95	2	286	g16550068	3.00E-40	unnamed protein product
694	2	95	2	286	g12834087	7.00E-38	evidence:NAS~hypothetical protein~putative
694	2	95	2	286	g7292012	2.00E-13	CG13907 gene product
695	2	196	110	697	g10438063	8.00E-74	unnamed protein product
695	2	196	110	697	g15277443	5.00E-63	Unknown (protein for MGC:19083)
695	2	196	110	697	g18027352	2.00E-14	unknown
696	3	352	162	1217	g14603078	0	Similar to RIKEN cDNA 4931428D14 gene
696	3	352	162	1217	g12845936	1.00E-174	evidence:NAS~hypothetical protein~putative
696	3	352	162	1217	g13543107	1.00E-173	RIKEN cDNA 4931428D14 gene
702	3	152	498	953	g16549297	2.00E-92	unnamed protein product
702	3	152	498	953	g18204863	2.00E-92	hypothetical protein MGC3020
702	3	152	498	953	g12653557	7.00E-92	Unknown (protein for MGC:3020)
703	3	84	96	347	g18314565	2.00E-41	Similar to signal recognition particle 9kD
703	3	84	96	347	g18490251	3.00E-21	signal recognition particle 9kD
703	3	84	96	347	g15929315	3.00E-21	signal recognition particle 9kD
704	3	107	3993	4313	g12006055	2.00E-56	DC42
706	3	362	246	1331	g3283879	0	unknown
706	3	362	246	1331	g6978018	0	SCHIP-1
706	3	362	246	1331	g6978022	0	SCHIP-1-D241/253
707	2	317	377	1327	g11610570	0	MOP-5
707	2	317	377	1327	g14042766	0	unnamed protein product
707	2	317	377	1327	g6942315	1.00E-180	hypothetical protein SBBI88

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
708	2	101	11	313	g7770147	6.00E-16	PRO1847
708	2	101	11	313	g10437752	6.00E-15	unnamed protein product
708	2	101	11	313	g6650810	3.00E-14	PRO1902
709	1	116	271	618	g16041132	9.00E-12	hypothetical protein
709	1	116	271	618	g10435559	1.00E-11	unnamed protein product
709	1	116	271	618	g10799024	2.00E-10	HC6
711	1	201	1	603	g7020571	1.00E-101	unnamed protein product
711	1	201	1	603	g12002684	1.00E-101	chromosome 9 open reading frame 6
711	1	201	1	603	g16041813	1.00E-101	hypothetical protein FLJ20457
713	3	563	3	1691	g16516599	0	unnamed protein product
713	3	563	3	1691	g16516597	0	unnamed protein product
713	3	563	3	1691	g4159682	0	Phosphatidylglycerophosphate synthase
714	2	373	119	1237	g12847516	1.00E-125	data source:SPTR, source key:Q9PTD5, evidence:ISS~putative~related to KIAA0009 PROTEIN
714	2	373	119	1237	g17512323	1.00E-124	Similar to.RIKEN cDNA 2610016C23 gene
714	2	373	119	1237	g12855709	1.00E-124	data source:SPTR, source key:Q15390, evidence:ISS~homolog to HYPOTHETICAL PROTEIN KIAA0009~putative
717	2	912	2	2737	g1136436	0	KIAA0188
717	2	912	2	2737	g7264655	0	Lpin1
717	2	912	2	2737	g12859810	0	data source:MGD, source key:MGI:1891340, evidence:ISS~lipin 1~putative
718	2	601	2	1804	g10954048	9.00E-24	ovarian fibroin-like substance-1
718	2	601	2	1804	g159712	3.00E-23	dragline silk fibroin
718	2	601	2	1804	g17063211	3.00E-23	dragline silk protein
720	3	132	768	1163	g16550108	9.00E-22	unnamed protein product
720	3	132	768	1163	g13624461	9.00E-22	dJ259A10.1 (ssDNA binding protein (SEB4D))
720	3	132	768	1163	g8895698	6.00E-18	RRM-containing protein SEB-4
723	1	332	1156	2151	g15214686	4.00E-81	Unknown (protein for IMAGE:4537124)
723	1	332	1156	2151	g12858533	2.00E-30	data source:SPTR, source key:Q9V540, evidence:ISS~putative~related to CG8058 PROTEIN
725	2	219	2	658	g13448609	1.00E-114	GAJ
725	2	219	2	658	g12847934	1.00E-102	data source:SPTR, source key:Q09739, evidence:ISS~putative~related to HYPOTHETICAL 24.2 KDA PROTEIN C13A11.03 IN CHROMOSOME I
725	2	219	2	658	g984224	2.00E-31	hypothetical coiled-coil protein
726	3	208	126	749	g17862302	8.00E-24	LD21733p

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
726	3	208	126	749	g7299099	8.00E-24	CG8379 gene product
727	2	470	2	1411	g13559033	0	bA11M20.3.1 (novel protein similar to Pleurodeles waltlii RAP55 protein, isoform 1)
727	2	470	2	1411	g13559032	1.00E-138	bA11M20.3.2 (novel protein similar to Pleurodeles waltlii RAP55 protein, isoform 2)
727	2	470	2	1411	g16877144	4.00E-94	Unknown (protein for MGC:10135)
728	3	212	3	638	g16551687	1.00E-106	unnamed protein product
728	3	212	3	638	g13442784	1.00E-106	DRCTNNB1A
728	3	212	3	638	g17511709	1.00E-106	down-regulated by Ctnnb1, a
729	2	115	1289	1633	g3413884	4.00E-60	KIAA0461 perotein
729	2	115	1289	1633	g5101774	4.00E-60	KIAA0461/245 protein
729	2	115	1289	1633	g927300	9.00E-05	ORF; similar to Drosophila supressor of hairy wing protein, Swiss-Prot Accession Number
730	2	599	5	1801	g15208233	0	hypothetical protein
730	2	599	5	1801	g15080468	2.00E-68	Similar to RIKEN cDNA 1110018J12 gene
730	2	599	5	1801	g12834655	1.00E-62	data source:SPTR, source key:P11055, evidence:ISS~homolog to MYOSIN HEAVY CHAIN, FAST SKELETAL MUSCLE, EMBRYONIC (MUSCLE EMBRYONIC MYOSIN HEAVY CHAIN) (SMHCE)~putative
733	1	313	1	939	g13625166	1.00E-171	RALBP1
733	1	313	1	939	g15706481	1.00E-171	Unknown (protein for MGC:16228)
733	1	313	1	939	g2677843	1.00E-163	RalBP1-associated EH domain protein Reps1
734	2	254	83	844	g12654495	1.00E-128	Unknown (protein for IMAGE:2822295)
734	2	254	83	844	g13279332	1.00E-128	Unknown (protein for IMAGE:2822295)
734	2	254	83	844	g13879370	2.00E-58	Unknown (protein for MGC:7867)
735	3	137	294	704	g17221829	3.00E-41	TDC1
735	3	137	294	704	g14602501	3.00E-41	hypothetical protein DKFZp566I133
735	3	137	294	704	g13185293	3.00E-41	unnamed protein product
738	1	147	142	582	g9104819	4.00E-05	hypothetical protein
739	3	194	3	584	g3738323	9.00E-67	hypothetical protein
739	3	194	3	584	g7269951	3.00E-53	putative protein
739	3	194	3	584	g13111782	4.00E-20	Similar to HSPC171 protein
744	1	607	940	2760	g7959271	0	KIAA1505 protein
744	1	607	940	2760	g9929955	1.00E-148	hypothetical protein
744	1	607	940	2760	g15208049	1.00E-127	hypothetical protein
746	3	224	192	863	g6330331	1.00E-112	KIAA1189 protein

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
746	3	224	192	863	g12861409	5.00E-46	data source:SPTR, source key:Q9ULN1, evidence:ISS--homolog to KIAA1189 PROTEIN (FRAGMENT)--putative
748	1	311	781	1713	g10436681	1.00E-177	unnamed protein product
748	1	311	781	1713	g5912126	1.00E-176	hypothetical protein
749	3	307	252	1172	g12698087	1.00E-180	KIAA1771 protein
749	3	307	252	1172	g16550229	1.00E-179	unnamed protein product
749	3	307	252	1172	g14597918	1.00E-151	human CLASP-3
751	1	491	274	1746	g16553996	0	unnamed protein product
751	1	491	274	1746	g10438804	1.00E-130	unnamed protein product
751	1	491	274	1746	g13938187	1.00E-130	hypothetical protein FLJ22419
752	3	545	324	1958	g16878013	0	chromosome 12 open reading frame 22
752	3	545	324	1958	g12274931	0	hypothetical protein
752	3	545	324	1958	g18146658	0	TGF-beta induced apotosis protein 12
754	1	123	223	591	g10799024	5.00E-15	HC6
754	1	123	223	591	g10436743	3.00E-14	unnamed protein product
754	1	123	223	591	g18027740	1.00E-11	unknown
755	2	71	575	787	g16550881	4.00E-05	unnamed protein product
756	3	193	174	752	g17512047	1.00E-110	Unknown (protein for MGC:20579)
756	3	193	174	752	g13365915	5.00E-39	hypothetical protein
756	3	193	174	752	g7020988	3.00E-38	unnamed protein product
757	2	202	452	1057	g16553318	6.00E-95	unnamed protein product
757	2	202	452	1057	g13097084	5.00E-18	Unknown (protein for MGC:7041)
757	2	202	452	1057	g6807802	1.00E-07	hypothetical protein
760	3	438	285	1598	g434765	0	ORF
760	3	438	285	1598	g12804871	0	nucleolar phosphoprotein p130
760	3	438	285	1598	g663008	0	nucleolar phosphoprotein p130
763	2	595	653	2437	g10047245	0	KIAA1585 protein
763	2	595	653	2437	g7022646	8.00E-97	unnamed protein product
763	2	595	653	2437	g3377722	1.00E-14	male-specific lethal-2
764	3	947	3	2843	g7243155	0	KIAA1387 protein
764	3	947	3	2843	g13623235	0	Similar to hypothetical protein FLJ20707
764	3	947	3	2843	g13905156	0	Unknown (protein for MGC:11798)

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
776	2	68	2	205	g18480246	3.00E-30	olfactory receptor MOR138-3
776	2	68	2	205	g15293707	7.00E-26	olfactory receptor
776	2	68	2	205	g9652309	6.00E-21	M12 odorant receptor
777	3	184	21	572	g13560108	1.00E-101	bA261N11.2.1 (novel protein, isoform 1)
777	3	184	21	572	g12837694	7.00E-81	MRNA, COMPLETE CDS, CLONE:1-107~data source:SPTR, source key:Q9JMG4, evidence:ISS~putative
777	3	184	21	572	g7259234	7.00E-81	contains transmembrane (TM) region
778	3	166	6	503	g5869925	4.00E-24	olfactory receptor
778	3	166	6	503	g18479780	4.00E-24	olfactory receptor MOR262-4
778	3	166	6	503	g8919697	4.00E-24	olfactory receptor
779	2	210	14	643	g12853606	6.00E-57	data source:SPTR, source key:O44231, evidence:ISS~putative~related to OUTER ARM DYNEIN LIGHT CHAIN 1
779	2	210	14	643	g12840067	1.00E-52	data source:SPTR, source key:O44231, evidence:ISS~putative~related to OUTER ARM DYNEIN LIGHT CHAIN 1
779	2	210	14	643	g2760163	2.00E-24	outer arm dynein light chain 1
780	2	109	644	970	g13276655	2.00E-25	hypothetical protein
780	2	109	644	970	g17028424	7.00E-25	Similar to calcium/calmodulin-dependent protein kinase kinase 1, alpha
780	2	109	644	970	g18308166	7.00E-25	calcium/calmodulin-dependent protein kinase kinase alpha
781	1	130	1	390	g6705973	3.00E-05	pBS4A5
781	1	130	1	390	g14789624	3.00E-05	Unknown (protein for MGC:18335)
781	1	130	1	390	g3738263	3.00E-05	cytochrome P-450
782	3	224	186	857	g4062502	1.00E-121	ProW protein homolog
782	3	224	186	857	g1787165	1.00E-121	putative transport system permease protein
782	3	224	186	857	g4583569	1.00E-113	putative aliphatic sulfonate transport membrane component
783	2	91	1724	1996	g16549456	4.00E-18	unnamed protein product
783	2	91	1724	1996	g18027424	5.00E-16	unknown
783	2	91	1724	1996	g12698155	2.00E-14	hypothetical protein
784	3	185	3	557	g16553692	1.00E-103	unnamed protein product
784	3	185	3	557	g16580688	2.00E-98	hypothetical protein
784	3	185	3	557	g14091950	7.00E-56	L-threonine 3-dehydrogenase
787	1	227	76	756	g16554793	2.00E-05	no on or off transient A
787	1	227	76	756	g16554785	2.00E-05	no on or off transient A

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
787	1	227	76	756	g16554787	2.00E-05	no on or off transient A
788	1	70	2479	2688	g16924282	8.00E-21	Unknown (protein for MGC:27375)
788	1	70	2479	2688	g10336831	5.00E-19	IgA regulatory protein
790	1	45	55	189	g16878329	9.00E-08	Unknown (protein for MGC:29628)
790	1	45	55	189	g12804415	9.00E-08	Similar to hypothetical protein FLJ10891
790	1	45	55	189	g7023216	9.00E-08	unnamed protein product
792	3	109	141	467	g2587027	2.00E-20	HERV-E envelope glycoprotein
792	3	109	141	467	g2587024	2.00E-20	HERV-E envelope glycoprotein
792	3	109	141	467	g1049232	8.00E-19	HERV-E envelope protein
793	2	145	920	1354	g2587027	2.00E-21	HERV-E envelope glycoprotein
793	2	145	920	1354	g2587024	2.00E-21	HERV-E envelope glycoprotein
793	2	145	920	1354	g1049232	2.00E-19	HERV-E envelope protein
794	2	56	233	400	g6690227	1.00E-13	PRO0478
794	2	56	233	400	g186774	3.00E-10	zinc finger protein
794	2	56	233	400	g9929995	1.00E-09	hypothetical protein
796	3	288	108	971	g14249961	1.00E-109	Similar to hypothetical protein AB030201
796	3	288	108	971	g14789776	8.00E-87	Similar to hypothetical protein AB030201
796	3	288	108	971	g7259296	2.00E-86	contains transmembrane (TM) region
797	2	103	953	1261	g16553789	2.00E-12	unnamed protein product
797	2	103	953	1261	g11493409	6.00E-08	PRO0898
797	2	103	953	1261	g16877294	1.00E-07	Similar to hypothetical protein PRO1722
800	1	249	577	1323	g10435262	1.00E-139	unnamed protein product
800	1	249	577	1323	g16877653	1.00E-138	Similar to KIAA0643 protein
800	1	249	577	1323	g3327100	1.00E-109	KIAA0643 protein
802	1	102	214	519	g13506805	5.00E-48	thymic stromal co-transporter
802	1	102	214	519	g16550334	1.00E-47	unnamed protein product
802	1	102	214	519	g8131858	1.00E-38	putative thymic stromal co-transporter TSCOT
804	3	266	777	1574	g9963761	3.00E-23	cd003 protein
805	1	63	289	477	g14249973	4.00E-14	Similar to hypothetical protein PRO1722
805	1	63	289	477	g18490197	7.00E-14	Unknown (protein for MGC:23782)
805	1	63	289	477	g6650810	1.00E-13	PRO1902
806	3	122	495	860	g15667843	1.00E-48	melanin-concentrating hormone receptor MCH-R2

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
806	3	122	495	860	g14164383	1.00E-48	G protein-coupled receptor
806	3	122	495	860	g13604342	1.00E-48	G protein-coupled receptor MCH2
814	2	717	2	2152	g16041704	0	hypothetical protein FLJ23322
814	2	717	2	2152	g10438323	0	unnamed protein product
814	2	717	2	2152	g10439967	0	unnamed protein product
815	1	153	508	966	g6172225	1.00E-92	ST2V
815	1	153	508	966	g220077	7.00E-54	ST2 protein
815	1	153	508	966	g5456908	7.00E-54	ST2L
816	2	146	92	529	g12850332	1.00E-34	Protein phosphatase 2C containing protein-data source:Pfam, source key:PF00481, evidence:ISS-putative
816	2	146	92	529	g16552416	6.00E-16	unnamed protein product
817	3	131	216	608	g12852098	1.00E-60	data source:SPTR, source key:O14563, evidence:ISS-homolog to GLUTAMYL-TRNA SYNTHETASE (FRAGMENT)-putative
817	3	131	216	608	g7294109	5.00E-35	CG4573 gene product
817	3	131	216	608	g2688265	5.00E-27	glutamyl-tRNA synthetase (gltX)
819	1	453	1	1359	g14042460	0	unnamed protein product
819	1	453	1	1359	g13623647	0	Similar to RIKEN cDNA 2700091N06 gene
819	1	453	1	1359	g12849446	1.00E-170	evidence:NAS-hypothetical protein~putative
820	3	288	594	1457	g12836212	2.00E-64	evidence:NAS-hypothetical protein~putative
820	3	288	594	1457	g18043476	2.00E-64	RIKEN cDNA 1200015A19 gene
820	3	288	594	1457	g17512106	8.00E-31	Similar to RIKEN cDNA 1200015A19 gene
822	3	282	804	1649	g11990420	1.00E-149	MQP-3
822	3	282	804	1649	g7022892	1.00E-149	unnamed protein product
822	3	282	804	1649	g18606385	1.00E-148	hypothetical protein FLJ10701
824	2	149	2	448	g9501799	7.00E-76	mitochondrial import receptor Tom22
824	2	149	2	448	g10716801	7.00E-76	Tom22
824	2	149	2	448	g10437092	7.00E-76	unnamed protein product
827	1	195	1	585	g6808095	7.00E-81	hypothetical protein
827	1	195	1	585	g4589678	7.00E-81	KIAA1014 protein
827	1	195	1	585	g10434696	6.00E-76	unnamed protein product
829	2	429	2	1288	g10862874	0	dJ927M24.2 (KIAA1219)
829	2	429	2	1288	g6330590	1.00E-162	KIAA1219 protein

Table 5.

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
829	2	429	2	1288	g17391470	7.00E-95	Unknown (protein for IMAGE:4693777)
830	2	65	2	196	g14388555	1.00E-33	hypothetical protein
830	2	65	2	196	g12854823	2.00E-22	data source:SPTR, source key:Q9W232, evidence:ISS~putative~related to CG17807 PROTEIN
830	2	65	2	196	g7959173	1.00E-07	KIAA1456 protein
832	2b	90	1130	1399	g3002527	2.00E-22	neuronal thread protein AD7c-NTP
832	2b	90	1130	1399	g16877294	3.00E-22	Similar to hypothetical protein PRO1722
832	2b	90	1130	1399	g10439739	5.00E-22	unnamed protein product
835	3	367	369	1469	g12855517	1.00E-162	data source:SPTR, source key:Q9VS60, evidence:ISS~putative~related to CG8576 PROTEIN
835	3	367	369	1469	g18044462	1.00E-131	Unknown (protein for MGC:30540)
835	3	367	369	1469	g14035948	6.00E-93	unnamed protein product
838	1	207	340	960	g16553789	5.00E-13	unnamed protein product
838	1	207	340	960	g11493409	1.00E-12	PRO0898
838	1	207	340	960	g7770147	2.00E-12	PRO1847
839	2	90	578	847	g16566353	2.00E-11	putative ion channel protein CATSPER2 variant 1
839	2	90	578	847	g16566356	2.00E-11	putative ion channel protein CATSPER2 variant 2
839	2	90	578	847	g16566350	3.00E-10	putative ion channel protein CATSPER2
840	2	122	305	670	g10437485	1.00E-28	unnamed protein product
840	2	122	305	670	g10437569	1.00E-27	unnamed protein product
840	2	122	305	670	g7020625	1.00E-26	unnamed protein product
841	2	107	128	448	g3413912	2.00E-37	KIAA0475 protein
841	2	107	128	448	g18044412	9.00E-36	Similar to KIAA0475 gene product
841	2	107	128	448	g13278492	1.00E-05	Unknown (protein for MGC:7673)
843	3	91	702	974	g12698182	1.00E-11	hypothetical protein
843	3	91	702	974	g16552221	2.00E-11	unnamed protein product
843	3	91	702	974	g14198309	4.00E-11	Similar to proline-serine-threonine phosphatase-interacting protein 2
844	2	285	2	856	g9255809	1.00E-149	PMEPA1 protein
844	2	285	2	856	g15824469	1.00E-149	solid tumor-associated 1 protein
844	2	285	2	856	g16303742	1.00E-149	STAG1/PMEPA1
847	2	363	2	1090	g14714684	1.00E-166	Unknown (protein for IMAGE:3482764)
847	2	363	2	1090	g12850324	1.00E-165	data source:SPTR, source key:Q9VS51, evidence:ISS~putative~related to CG8596 PROTEIN
847	2	363	2	1090	g17861694	5.00E-50	GH22722p
848	2	745	1220	3454	g7243081	0	KIAA1350 protein

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
848	2	745	1220	3454	g18490104	0	Unknown (protein for IMAGE:4236151)
848	2	745	1220	3454	g16924225	1.00E-108	Unknown (protein for MGC:22206)
849	2	134	746	1147	g12005635	2.00E-73	AD031
850	1	976	1	2928	g10434944	0	unnamed protein product
850	1	976	1	2928	g7300581	1.00E-125	CG4845 gene product
850	1	976	1	2928	g15145395	3.00E-52	Hypothetical protein R13F6.10
853	2	155	239	703	g16566353	3.00E-65	putative ion channel protein CATSPER2 variant 1
853	2	155	239	703	g16566356	3.00E-65	putative ion channel protein CATSPER2 variant 2
853	2	155	239	703	g16566350	8.00E-26	putative ion channel protein CATSPER2
854	1	163	10	498	g9837292	2.00E-24	C-type lectin
854	1	163	10	498	g6651065	2.00E-24	lectin-like NK cell receptor LLT1
854	1	163	10	498	g18044358	2.00E-24	Similar to lectin-like NK cell receptor
855	1	123	199	567	g12844231	2.00E-39	evidence:NAS~putative~unclassifiable
855	1	123	199	567	g517115	5.00E-16	KIAA0032
855	1	123	199	567	g12856817	6.00E-16	Regulator of chromosome condensation (RCC1) containing protein~data source:InterPro, source key:IPR000408, evidence:ISS~putative
856	3	138	3	416	g17390179	5.00E-61	Similar to RIKEN cDNA 9030409E16 gene
856	3	138	3	416	g12858225	5.00E-59	evidence:NAS~hypothetical protein~putative
856	3	138	3	416	g7303701	1.00E-07	CG12341 gene product
858	2	300	50	949	g12654927	1.00E-132	Unknown (protein for MGC:5509)
858	2	300	50	949	g13905264	1.00E-112	Similar to hypothetical protein MGC5509
858	2	300	50	949	g9022437	2.00E-19	ashwin
860	2	70	383	592	g12698182	2.00E-15	hypothetical protein
860	2	70	383	592	g7021164	9.00E-14	unnamed protein product
860	2	70	383	592	g16876883	1.00E-10	Unknown (protein for IMAGE:4075924)
862	1	73	295	513	g16549456	2.00E-19	unnamed protein product
862	1	73	295	513	g7959267	4.00E-16	KIAA1503 protein
862	1	73	295	513	g18027424	1.00E-15	unknown
864	1	206	394	1011	g13623425	3.00E-54	Similar to KIAA0445 gene product
864	1	206	394	1011	g15620903	6.00E-46	KIAA1922 protein
864	1	206	394	1011	g8979803	5.00E-45	dJ37C10.5 (KIAA0445)
866	3	87	3	263	g12804713	3.00E-39	Unknown (protein for MGC:2492)

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
866	3	87	3	263	g12847677	9.00E-30	data source:SPTR, source key:Q9U5I9, evidence:ISS~putative~related to CENTRIN,
866	3	87	3	263	g12848210	1.00E-29	data source:SPTR, source key:Q9U5J0, evidence:ISS~putative~related to PUTATIVE CENTRIN (FRAGMENT)
867	2	149	89	535	g4200446	3.00E-51	FYVE finger-containing phosphoinositide kinase
868	2	445	2	1336	g7295961	1.00E-117	CG9867 gene product
868	2	445	2	1336	g16182556	1.00E-117	GH05422p
868	2	445	2	1336	g3947579	1.00E-30	predicted using Genefinder
869	2	216	224	871	g1633564	1.00E-102	C8
869	2	216	224	871	g12803453	1.00E-102	Similar to gene rich cluster, C8 gene
869	2	216	224	871	g12805099	2.00E-63	gene rich cluster, C8 gene
870	3	77	132	362	g10440282	3.00E-12	unnamed protein product
870	3	77	132	362	g14388331	2.00E-09	hypothetical protein
870	3	77	132	362	g16552221	4.00E-09	unnamed protein product
872	3	402	90	1295	g8102033	0	TRF2-interacting telomeric RAP1 protein
872	3	402	90	1295	g13543358	0	TRF2-interacting telomeric RAP1 protein
872	3	402	90	1295	g13325304	0	TRF2-interacting telomeric RAP1 protein
873	3	86	3	260	g3395506	7.00E-30	dJ511E16.2 (putative protein based on ESTs)
873	3	86	3	260	g18606260	6.00E-23	Similar to hypothetical protein dJ511E16.2
874	2	144	212	643	g12833402	2.00E-47	evidence:NAS~hypothetical protein~putative
874	2	144	212	643	g12843375	2.00E-47	evidence:NAS~hypothetical protein~putative
875	3	279	192	1028	g14495648	1.00E-158	Unknown (protein for MGC:15606)
875	3	279	192	1028	g16549254	1.00E-158	unnamed protein product
875	3	279	192	1028	g12859694	6.00E-38	data source:SPTR, source key:Q05004, evidence:ISS~homolog to BRUSH BORDER 61.9 KDA PROTEIN PRECURSOR~putative
876	2	69	2	208	g13624098	7.00E-16	cervical cancer 1 protooncogene protein p40
876	2	69	2	208	g16588706	3.00E-15	cervical cancer protooncogene-2 protein
876	2	69	2	208	g15077022	1.00E-13	cervical cancer receptor
877	1	116	973	1320	g16566359	2.00E-11	putative ion channel protein CATSPER2 variant 3
877	1	116	973	1320	g16566353	2.00E-11	putative ion channel protein CATSPER2 variant 1
877	1	116	973	1320	g16566356	2.00E-11	putative ion channel protein CATSPER2 variant 2
878	2	618	2	1855	g6329755	0	KIAA1126 protein
878	2	618	2	1855	g4680229	4.00E-52	DNb-5

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
878	2	618	2	1855	g15004313	2.00E-40	membrane-associated transporter protein B
880	2	197	65	655	g12653037	4.00E-70	Unknown (protein for IMAGE:3355813)
880	2	197	65	655	g15209730	2.00E-66	unnamed protein product
880	2	197	65	655	g12861881	4.00E-42	evidence:NAS-hypothetical protein-putative
881	3	132	2412	2807	g2852636	7.00E-05	unknown
882	2	197	56	646	g13937819	1.00E-101	Unknown (protein for MGC:12335)
882	2	197	56	646	g4468307	9.00E-95	dJ413H6:1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein)
882	2	197	56	646	g191315	5.00E-66	androgen-dependent expressed protein
885	3	220	426	1085	g18043306	1.00E-92	RIKEN cDNA 1810033A06 gene
885	3	220	426	1085	g12841374	1.00E-92	data source:SPTR, source key:Q9NRU6, evidence:ISS-homolog to human X 009 PROTEIN-putative
885	3	220	426	1085	g7301782	7.00E-34	CG2006 gene product
886	2	365	2	1096	g17390000	0	Similar to RIKEN cDNA 5730455O13 gene
886	2	365	2	1096	g12857019	1.00E-112	data source:SPTR, source key:O81652, evidence:ISS-putative-related to PHYB1
886	2	365	2	1096	g14189976	1.00E-111	PRO2972
887	3	109	48	374	g10437569	4.00E-28	unnamed protein product
887	3	109	48	374	g10437485	3.00E-26	unnamed protein product
887	3	109	48	374	g9280152	3.00E-25	unnamed portein product
888	1	106	43	360	g10437485	2.00E-15	unnamed protein product
888	1	106	43	360	g14043141	1.00E-14	Unknown (protein for MGC:15483)
888	1	106	43	360	g10441877	3.00E-14	unknown
889	1	157	112	582	g10434098	1.00E-07	unnamed protein product
889	1	157	112	582	g18027726	3.00E-07	unknown
889	1	157	112	582	g854065	7.00E-06	U88
890	1	99	262	558	g10435559	6.00E-16	unnamed protein product
890	1	99	262	558	g10437485	2.00E-15	unnamed protein product
890	1	99	262	558	g9280152	2.00E-14	unnamed portein product
891	1	89	193	459	g14189960	7.00E-18	unnamed protein product
891	1	89	193	459	g8980667	2.00E-17	PRO0764
891	1	89	193	459	g10437569	8.00E-17	PADI-H protein
892	1	118	844	1197	g2072957	1.00E-08	unnamed protein product
892	1	118	844	1197	g2072966	2.00E-08	p40

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
892	1	118	844	1197	g337663	9.00E-08	ORF1; putative
893	1	170	1	510	g10802923	4.00E-08	SecY-independent transporter protein
893	1	170	1	510	g5869819	2.00E-07	NADH-ubiquinone oxidoreductase subunit 1
893	1	170	1	510	g13359187	8.00E-07	KIAA1657 protein
896	2	238	392	1105	g12845540	1.00E-67	data source:SPTR, source key:Q9HA82, evidence:ISS~homolog to CDNA FLJ12089 FIS, CLONE HEMBB1002550, WEAKLY SIMILAR TO HYPOTHETICAL UOG-1
896	2	238	392	1105	g13936285	1.00E-67	TRH4
896	2	238	392	1105	g14715021	3.00E-50	Similar to RIKEN cDNA 2310081H14 gene
897	3	131	381	773	g3176973	9.00E-33	BCE-1
898	3	62	300	485	g16550580	3.00E-11	unnamed protein product
898	3	62	300	485	g6690248	7.00E-10	PRO0657
898	3	62	300	485	g288145	1.00E-09	put. ORF
900	2	64	2	193	g17390202	3.00E-28	Similar to RIKEN cDNA 2510005D08 gene
900	2	64	2	193	g14035896	3.00E-28	unnamed protein product
900	2	64	2	193	g12848605	1.00E-23	data source:SPTR, source key:Q21541, evidence:ISS~putative~related to M142.5 PROTEIN
901	1	95	58	342	g10436992	5.00E-41	unnamed protein product
901	1	95	58	342	g13784943	5.00E-35	Unknown (protein for MGC:11761)
902	3	122	192	557	g6650810	2.00E-26	PRO1902
902	3	122	192	557	g12698182	2.00E-22	hypothetical protein
902	3	122	192	557	g16553789	9.00E-22	unnamed protein product
908	1	94	94	375	g17390188	7.00E-47	Similar to RIKEN cDNA 1110058L19 gene
908	1	94	94	375	g12841765	9.00E-32	data source:SPTR, source key:Q9VLU6, evidence:ISS~putative~related to CG7224 PROTEIN
908	1	94	94	375	g12835436	9.00E-32	data source:SPTR, source key:Q9VLU6, evidence:ISS~putative~related to CG7224 PROTEIN
910	3	1027	6	3086	g4240311	0	KIAA0911 protein
910	3	1027	6	3086	g11558246	0	calsyntenin-1 protein
910	3	1027	6	3086	g11558248	0	calsyntenin-1 protein
911	3	190	3	572	g14036042	1.00E-104	unnamed protein product
911	3	190	3	572	g18088345	2.00E-91	Similar to RIKEN cDNA 1110066C01 gene
911	3	190	3	572	g12849796	8.00E-78	data source:SPTR, source key:Q9NZE8, evidence:ISS~homolog to MITOCHONDRIAL 39S RIBOSOMAL PROTEIN L35 (MRP-L35)~putative
912	3	549	3	1649	g15277565	0	RIKEN cDNA 2510039O18 gene
912	3	549	3	1649	g12846932	0	data source:SPTR, source key:Q9VQ60, evidence:ISS~putative~related to CG7289 PROTEIN

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
912	3	549	3	1649	g13325391	1.00E-138	Similar to RIKEN cDNA 2510039O18 gene
913	3	194	225	806	g13543692	1.00E-87	COBW-like protein
913	3	194	225	806	g13177623	1.00E-87	dopamine-responsive protein
913	3	194	225	806	g15488579	1.00E-87	COBW-like protein
916	2	58	338	511	g6690248	6.00E-05	PRO0657
917	2	81	53	295	g12053359	6.00E-07	hypothetical protein
918	2	248	296	1039	g18490618	1.00E-142	Similar to RIKEN cDNA 1700048E23 gene
918	2	248	296	1039	g12839952	1.00E-117	data source:SPTR, source key:O73884, evidence:ISS~putative~related to PUTATIVE PHOSPHATASE
918	2	248	296	1039	g3218467	6.00E-57	putative phosphatase
919	2	128	542	925	g14042106	4.00E-72	unnamed protein product
920	3	439	231	1547	g7023022	5.00E-88	unnamed protein product
920	3	439	231	1547	g14030861	2.00E-36	paraneoplastic neuronal antigen MA1
920	3	439	231	1547	g18478557	9.00E-36	paraneoplastic onconeuronal protein MA1
921	2	193	149	727	g12746410	5.00E-35	coenzyme A diphosphatase
921	2	193	149	727	g12836479	7.00E-35	data source:MGD, source key:MGI:1914778, evidence:ISS~nudix (nucleoside diphosphate linked moiety X)-type motif 7~putative
921	2	193	149	727	g12847124	2.00E-33	data source:MGD, source key:MGI:1914778, evidence:ISS~nudix (nucleoside diphosphate linked moiety X)-type motif 7~putative
922	3	305	3	917	g16024938	4.00E-46	4-1BB-mediated signaling molecule
922	3	305	3	917	g12845847	3.00E-34	evidence:NAS~hypothetical protein~putative
922	3	305	3	917	g18490950	2.00E-33	RIKEN cDNA 2410005L11 gene
923	2	142	1244	1669	g6562162	1.00E-71	hypothetical protein
923	2	142	1244	1669	g695370	1.00E-46	thyroid receptor interactor
923	2	142	1244	1669	g3193258	1.00E-46	proteasome subunit SUG1
927	3	76	309	536	g12698192	3.00E-07	hypothetical protein
927	3	76	309	536	g16550881	5.00E-07	unnamed protein product
927	3	76	309	536	g15929032	6.00E-06	Similar to RIKEN cDNA 9430029K10 gene
931	2	75	62	286	g10437485	5.00E-10	unnamed protein product
931	2	75	62	286	g16041132	9.00E-10	hypothetical protein
931	2	75	62	286	g7020625	1.00E-09	unnamed protein product
934	3	554	3	1664	g6599215	0	hypothetical protein

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
934	3	554	3	1664	g7023623	0	unnamed protein product
934	3	554	3	1664	g3549261	1.00E-13	interaptin
935	3	266	1698	2495	g7019969	1.00E-149	unnamed protein product
935	3	266	1698	2495	g12805451	1.00E-106	Similar to hypothetical protein FLJ20093
935	3	266	1698	2495	g10438722	7.00E-89	unnamed protein product
937	1	205	277	891	g12847516	1.00E-60	data source:SPTR, source key:Q9PTD5, evidence:ISS~putative~related to KIAA0009 PROTEIN
937	1	205	277	891	g12855709	3.00E-60	data source:SPTR, source key:Q15390, evidence:ISS~homolog to HYPOTHETICAL PROTEIN KIAA0009~putative
937	1	205	277	891	g17512323	6.00E-59	Similar to RIKEN cDNA 2610016C23 gene
938	2	227	386	1066	g16550264	1.00E-112	unnamed protein product
938	2	227	386	1066	g16924243	1.00E-72	Unknown (protein for IMAGE:4049523)
938	2	227	386	1066	g1504016	4.00E-09	no similarities to reported gene products
939	3	81	3	245	g14717079	1.00E-40	dJ469A13.2 (Novel protein)
939	3	81	3	245	g12857138	1.00E-21	data source:SPTR, source key:Q9H8P4, evidence:ISS~homolog to CDNA FLJ13346 FIS, CLONE OVARC1002107~putative
939	3	81	3	245	g12839239	1.00E-21	data source:SPTR, source key:Q9H8P4, evidence:ISS~homolog to CDNA FLJ13346 FIS, CLONE OVARC1002107~putative
940	1	646	1	1938	g13111835	0	hypothetical protein FLJ20333
940	1	646	1	1938	g7243047	0	KIAA1333 protein
940	1	646	1	1938	g7020359	0	unnamed protein product
943	3	335	3	1007	g6330416	0	KIAA1201 protein
943	3	335	3	1007	g15559417	3.00E-66	Unknown (protein for MGC:20455)
943	3	335	3	1007	g7959333	3.00E-66	KIAA1533 protein
945	2	154	50	511	g14043111	4.00E-28	Similar to ubiquitin associated and SH3 domain containing, A
945	2	154	50	511	g16304176	4.00E-28	nm23-phosphorylated unknown substrate
945	2	154	50	511	g7799912	1.00E-11	UBASH3A protein
947	3	121	432	794	g1915967	2.00E-62	small acidic protein
947	3	121	432	794	g16741003	2.00E-62	small acidic protein
947	3	121	432	794	g13937979	2.00E-62	small acidic protein
948	3	137	888	1298	g11493508	4.00E-29	PRO0522
948	3	137	888	1298	g15080674	4.00E-18	RanBPM
948	3	137	888	1298	g13194576	4.00E-18	RANBPM

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Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
950	1	127	202	582	g16553676	4.00E-63	unnamed protein product
950	1	127	202	582	g12847853	3.00E-15	data source:MGD, source key:MGI:1100877, evidence:ISS~putative~transforming growth factor beta regulated gene 1
951	2	74	65	286	g16549456	1.00E-15	unnamed protein product
951	2	74	65	286	g15680195	2.00E-13	Similar to hypothetical protein FLJ11267
951	2	74	65	286	g7023820	2.00E-13	unnamed protein product
953	3	196	144	731	g15012072	6.00E-93	Similar to DKFZP566K023 protein
953	3	196	144	731	g7018410	6.00E-93	hypothetical protein
953	3	196	144	731	g13559035	9.00E-92	dJ586O15.1 (hypothetical 22.1 KDA protein)
954	2	349	2	1048	g14017777	0	MEGF10 protein (KIAA1780)
954	2	349	2	1048	g17017251	5.00E-43	MEGF12
954	2	349	2	1048	g17386053	5.00E-43	Jedi protein
955	2	359	2	1078	g12405521	4.00E-68	unnamed protein product
955	2	359	2	1078	g18606449	2.00E-59	germ cell-specific gene 1
955	2	359	2	1078	g12839367	9.00E-37	data source:MGD, source key:MGI:1194499, evidence:ISS~germ cell-specific gene 1~putative
956	2	380	155	1294	g14017869	0	KIAA1826 protein
956	2	380	155	1294	g15928503	0	Similar to KIAA1826 protein
956	2	380	155	1294	g14042730	5.00E-98	unnamed protein product
959	3	115	333	677	g16550502	2.00E-51	unnamed protein product
959	3	115	333	677	g14290546	2.00E-51	Similar to RIKEN cDNA 2410003C20 gene
959	3	115	333	677	g12804121	2.00E-51	Unknown (protein:for IMAGE:3954132)
962	3	74	2505	2726	g10433567	1.00E-08	unnamed protein product
962	3	74	2505	2726	g18490197	3.00E-08	Unknown (protein for MGC:23782)
962	3	74	2505	2726	g12698182	5.00E-08	hypothetical protein
964	1	111	250	582	g10437569	8.00E-20	unnamed protein product
964	1	111	250	582	g14189960	4.00E-19	PRO0764
964	1	111	250	582	g15214765	9.00E-19	Similar to hypothetical protein
969	2	216	2	649	g307155	4.00E-97	MAC30
969	2	216	2	649	g17390346	3.00E-84	Unknown (protein for MGC:25841)
969	2	216	2	649	g3831458	6.00E-08	hypothetical protein
970	3	109	102	428	g4200241	5.00E-26	hypothetical protein
970	3	109	102	428	g12248791	3.00E-20	syntaxin 12

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Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
970	3	109	102	428	g14715019	3.00E-20	Unknown (protein for MGC:6471)
974	3	565	240	1934	g14278953	0	Mid-1-related chloride channel 1
974	3	565	240	1934	g13096892	0	Similar to KIAA0761 protein
974	3	565	240	1934	g4588787	0	unknown
975	2	352	2	1057	g18088178	1.00E-134	Unknown (protein for IMAGE:3882977)
975	2	352	2	1057	g10636484	4.00E-81	polyglutamine-containing protein
975	2	352	2	1057	g14017947	4.00E-81	KIAA1865 protein
976	1	349	976	2022	g14549207	0	URAX1
976	1	349	976	2022	g17907795	0	TGF-beta induced apotosis protein 3
976	1	349	976	2022	g17049034	0	unnamed protein product
978	3	274	2046	2867	g7020399	1.00E-58	unnamed protein product
978	3	274	2046	2867	g10435659	1.00E-17	unnamed protein product
978	3	274	2046	2867	g17132941	2.00E-11	ORF_ID:alr3807~hypothetical protein
983	3	839	18	2534	g10880933	0	putative prostate cancer susceptibility protein HPC2/ELAC2
983	3	839	18	2534	g12804973	0	putative prostate cancer susceptibility protein
983	3	839	18	2534	g13278771	0	putative prostate cancer susceptibility protein
985	3	196	570	1157	g12005505	1.00E-107	AD029
985	3	196	570	1157	g12697953	1.00E-106	KIAA1704 protein
985	3	196	570	1157	g7920153	7.00E-93	lipopolysaccharide specific response-7 protein
986	2	755	2	2266	g7022590	0	unnamed protein product
986	2	755	2	2266	g10435073	0	unnamed protein product
986	2	755	2	2266	g7959163	0	KIAA1452 protein
1001	3	335	252	1256	g16550386	1.00E-154	unnamed protein product
1001	3	335	252	1256	g12836009	1.00E-120	evidence:NAS~hypothetical protein~putative
1001	3	335	252	1256	g296164	3.00E-09	156 kDa Protein
1002	3	168	744	1247	g12002207	6.00E-98	chymotrypsin-like protein
1002	3	168	744	1247	g6581056	4.00E-95	CHORD containing protein-1
1002	3	168	744	1247	g17390873	6.00E-92	RIKEN cDNA 1110001O09 gene
1003	1	172	112	627	g2587027	1.00E-19	HERV-E envelope glycoprotein
1003	1	172	112	627	g2587024	1.00E-19	HERV-E envelope glycoprotein
1003	1	172	112	627	g1049232	5.00E-17	HERV-E envelope protein
1005	3	123	1155	1523	g13276669	2.00E-53	hypothetical protein

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1008	1	154	247	708	g17430957	9.00E-17	HYPOTHETICAL TRANSMEMBRANE PROTEIN
1008	1	154	247	708	g3594	1.00E-09	carboxypeptidase s
1008	1	154	247	708	g1008367	1.00E-09	ORF YIL172w
1009	2	270	2	811	g17512162	1.00E-153	Unknown (protein for MGC:29802)
1009	2	270	2	811	g15082287	1.00E-153	Unknown (protein for IMAGE:3502817)
1009	2	270	2	811	g2522348	4.00E-46	Na/taurocholate cotransporting polypeptide 1
1013	2	109	140	466	g2587027	2.00E-20	HERV-E envelope glycoprotein
1013	2	109	140	466	g2587024	2.00E-20	HERV-E envelope glycoprotein
1013	2	109	140	466	g1049232	8.00E-19	HERV-E envelope protein
1014	3	69	30	236	g6114601	7.00E-24	stromal antigen 3, (STAG3)
1014	3	69	30	236	g13195163	4.00E-10	stromal antigen 3
1014	3	69	30	236	g3090423	3.00E-08	stag3
1017	3	118	3	356	g14009459	1.00E-06	protocadherin-beta11
1017	3	118	3	356	g5457029	1.00E-06	protocadherin beta 11
1017	3	118	3	356	g5457035	4.00E-06	protocadherin beta 14
1019	2	138	98	511	g16550813	9.00E-42	unnamed protein product
1019	2	138	98	511	g2792016	1.00E-40	olfactory receptor
1019	2	138	98	511	g4092819	1.00E-40	BC319430_5
1020	1	359	163	1239	g15131403	2.00E-80	dJ85M6.3 (similar to testis-specific protein PBS13)
1020	1	359	163	1239	g7023926	2.00E-80	unnamed protein product
1020	1	359	163	1239	g17426495	4.00E-60	bA353I17.2 (testis specific protein similar to TCP11 (t-complex 11 (a murine tcp homolog)))
1021	2	79	188	424	g7020440	6.00E-20	unnamed protein product
1021	2	79	188	424	g6690252	5.00E-16	PRO0663
1021	2	79	188	424	g16552221	1.00E-15	unnamed protein product
1022	2	380	2	1141	g6683126	1.00E-128	KIAA0339 protein
1022	2	380	2	1141	g17016489	3.00E-18	wsv091
1022	2	380	2	1141	g9837385	3.00E-18	retinitis pigmentosa GTPase regulator-like protein
1023	3	594	216	1997	g15990553	1.00E-173	Unknown (protein for MGC:23445)
1023	3	594	216	1997	g16041702	1.00E-122	Unknown (protein for MGC:17998)
1023	3	594	216	1997	g7295275	1.00E-36	CG8616 gene product
1024	3	233	3	701	g14272632	1.00E-126	unnamed protein product
1024	3	233	3	701	g16551700	1.00E-108	unnamed protein product

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1024	3	233	3	701	g12843884	1.00E-79	evidence:NAS~hypothetical protein~putative
1025	3	325	3	977	g12654711	1.00E-178	Unknown (protein for MGC:3169)
1025	3	325	3	977	g10438670	1.00E-178	unnamed protein product
1025	3	325	3	977	g15928500	1.00E-163	Similar to hypothetical protein MGC3169
1026	2	256	908	1675	g15079262	1.00E-44	Unknown (protein for IMAGE:3154539)
1026	2	256	908	1675	g13544043	2.00E-23	Unknown (protein for IMAGE:3627317)
1026	2	256	908	1675	g12003980	2.00E-23	spinster-like protein
1027	1	260	610	1389	g18043473	1.00E-106	DP-ribosylation-like factor 6 interacting protein 6
1027	1	260	610	1389	g12854930	1.00E-105	DP-ribosylation-like factor 6 interacting protein 6~data source:MGD, source key:MGI:1929507, evidence:ISS~putative
1027	1	260	610	1389	g12846953	1.00E-103	DP-ribosylation-like factor 6 interacting protein 6~data source:MGD, source key:MGI:1929507, evidence:ISS~putative
1030	3	207	831	1451	g14717079	1.00E-110	dJ469A13.2 (Novel protein)
1030	3	207	831	1451	g12857138	1.00E-71	data source:SPTR, source key:Q9H8P4, evidence:ISS~homolog to CDNA FLJ13346 FIS, CLONE OVARC1002107~putative
1030	3	207	831	1451	g12839239	1.00E-71	data source:SPTR, source key:Q9H8P4, evidence:ISS~homolog to CDNA FLJ13346 FIS, CLONE OVARC1002107~putative
1032	3	313	30	968	g14198207	1.00E-179	Similar to CG4452 gene product
1032	3	313	30	968	g4200234	1.00E-176	hypothetical protein
1032	3	313	30	968	g4200238	1.00E-154	hypothetical protein
1033	1	91	472	744	g9967222	3.00E-22	hypothetical protein
1034	1	561	1	1683	g3882183	0	KIAA0731 protein
1034	1	561	1	1683	g7022373	5.00E-56	unnamed protein product
1034	1	561	1	1683	g10726821	9.00E-32	larp gene product
1035	3	91	288	560	g12698182	1.00E-11	hypothetical protein
1035	3	91	288	560	g16552221	2.00E-11	unnamed protein product
1035	3	91	288	560	g14198309	4.00E-11	Similar to proline-serine-threonine phosphatase-interacting protein 2
1037	1	79	928	1164	g288145	8.00E-08	put. ORF
1037	1	79	928	1164	g6690248	1.00E-07	PRO0657
1037	1	79	928	1164	g9955914	6.00E-06	platelet glycoprotein VI-3
1038	1	213	1	639	g12847051	1.00E-107	evidence:NAS~hypothetical protein~putative
1038	1	213	1	639	g16549898	1.00E-107	unnamed protein product

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Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1038	1	213	1	639	g16877037	3.00E-71	Similar to RIKEN cDNA 2600001B17 gene
1039	3	148	450	893	g14042588	2.00E-54	unnamed protein product
1039	3	148	450	893	g14042283	2.00E-54	unnamed protein product
1039	3	148	450	893	g14035872	2.00E-54	unnamed protein product
1042	1	305	70	984	g16307277	1.00E-140	putative protein tyrosine kinase
1042	1	305	70	984	g14715460	1.00E-140	Nori-2p
1042	1	305	70	984	g9588402	1.00E-140	dJ28H20.2 (novel protein)
1043	3	162	3	488	g18490805	2.00E-93	hypothetical protein SP192
1043	3	162	3	488	g10503966	2.00E-93	unknown
1043	3	162	3	488	g10437401	2.00E-93	unnamed protein product
1045	3	1093	3	3281	g5733726	0	gamma-synergin
1045	3	1093	3	3281	g5733728	0	gamma-synergin
1045	3	1093	3	3281	g7341344	0	gamma-synergin
1047	1	515	721	2265	g12804973	0	putative prostate cancer susceptibility protein
1047	1	515	721	2265	g10880933	0	putative prostate cancer susceptibility protein HPC2/ELAC2
1047	1	515	721	2265	g13278771	0	putative prostate cancer susceptibility protein
1048	3	104	762	1073	g12849011	3.00E-17	Zinc finger, C2H2 type containing protein–data source:Pfam, source key:PF00096, evidence:ISS~putative
1049	3	177	3	533	g12844368	7.00E-82	evidence:NAS~hypothetical protein~putative
1049	3	177	3	533	g13358924	2.00E-79	hypothetical protein
1049	3	177	3	533	g13623489	5.00E-26	Unknown (protein for IMAGE:4109498)
1050	2	330	2	991	g10436267	1.00E-178	unnamed protein product
1050	2	330	2	991	g16359295	1.00E-152	Similar to hypothetical protein FLJ13955
1050	2	330	2	991	g5459205	6.00E-75	dJ462O23.2 (novel protein)
1052	3	206	3	620	g12834129	1.00E-105	data source:SPTR, source key:Q9VEZ4, evidence:ISS~putative~related to CG5013 PROTEIN
1052	3	206	3	620	g12855876	1.00E-57	Beta defensin containing protein–data source:Pfam, source key:PF00711, evidence:ISS~putative
1052	3	206	3	620	g7300099	2.00E-42	CG5013 gene product
1057	2	3021	2	9064	g7243035	0	KIAA1327 protein
1057	2	3021	2	9064	g2384711	0	antigen containing epitope to monoclonal antibody MMS-85/12
1057	2	3021	2	9064	g10438646	0	unnamed protein product
1058	1	168	70	573	g10047243	2.00E-63	KIAA1584 protein
1058	1	168	70	573	g6468312	2.00E-38	hypothetical protein

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1058	1	168	70	573	g7019973	2.00E-38	unnamed protein product
1060	3	1036	3	3110	g7271903	0	DWF-1
1060	3	1036	3	3110	g7141125	0	Ellis-van Creveld syndrome protein
1060	3	1036	3	3110	g7141127	0	Ellis-van Creveld syndrome protein
1061	3	470	159	1568	g9828190	0	FLAMINGO 1
1061	3	470	159	1568	g1665821	0	Similar to D.melanogaster cadherin-related tumor suppressor
1061	3	470	159	1568	g6681360	1.00E-176	MEGF3
1062	1	194	556	1137	g14133213	7.00E-33	KIAA0732 protein
1064	3	389	3	1169	g4884468	1.00E-159	hypothetical protein
1064	3	389	3	1169	g15929494	1.00E-141	Unknown (protein for MGC:10151)
1064	3	389	3	1169	g18380937	1.00E-128	Unknown (protein for MGC:4713)
1065	2	235	119	823	g14198207	4.00E-69	Similar to CG4452 gene product
1065	2	235	119	823	g4200234	8.00E-63	hypothetical protein
1065	2	235	119	823	g4200238	5.00E-58	hypothetical protein
1069	1	212	1285	1920	g10504263	1.00E-114	betaPix-b
1069	1	212	1285	1920	g10504266	1.00E-114	betaPix-c
1069	1	212	1285	1920	g15420378	1.00E-61	betaPix-d
1071	2	284	170	1021	g13442786	1.00E-107	Drctnnb1a
1071	2	284	170	1021	g16551687	1.00E-106	unnamed protein product
1071	2	284	170	1021	g17511709	1.00E-106	down-regulated by Ctnnb1, a
1073	1	304	226	1137	g13625186	1.00E-173	RNA binding protein
1073	1	304	226	1137	g14042167	1.00E-172	unnamed protein product
1073	1	304	226	1137	g12853682	1.00E-154	data source:SPTR, source key:P10962, evidence:ISS~putative~related to MAK16 PROTEIN
1074	2	434	86	1387	g12846470	0	data source:SPTR, source key:O46078, evidence:ISS~putative~related to EG:39E1.1 PROTEIN (CG11596 PROTEIN)
1074	2	434	86	1387	g10728401	8.00E-88	EG:39E1.1 gene product
1074	2	434	86	1387	g15292213	8.00E-88	LD42227p
1075	1	99	124	420	g15620859	2.00E-44	KIAA1900 protein
1075	1	99	124	420	g16549994	2.00E-44	unnamed protein product
1076	1	84	397	648	g299471	1.00E-08	X-linked retinopathy protein
1076	1	84	397	648	g12698182	5.00E-08	hypothetical protein
1076	1	84	397	648	g10433567	4.00E-07	unnamed protein product

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1078	3	146	3	440	g13359183	4.00E-27	KIAA1655 protein
1078	3	146	3	440	g10439739	3.00E-24	unnamed protein product
1078	3	146	3	440	g14249973	2.00E-23	Similar to hypothetical protein PRO1722
1079	2	208	143	766	g14574118	1.00E-17	Hypothetical protein F22B7.10
1079	2	208	143	766	g16553246	3.00E-15	unnamed protein product
1079	2	208	143	766	g7293494	9.00E-06	CG6659 gene product
1081	2	54	305	466	g6690248	3.00E-10	PRO0657
1081	2	54	305	466	g16550580	1.00E-08	unnamed protein product
1081	2	54	305	466	g288145	1.00E-08	put. ORF
1084	1	111	892	1224	g4309949	5.00E-39	similar to MLN 64; similar to I38027 (PID:g2135214)
1084	1	111	892	1224	g13111774	5.00E-39	Similar to steroidogenic acute regulatory protein related
1084	1	111	892	1224	g13543615	5.00E-39	Unknown (protein for MGC:14607)
1088	3	375	792	1916	g12655913	0	sprouty-4A
1088	3	375	792	1916	g4850326	1.00E-169	sprouty-4
1088	3	375	792	1916	g5917720	1.00E-169	sprouty 4
1090	1	46	1	138	g12852725	4.00E-06	data source:SPTR, source key:Q9VBL1, evidence:ISS~putative~related to CG5901 PROTEIN
1091	3	227	186	866	g10041644	1.00E-34	unnamed protein product
1091	3	227	186	866	g10041654	1.00E-34	unnamed protein product
1091	3	227	186	866	g10041649	3.00E-30	unnamed protein product
1093	3	101	552	854	g7770147	6.00E-16	PRO1847
1093	3	101	552	854	g10437752	6.00E-15	unnamed protein product
1093	3	101	552	854	g6650810	3.00E-14	PRO1902
1094	1	126	619	996	g16041152	2.00E-16	hypothetical protein
1094	1	126	619	996	g10435380	2.00E-09	unnamed protein product
1095	2	67	194	394	g522145	4.00E-07	B-cell growth factor
1097	3	430	39	1328	g16877653	0	Similar to KIAA0643 protein
1097	3	430	39	1328	g3327100	0	KIAA0643 protein
1097	3	430	39	1328	g10435262	1.00E-138	unnamed protein product
1101	3	224	288	959	g12855287	3.00E-65	evidence:NAS~hypothetical protein~putative
1101	3	224	288	959	g4200330	8.00E-22	dJ821D11.1 (PUTATIVE protein)
1102	2	958	164	3037	g16306780	0	Unknown (protein for IMAGE:3461401)
1102	2	958	164	3037	g16552089	0	unnamed protein product

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1102	2	958	164	3037	g12857435	1.00E-105	evidence:NAS~putative~unclassifiable
1106	3	302	210	1115	g14272790	1.00E-156	unnamed protein product
1106	3	302	210	1115	g15209786	1.00E-146	unnamed protein product
1106	3	302	210	1115	g7303350	1.00E-12	CG12251 gene product
1107	3	312	72	1007	g15079708	1.00E-151	Similar to KIAA0514 gene product
1107	3	312	72	1007	g3043552	1.00E-151	KIAA0514 protein
1108	1	402	910	2115	g14388555	0	hypothetical protein
1108	1	402	910	2115	g12854823	8.00E-96	data source:SPTR, source key:Q9W232, evidence:ISS~putative~related to CG17807 PROTEIN
1108	1	402	910	2115	g7291441	6.00E-89	CG17807 gene product
1110	2	359	2	1078	g12405521	4.00E-68	unnamed protein product
1110	2	359	2	1078	g18606449	2.00E-59	germ-cell-specific gene 1
1110	2	359	2	1078	g12839367	9.00E-37	data source:MGD, source key:MGI:1194499, evidence:ISS~germ cell-specific gene 1~putative
1111	1	287	1	861	g14714684	1.00E-135	Unknown (protein for IMAGE:3482764)
1111	1	287	1	861	g12850324	1.00E-134	data source:SPTR, source key:Q9VS51, evidence:ISS~putative~related to CG8596 PROTEIN
1111	1	287	1	861	g17861694	1.00E-29	GH22722p
1112	2	62	308	493	g12963869	2.00E-24	gene trap ankyrin repeat containing protein
1112	2	62	308	493	g10438501	7.00E-07	unnamed protein product
1112	2	62	308	493	g7020282	1.00E-05	unnamed protein product
1113	3	396	480	1667	g14250716	2.00E-17	Unknown (protein for MGC:13310)
1113	3	396	480	1667	g16877906	1.00E-16	Unknown (protein for IMAGE:3344281)
1113	3	396	480	1667	g15030268	1.00E-13	Unknown (protein for MGC:9923)
1114	3	962	3	2888	g13625166	0	RALBP1
1114	3	962	3	2888	g15706481	0	Unknown (protein for MGC:16228)
1114	3	962	3	2888	g2677843	0	RalBP1-associated EH domain protein Reps1
1115	1	97	1	291	g3047242	1.00E-13	melastatin
1115	1	97	1	291	g3243075	2.00E-13	melastatin 1
1115	1	97	1	291	g8131903	2.00E-06	transient receptor potential-related protein
1116	1	211	1	633	g1304179	2.00E-05	fibrinogen A-alpha-chain
1116	1	211	1	633	g3789960	2.00E-05	fibrinogen A-alpha chain
1116	1	211	1	633	g531261	5.00E-05	5E5 antigen
1117	1	124	562	933	g12698182	1.00E-29	hypothetical protein
1117	1	124	562	933	g7020440	7.00E-24	unnamed protein product

Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1117	1	124	562	933	g11493483	3.00E-23	PRO2550
1118	1	142	61	486	g14041976	1.00E-38	unnamed protein product
1118	1	142	61	486	g5689553	1.00E-38	KIAA1108 protein
1118	1	142	61	486	g988221	2.00E-35	Tbc1
1119	1	1294	184	4065	g7228149	0	ATFa-associated factor
1119	1	1294	184	4065	g7022872	0	unnamed protein product
1119	1	1294	184	4065	g5101772	0	p621
1120	3	188	3	566	g12804117	7.00E-39	Unknown (protein for MGC:11276)
1120	3	188	3	566	g12652917	1.00E-26	Unknown (protein for MGC:2694)
1120	3	188	3	566	g12851605	3.00E-26	DNA segment, Chr 7, Wayne State University 86, expressed~data source:MGD, source key:MGI:106442, evidence:ISS~putative
1121	1	177	43	573	g11932167	2.00E-40	dJ659119.1 (KIAA0435 protein)
1121	1	177	43	573	g2662151	2.00E-40	KIAA0435
1123	3	80	48	287	g10433567	8.00E-09	unnamed protein product
1123	3	80	48	287	g10440282	8.00E-07	unnamed protein product
1123	3	80	48	287	g14388331	8.00E-07	hypothetical protein
1124	3	507	552	2072	g16549800	0	unnamed protein product
1124	3	507	552	2072	g12852088	1.00E-138	data source:SPTR, source key:Q14699, evidence:ISS~homolog to HYPOTHETICAL PROTEIN KIAA0084 (HA2022) (FRAGMENT)~putative
1124	3	507	552	2072	g577299	7.00E-61	The ha2022 gene product is novel.
1125	2	114	119	460	g14139788	2.00E-46	unnamed protein product
1125	2	114	119	460	g12405797	2.00E-46	unnamed protein product
1125	2	114	119	460	g12405805	2.00E-46	unnamed protein product
1126	3	62	300	485	g16550580	3.00E-11	unnamed protein product
1126	3	62	300	485	g6690248	7.00E-10	PRO0657
1126	3	62	300	485	g288145	1.00E-09	put. ORF
1128	1	54	436	597	g10435738	1.00E-08	unnamed protein product
1128	1	54	436	597	g14042822	3.00E-07	unnamed protein product
1128	1	54	436	597	g2810991	6.00E-07	KRAB-zinc finger protein KZF-1
1129	1	181	34	576	g4205084	4.00E-40	WW domain binding protein-1
1129	1	181	34	576	g14603081	4.00E-40	Similar to WW domain binding protein 1
1129	1	181	34	576	g18044295	2.00E-38	Similar to WW domain binding protein 1

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Table 5

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1131	2	107	569	889	g5726235	2.00E-19	unknown protein U5/2
1132	2	115	434	778	g7544146	2.00E-28	vanilloid receptor type 1 like protein 1
1132	2	115	434	778	g6782444	2.00E-28	vanilloid receptor splice variant
1132	2	115	434	778	g5263196	2.00E-28	stretch-inhibiable nonselective channel (SIC)
1133	1	180	154	693	g7243155	6.00E-82	KIAA1387 protein
1133	1	180	154	693	g13623235	5.00E-21	Similar to hypothetical protein FLJ20707
1133	1	180	154	693	g13905156	5.00E-21	Unknown (protein for MGC:11798)
1135	1	57	328	498	g10437485	9.00E-10	unnamed protein product
1135	1	57	328	498	g7020292	1.00E-09	unnamed protein product
1135	1	57	328	498	g9280152	1.00E-08	unnamed portein product
1136	3	129	405	791	g10439739	6.00E-26	unnamed protein product
1136	3	129	405	791	g13359183	1.00E-25	KIAA1655 protein
1136	3	129	405	791	g3002527	2.00E-25	neuronal thread protein AD7c-NTP
1137	1	546	1321	2958	g13158006	0	unnamed protein product
1137	1	546	1321	2958	g13158008	0	unnamed protein product
1137	1	546	1321	2958	g17225574	0	LIM domain only 7
1138	2	199	668	1264	g10438571	3.00E-97	unnamed protein product
1142	3	398	504	1697	g10436616	1.00E-129	unnamed protein product
1142	3	398	504	1697	g14286252	5.00E-71	Similar to hypothetical protein FLJ14213
1142	3	398	504	1697	g10503959	1.00E-58	unknown.
1145	2	1711	1151	6283	g7959279	0	KIAA1509 protein
1145	2	1711	1151	6283	g10434073	0	unnamed protein product
1145	2	1711	1151	6283	g6563224	1.00E-142	unknown
1146	2	314	227	1168	g11342658	1.00E-158	transmembrane chemokine CXCL16
1146	2	314	227	1168	g14042031	1.00E-156	unnamed protein product
1146	2	314	227	1168	g11139544	1.00E-146	SRPSOX

TABLE 6

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	Mismatch <50%
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less; Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises as least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6; Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less; Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value= 1.0E-3 or less; Signal peptide hits: Score= 0 or greater

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TABLE 6

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score≥GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol., Glasgow et al., eds, The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

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CLAIMS

What is claimed is:

1. An isolated polynucleotide selected from the group consisting of:

5   a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting
of NO:1-567,

b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least about
90% identical to a polynucleotide sequence selected from the group consisting of NO:1-567,

c) a polynucleotide complementary to the polynucleotide of a),

10   d) a polynucleotide complementary to the polynucleotide of b), and

e) an RNA equivalent of a)-d).

2. An isolated polynucleotide of claim 1, comprising a polynucleotide sequence selected from
the group consisting of SEQ ID NO:1-567.

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3. An isolated polynucleotide comprising at least about 60 contiguous nucleotides of a
polynucleotide of claim 1.

4. A composition for the detection of expression of secretory polynucleotides comprising at

20   least one of the polynucleotides of claim 1 and a detectable label.

5. A method for detecting a target polynucleotide in a sample, said target polynucleotide
having a sequence of a polynucleotide of claim 1, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction

25   amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment
thereof, and, optionally, if present, the amount thereof.

6. A method for detecting a target polynucleotide in a sample, said target polynucleotide

30   comprising a sequence of a polynucleotide of claim 1, the method comprising:

a) hybridizing the sample with a probe comprising at least about 20 contiguous nucleotides
comprising a sequence complementary to said target polynucleotide in the sample, and which probe
specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex
is formed between said probe and said target polynucleotide or fragments thereof, and

35   b) detecting the presence or absence of said hybridization complex, and, optionally, if present,

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the amount thereof.

7. A method of claim 5, wherein the probe comprises at least about 30 contiguous nucleotides.

8. A method of claim 5, wherein the probe comprises at least about 60 contiguous nucleotides.

9. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 1.

10. A cell transformed with a recombinant polynucleotide of claim 9.

11. A transgenic organism comprising a recombinant polynucleotide of claim 9.

12. A method for producing a secretory polypeptide, the method comprising:
a) culturing a cell under conditions suitable for expression of the secretory polypeptide, wherein said cell is transformed with a recombinant polynucleotide of claim 9, and
b) recovering the secretory polypeptide so expressed.

13. A purified secretory polypeptide (SPTM) encoded by at least one of the polynucleotides of claim 2.

14. An isolated antibody which specifically binds to a secretory polypeptide of claim 13.

15. A method of identifying a test compound which specifically binds to the secretory polypeptide of claim 13, the method comprising:
a) providing a test compound;
b) combining the secretory polypeptide with the test compound for a sufficient time and under suitable conditions for binding; and
c) detecting binding of the secretory polypeptide to the test compound, thereby identifying the test compound which specifically binds the secretory polypeptide.

16. A microarray wherein at least one element of the microarray is a polynucleotide of claim 3.

17. A method for generating a transcript image of a sample which contains polynucleotides, the method comprising:

    a) labeling the polynucleotides of the sample,

    b) contacting the elements of the microarray of claim 16 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and

    c) quantifying the expression of the polynucleotides in the sample.

18. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence of claim 1, the method comprising:

    a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

    b) detecting altered expression of the target polynucleotide, and

    c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

19. A method for assessing toxicity of a test compound, said method comprising:

    a) treating a biological sample containing nucleic acids with the test compound;

    b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least about 20 contiguous nucleotides of a polynucleotide of claim 1 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 1 or fragment thereof;

    c) quantifying the amount of hybridization complex; and

    d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

20. An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first oligonucleotide or polynucleotide sequence specifically hybridizable with at least about 30 contiguous nucleotides of a target polynucleotide, said target polynucleotide having a sequence of claim 1.

21. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least about 30 contiguous nucleotides of said target polynucleotide.

22. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least about 60 contiguous nucleotides of said target polynucleotide

23. An array of claim 20, which is a microarray.

24. An array of claim 20, further comprising said target polynucleotide hybridized to said first oligonucleotide or polynucleotide.

25. An array of claim 20, wherein a linker joins at least one of said nucleotide molecules to said solid substrate.

26. An array of claim 20, wherein each distinct physical location on the substrate contains multiple nucleotide molecules having the same sequence, and each distinct physical location on the substrate contains nucleotide molecules having a sequence which differs from the sequence of nucleotide molecules at another physical location on the substrate.

27. An isolated polypeptide selected from the group consisting of:

a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146,

b) a naturally occurring polypeptide comprising an amino acid sequence at least about 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146,

c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146, and

d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:568-1146.

28. An isolated polypeptide of claim 27, comprising a polypeptide sequence selected from the group consisting of SEQ ID NO:568-1146.